

SEQUENCE LISTING

JCS41 U.S. PRO
10/037270
01/04/02

<110> Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yuning
Wang, Dunrui
Wang, Zhiwei
Tillinghast, John
Drmanac, Radoje T.

<120> Novel Nucleic Acids and
Polypeptides

<130> 784CIP2B

<140> To Be Assigned
<141>

<150> 09/552,317
<151> 2000-04-25

<150> 09/488,725
<151> 2000-01-21

<160> 1104

<170> pt_FL_genes Version 1.0

<210> 1
<211> 2063
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1677)

<400> 1

atg agg ttc tcg ctg gac aag gac acg gga ctc atc atg ctg att gcc 48
Met Arg Phe Ser Leu Asp Lys Asp Thr Gly Leu Ile Met Leu Ile Ala
1 5 10

agg ctg gac tat gag ctc atc cag cgc ttc acc ctg acg atc att gcc 96
Arg Leu Asp Tyr Glu Leu Ile Gln Arg Phe Thr Leu Thr Ile Ile Ala
17 22 27 32

cgg gac ggg ggc ggc gag gag acc aca ggc cgg gtc agg atc aat gtg 144
Arg Asp Gly Gly Gly Glu Glu Thr Thr Gly Arg Val Arg Ile Asn Val
33 38 43 48

ttg gat gtc aac gac aac gtg ccc acc ttc cag aag gat gcc tac gtg 192
Leu Asp Val Asn Asp Asn Val Pro Thr Phe Gln Lys Asp Ala Tyr Val
49 54 59 64

ggc gct ctg cgg gag aac gag cct tct gtc aca cag ctg gtg cgg ctc 240
Gly Ala Leu Arg Glu Asn Glu Pro Ser Val Thr Gln Leu Val Arg Leu
65 70 75 80

cgg gca aca gat gaa gac tcc cct ccc aac aac cag atc acc tac agc 288
Arg Ala Thr Asp Glu Asp Ser Pro Pro Asn Asn Gln Ile Thr Tyr Ser
81 86 91 96

att gtc agt gca tct gcc ttt ggc agc tac ttc gac atc agc ctg tac 336
Ile Val Ser Ala Ser Ala Phe Gly Ser Tyr Phe Asp Ile Ser Leu Tyr
97 102 107 112

gag ggc tat gga gtg atc agc gtc agt cgc ccc ctg gat tat gaa cag 384
Glu Gly Tyr Gly Val Ile Ser Val Ser Arg Pro Leu Asp Tyr Glu Gln
113 118 123 128

ata tcc aat ggg ctg att tat ctg acg gtc atg gcc atg gat gct ggc 432
Ile Ser Asn Gly Leu Ile Tyr Leu Thr Val Met Ala Met Asp Ala Gly
129 134 139 144

aac ccc cct ctc aac agc acc gtc cct gtc acc atc gag gtg ttt gat 480
Asn Pro Pro Leu Asn Ser Thr Val Pro Val Thr Ile Glu Val Phe Asp
145 150 155 160

gag aat gac gac cct ccc acc ttc agc aag ccc gcc tac ttc gtc tcc 528
Glu Asn Asp Asp Pro Pro Thr Phe Ser Lys Pro Ala Tyr Phe Val Ser
161 166 171 176

gtg gtg gag aac atc atg gca gga gcc acg gtg ctg ttc ctg aat gcc 576
Val Val Glu Asn Ile Met Ala Gly Ala Thr Val Leu Phe Leu Asn Ala
177 182 187 192

aca gac ctg gac cgc tcc cgg gag tac ggc cag gag tcc atc atc tac 624
Thr Asp Leu Asp Arg Ser Arg Glu Tyr Gly Gln Glu Ser Ile Ile Tyr
193 198 203 208

tcc ttg gaa ggc tcc acc cag ttt cgg atc aat gcc cgc tca ggg gaa 672
Ser Leu Glu Gly Ser Thr Gln Phe Arg Ile Asn Ala Arg Ser Gly Glu
209 214 219 224

atc acc acc acg tct ctg ctt gac cga gag acc aag tct gaa tac atc Ile Thr Thr Thr Ser Leu Leu Asp Arg Glu Thr Lys Ser Glu Tyr Ile 225 230 235 240	720
ctc atc gtt cgc gca gtg gac ggg ggt gtg ggc cac aac cag aaa act Leu Ile Val Arg Ala Val Asp Gly Gly Val Gly His Asn Gln Lys Thr 241 246 251 256	768
ggc atc gcc acc gta aac atc acc ctc ctg gac atc aac gac aac cac Gly Ile Ala Thr Val Asn Ile Thr Leu Leu Asp Ile Asn Asp Asn His 257 262 267 272	816
ccc acg tgg aag gac gca ccc tac tac atc aac ctg gtg gag atg acc Pro Thr Trp Lys Asp Ala Pro Tyr Tyr Ile Asn Leu ⁸ Val Glu Met Thr 273 278 283 288	864
cct cca gac tct gac gtg acc acg gtg gtg gct gtt gac cca gac ctg Pro Pro Asp Ser Asp Val Thr Thr Val Val Ala Val Asp Pro Asp Leu 289 294 299 304	912
ggg gag aat ggc acc ctg gtg tac agc atc cag cca ccc aac aag ttc Gly Glu Asn Gly Thr Leu Val Tyr Ser Ile Gln Pro Pro Asn Lys Phe 305 310 315 320	960
tac agc ctc aac agc acc acg ggc aag atc cgc acc acc cac gcc atg Tyr Ser Leu Asn Ser Thr Thr Gly Lys Ile Arg Thr Thr His Ala Met 321 326 331 336	1008
ctg gac cgg gag aac ccc gac ccc cat gag gcc gag ctg atg cgc aaa Leu Asp Arg Glu Asn Pro Asp Pro His Glu Ala Glu Leu Met Arg Lys 337 342 347 352	1056
atc gtc gtc tct gtt act gac tgt ggc agg ccc cct ctg aaa gcc acc Ile Val Val Ser Val Thr Asp Cys Gly Arg Pro Pro Leu Lys Ala Thr 353 358 363 368	1104
agc agt gcc aca gtg ttt gtg aac ctc ttg gat ctc aat gac aat gac Ser Ser Ala Thr Val Phe Val Asn Leu Leu Asp Leu Asn Asp Asn Asp 369 374 379 384	1152
ccc acc ttt cag aac ctg cct ttt gtg gcc gag gtg ctt gaa ggc atc Pro Thr Phe Gln Asn Leu Pro Phe Val Ala Glu Val Leu Glu Gly Ile 385 390 395 400	1200
ccg gcg ggg gtc tcc atc tac caa gtg gtg gcc atc gac ctc gat gag Pro Ala Gly Val Ser Ile Tyr Gln Val Val Ala Ile Asp Leu Asp Glu 401 406 411 416	1248
ggc ctg aac ggc ctg gtg tcc tac cgc atg ccg gtg ggc atg ccc cgc Gly Leu Asn Gly Leu Val Ser Tyr Arg Met Pro Val Gly Met Pro Arg 417 422 427 432	1296
atg gac ttc ctc atc aac agc agc agc ggc gtg gtg gtc acc acc acc Met Asp Phe Leu Ile Asn Ser Ser Ser Gly Val Val Val Thr Thr Thr 433 438 443 448	1344
gag ctg gac cgc gag cgc atc gcg gag tac cag ctg ccg gtg gtg gcc	1392

[illegible]

atggtttttag ctcaaaaaaaaa aaa 2063

gtctgaggag ctggggaagg aacaaagcga ggcttgctgg cggcggctgg gctccggcgg 120

ggccgcgggg tgccggggcct gcggggcggcg gcccgggcgg agcgttgagg ggaaggagggt 180
ggcatcgccg tccgcgcggg ccccggcc atg aac ggg ctc ccc tcg gca gag 232
Met Asn Gly Leu Pro Ser Ala Glu
1 5
gcg ccg ggc ggg gcg ggc tgc gct ttg gcc ggg ctc cca ccg ctg ccg 280
Ala Pro Gly Gly Ala Gly Cys Ala Leu Ala Gly Leu Pro Pro Leu Pro
9 14 19 24
cgc ggc ctc agc ggc ctc ctt aat gcg agc ggg ggc tcg tgg cgg gag 328
Arg Gly Leu Ser Gly Leu Leu Asn Ala Ser Gly Gly Ser Trp Arg Glu
25 30 35 40
ctg gag cgc gtc tac agc cag cgc agc cgc atc cac gac gag ctg agc 376
Leu Glu Arg Val Tyr Ser Gln Arg Ser Arg Ile His Asp Glu Leu Ser
41 46 51 56
cgc gcc gcc cgc gcc ccg gac ggg ccc cgc cac gcc gcc ggc gcc gcc 424
Arg Ala Ala Arg Ala Pro Asp Gly Pro Arg His Ala Ala Gly Ala Ala
57 62 67 72
aac gcg gga ccc gca gcc ggc ccg cgt cgt cct gtc aac ctc gac tca 472
Asn Ala Gly Pro Ala Ala Gly Pro Arg Arg Pro Val Asn Leu Asp Ser
73 78 83 88
gcg ctg gcc gcg ctg cgc aag gag atg ttg tct gca ggt ggg gct gcg 520
Ala Leu Ala Ala Leu Arg Lys Glu Met Leu Ser Ala Gly Gly Ala Ala
89 94 99 104
gca gtt gga cat gtc ctt gtt gtg cca gct gtg ggg cct gta cga gtc 568
Ala Val Gly His Val Leu Val Val Pro Ala Val Gly Pro Val Arg Val
105 110 115 120
aat cca gga cta caa aca cct gtg cca aga cct gag ctt ctg cca gga 616
Asn Pro Gly Leu Gln Thr Pro Val Pro Arg Pro Glu Leu Leu Pro Gly
121 126 131 136
cct gtc atc ctc cct cca ttc gga cag ctc cta ccc acc gga tgc ggg 664
Pro Val Ile Leu Pro Pro Phe Gly Gln Leu Leu Pro Thr Gly Cys Gly
137 142 147 152
cct gtc tga cgacgag gagcctcccg atgccagcct gcctcctgac ccgccacccc 720
Pro Val *
153
ttactgtgcc ccagacgcac aatgcccgtg accagtggct gcaggatgcc ttccacatca 780
gcctctgaag ggctgggggg cagggggcat gcacccatgc aaaaggctca gaaactcccc 840
ctccggcaag ccctcagact tcggagcctg cgccttcccc cctaccgct cacctcacag 900
gagggccagg catgtattcc tcagaggcga aactgccaaa ctctttctcc tgtcttgggt 960
tggttgccac tggggcgggc atctagggtg cagcctctgc tcattggcact gggcctccag 1020

ttcttccaca tgtgtgcacc cccagcttgg ccaaccctca gccttgcggt ggggcccgaa 1080
 gcatcttccc ttccgcttgg cgtctctggg attgggatga gtgcctggct cccatctcct 1140
 cctcaccttt tgttgcctatc ggcagctgct ggctcagggg catccacact ccgggctctg 1200
 ggttcctctg ccttgaagg gctccaggac ccgtcccaat aaccacccac ggccaggagg 1260
 gccaaaggccc cgtgctggat atttaaattt aggggcccgt ctccagggcg cgtagataaa 1320
 taaatacact cagcgtcaaa aaaaaaaaaa aa 1352

<210> 3
 <211> 5143
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (501)..(4277)

<400> 3
 tgtgtcttga gactcgatat acctatctat tcgatgatga agatacccca ccagacccaa 60
 aaaaagagat ctctcgagga tccgaattcg cggccgcgtc gaccgcgccc ctgccgcggc 120
 ccctagctcg ggcctcaggg gcctccctt tccgggcagg ccgctcccggt cagcaaggca 180
 gtgagcaccg cggccagcag agggcgggtcc ggaccaagt ctgcagcggc gccattggcg 240
 tgtggaaaat gccaccagat ggcggttag gattgcagct ccgttgaagg cgcggccccc 300
 gctcccgaa ccccggcgac caccocgtaa caaccccccc acatcgggaa taacacaccg 360
 gagacttttg gggggaaact aggtcgatgg tcggcggcgc ccggatgggc agctgaggat 420
 tgcctttgag gttattttta aagttttgag ttgtacagca cttgattatt ttgctgcatt 480
 gtgaaaggac ctctccagca atg att act tca gaa tta cca gtg tta cag 530
 Met Ile Thr Ser Glu Leu Pro Val Leu Gln
 1 5
 gat tca act aat gaa act act gcc cat tcc gat gct ggc agc gag ctt 578
 Asp Ser Thr Asn Glu Thr Thr Ala His Ser Asp Ala Gly Ser Glu Leu
 11 16 21 26
 gaa gaa aca gag gtc aaa gga aaa aga aaa agg ggt cgt cct ggc cgg 626
 Glu Glu Thr Glu Val Lys Gly Lys Arg Lys Arg Gly Arg Pro Gly Arg
 27 32 37 42
 cct cca tct aca aat aag aaa cct cga aaa tct cca ggt gag aag agc 674
 Pro Pro Ser Thr Asn Lys Lys Pro Arg Lys Ser Pro Gly Glu Lys Ser
 43 48 53 58

aga att gaa gct gga att aga gga gca ggc cgt gga aga gct aat gga	722
Arg Ile Glu Ala Gly Ile Arg Gly Ala Gly Arg Gly Arg Ala Asn Gly	
59 64 69 74	
cac cct caa cag aat ggg gaa ggg gag cct gtc aca tta ttt gag gtg	770
His Pro Gln Gln Asn Gly Glu Gly Glu Pro Val Thr Leu Phe Glu Val	
75 80 85 90	
gtg aaa ctg ggg aaa agt gca atg cag tcc gtg gtg gat gac tgg att	818
Val Lys Leu Gly Lys Ser Ala Met Gln Ser Val Val Asp Asp Trp Ile	
91 96 101 106	
gaa tca tat aaa caa gac agg gac atc gca ctt ctg gat tta atc aac	866
Glu Ser Tyr Lys Gln Asp Arg Asp Ile Ala Leu Leu Asp Leu Ile Asn	
107 112 117 122	
ttt ttt atc cag tgt tca gga tgt cga ggt act gtg aga ata gag atg	914
Phe Phe Ile Gln Cys Ser Gly Cys Arg Gly Thr Val Arg Ile Glu Met	
123 128 133 138	
ttt cga aat atg cag aat gca gaa atc atc aga aaa atg act gaa gaa	962
Phe Arg Asn Met Gln Asn Ala Glu Ile Ile Arg Lys Met Thr Glu Glu	
139 144 149 154	
ttt gat gag gac agt ggt gat tat cct ctt acc atg cct gga cct cag	1010
Phe Asp Glu Asp Ser Gly Asp Tyr Pro Leu Thr Met Pro Gly Pro Gln	
155 160 165 170	
tgg aaa aaa ttt cgt tca aac ttt tgt gaa ttt att gga gtc ctg att	1058
Trp Lys Lys Phe Arg Ser Asn Phe Cys Glu Phe Ile Gly Val Leu Ile	
171 176 181 186	
cga cag tgt cag tat agc ata att tat gat gag tat atg atg gac aca	1106
Arg Gln Cys Gln Tyr Ser Ile Ile Tyr Asp Glu Tyr Met Met Asp Thr	
187 192 197 202	
gta atc tcc ctt ttg acg ggt ttg tca gac tcc cag gtc aga gct ttt	1154
Val Ile Ser Leu Leu Thr Gly Leu Ser Asp Ser Gln Val Arg Ala Phe	
203 208 213 218	
agg cat aca agt acc ctg gct gcc atg aag ctc atg act gct ctg gtg	1202
Arg His Thr Ser Thr Leu Ala Ala Met Lys Leu Met Thr Ala Leu Val	
219 224 229 234	
aat gtt gcc tta aac ctc agt att cat cag gat aat acc cag aga caa	1250
Asn Val Ala Leu Asn Leu Ser Ile His Gln Asp Asn Thr Gln Arg Gln	
235 240 245 250	
tat gaa gcc gag aga aat aaa atg att ggg aag aga gcc aat gaa agg	1298
Tyr Glu Ala Glu Arg Asn Lys Met Ile Gly Lys Arg Ala Asn Glu Arg	
251 256 261 266	
ttg gag tta cta ctt cag aaa cgc aaa gag ctg caa gaa aat cag gat	1346
Leu Glu Leu Leu Leu Gln Lys Arg Lys Glu Leu Gln Glu Asn Gln Asp	
267 272 277 282	
gaa atc gaa aat atg atg aac tct att ttt aag ggt ata ttt gtt cat	1394

507	512	517	522	
agt gct ctt ata gag	cta atg gtt tgt aca	att cgt caa gct gct gag	2114	
Ser Ala Leu Ile Glu	Leu Met Val Cys Thr	Ile Arg Gln Ala Ala Glu		
523	528	533	538	
gca cat cct cca gtg	gga agg ggt acc ggc	aag aga gtg cta act gcc	2162	
Ala His Pro Pro Val	Gly Arg Gly Thr Gly	Lys Arg Val Leu Thr Ala		
539	544	549	554	
aaa gaa agg aaa act	caa att gat gat aga	aac aaa ttg act gaa cat	2210	
Lys Glu Arg Lys Thr	Gln Ile Asp Asp Arg	Asn Lys Leu Thr Glu His		
555	560	565	570	
ttt att att aca ctt	cct atg tta ctg tca	aag tat tct gca gat gca	2258	
Phe Ile Ile Thr Leu	Pro Met Leu Leu Ser	Lys Tyr Ser Ala Asp Ala		
571	576	581	586	
gag aag gta gca aac	ttg cta caa atc cca	cag tat ttt gat tta gaa	2306	
Glu Lys Val Ala Asn	Leu Leu Gln Ile Pro	Gln Tyr Phe Asp Leu Glu		
587	592	597	602	
atc tac agc aca ggt	aga atg gaa aag cat	ctg gat gct tta tta aaa	2354	
Ile Tyr Ser Thr Gly	Arg Met Glu Lys His	Leu Asp Ala Leu Leu Lys		
603	608	613	618	
cag att aag ttt gtt	gtg gag aaa cac gta	gaa tca gat gtt cta gaa	2402	
Gln Ile Lys Phe Val	Val Glu Lys His Val	Glu Ser Asp Val Leu Glu		
619	624	629	634	
gcc tgc agt aaa acc	tat agt atc tta tgc	agt gaa gaa tat acc atc	2450	
Ala Cys Ser Lys Thr	Tyr Ser Ile Leu Cys	Ser Glu Glu Tyr Thr Ile		
635	640	645	650	
cag aac aga gtt gac	ata gct cga agc cag	ctg att gat gag ttt gta	2498	
Gln Asn Arg Val Asp	Ile Ala Arg Ser Gln	Leu Ile Asp Glu Phe Val		
651	656	661	666	
gat cga ttc aat cat	tct gtg gaa gac cta	ttg caa gag gga gaa gaa	2546	
Asp Arg Phe Asn His	Ser Val Glu Asp Leu	Leu Gln Glu Gly Glu Glu		
667	672	677	682	
gct gat gat gat gac	att tac aat gtt ctt	tct aca tta aag cgg tta	2594	
Ala Asp Asp Asp Asp	Ile Tyr Asn Val Leu	Ser Thr Leu Lys Arg Leu		
683	688	693	698	
act tct ttt cag aat	gca cat gat ctc aca	aaa tgg gat ctc ttt ggt	2642	
Thr Ser Phe Gln Asn	Ala His Asp Leu Thr	Lys Trp Asp Leu Phe Gly		
699	704	709	714	
aat tgc tac aga tta	ttg aag act gga att	gaa cat gga gcc atg cca	2690	
Asn Cys Tyr Arg Leu	Leu Lys Thr Gly Ile	Glu His Gly Ala Met Pro		
715	720	725	730	
gaa cag ata gtc gtg	caa gca ctg cag tgt	tcc cat tat tcg att ctt	2738	
Glu Gln Ile Val Val	Gln Ala Leu Gln Cys	Ser His Tyr Ser Ile Leu		
731	736	741	746	

ttg cag ttg gtg aaa att act gat ggc tct cct tcc aaa gag gat ttg	2786
Trp Gln Leu Val Lys Ile Thr Asp Gly Ser Pro Ser Lys Glu Asp Leu	
747 752 757 762	
ttg gta ttg agg aaa acg gtg aaa tcc ttt ttg gct gtt tgc cag cag	2834
Leu Val Leu Arg Lys Thr Val Lys Ser Phe Leu Ala Val Cys Gln Gln	
763 768 773 778	
tgc ctg tct aat gtt aat act cca gtg aaa gaa cag gct ttc atg tta	2882
Cys Leu Ser Asn Val Asn Thr Pro Val Lys Glu Gln Ala Phe Met Leu	
779 784 789 794	
ctc tgt gat ctt ctg atg att ttc agc cac caa tta atg aca ggt ggc	2930
Leu Cys Asp Leu Leu Met Ile Phe Ser His Gln Leu Met Thr Gly Gly	
795 800 805 810	
aga gag ggc ctt cag cct ttg gtg ttc aat cca gat act gga ctc caa	2978
Arg Glu Gly Leu Gln Pro Leu Val Phe Asn Pro Asp Thr Gly Leu Gln	
811 816 821 826	
tct gaa ctc ctc agt ttt gtg atg gat cac gtt ttt att gac caa gac	3026
Ser Glu Leu Leu Ser Phe Val Met Asp His Val Phe Ile Asp Gln Asp	
827 832 837 842	
gag gag aac cag agc atg gag ggt gat gaa gaa gat gaa gct aat aaa	3074
Glu Glu Asn Gln Ser Met Glu Gly Asp Glu Glu Asp Glu Ala Asn Lys	
843 848 853 858	
att gag gcc tta cat aaa aga agg aat cta ctt gct gct ttc agc aaa	3122
Ile Glu Ala Leu His Lys Arg Arg Asn Leu Leu Ala Ala Phe Ser Lys	
859 864 869 874	
ctt atc att tat gac att gtt gac atg cat gca gct gca gac atc ttc	3170
Leu Ile Ile Tyr Asp Ile Val Asp Met His Ala Ala Ala Asp Ile Phe	
875 880 885 890	
aaa cac tac atg aag tat tac aat gac tat ggt gat att att aag gaa	3218
Lys His Tyr Met Lys Tyr Tyr Asn Asp Tyr Gly Asp Ile Ile Lys Glu	
891 896 901 906	
aca ctg agt aaa acc agg cag att gat aaa att cag tgt gcc aag act	3266
Thr Leu Ser Lys Thr Arg Gln Ile Asp Lys Ile Gln Cys Ala Lys Thr	
907 912 917 922	
ctc att ctc agt ttg caa cag tta ttt aat gaa ctt gtt caa gag caa	3314
Leu Ile Leu Ser Leu Gln Gln Leu Phe Asn Glu Leu Val Gln Glu Gln	
923 928 933 938	
ggc ccc aac cta gat agg aca tct gcc cat gtc agt ggc att aaa gaa	3362
Gly Pro Asn Leu Asp Arg Thr Ser Ala His Val Ser Gly Ile Lys Glu	
939 944 949 954	
ctg gca cgt cgc ttt gcc ctt aca ttt gga ttg gac cag att aag aca	3410
Leu Ala Arg Arg Phe Ala Leu Thr Phe Gly Leu Asp Gln Ile Lys Thr	
955 960 965 970	

cga gaa gca gtt gcc aca ctt cac aag gat ggc ata gag ttt gca ttt	3458
Arg Glu Ala Val Ala Thr Leu His Lys Asp Gly Ile Glu Phe Ala Phe	
971 976 981 986	
aaa tac caa aat cag aaa gga caa gag tat cca cct cct aat ctg gct	3506
Lys Tyr Gln Asn Gln Lys Gly Gln Glu Tyr Pro Pro Pro Asn Leu Ala	
987 992 997 1002	
ttt ctt gaa gta cta agt gaa ttt tct tct aaa ctt ctt cga cag gac	3554
Phe Leu Glu Val Leu Ser Glu Phe Ser Ser Lys Leu Leu Arg Gln Asp	
1003 1008 1013 1018	
aaa aag aca gtt cat tca tac cta gag aaa ttc ctt acc gag cag atg	3602
Lys Lys Thr Val His Ser Tyr Leu Glu Lys Phe Leu Thr Glu Gln Met	
1019 1024 1029 1034	
atg gaa agg agg gag gat gta tgg ctt cca ctc atc tcc tat aga aat	3650
Met Glu Arg Arg Glu Asp Val Trp Leu Pro Leu Ile Ser Tyr Arg Asn	
1035 1040 1045 1050	
tca tta gtc act ggg ggt gaa gat gat aga atg tct gtg aac agt gga	3698
Ser Leu Val Thr Gly Gly Glu Asp Asp Arg Met Ser Val Asn Ser Gly	
1051 1056 1061 1066	
agt agc agc agc aaa acc tca tca gta agg aat aag aaa gga cga cct	3746
Ser Ser Ser Ser Lys Thr Ser Ser Val Arg Asn Lys Lys Gly Arg Pro	
1067 1072 1077 1082	
cca ctt cat aaa aaa cga gta gaa gat gag agt ctg gat aac aca tgg	3794
Pro Leu His Lys Lys Arg Val Glu Asp Glu Ser Leu Asp Asn Thr Trp	
1083 1088 1093 1098	
cta aac agg act gac acc atg att cag act cct ggc ccc ctg cca gca	3842
Leu Asn Arg Thr Asp Thr Met Ile Gln Thr Pro Gly Pro Leu Pro Ala	
1099 1104 1109 1114	
cca caa ctc aca tcc act gta ctg cgg gag aac agt cgg ccc atg gga	3890
Pro Gln Leu Thr Ser Thr Val Leu Arg Glu Asn Ser Arg Pro Met Gly	
1115 1120 1125 1130	
gac cag att caa gaa cct gag tct gaa cat ggt tct gaa cca gac ttt	3938
Asp Gln Ile Gln Glu Pro Glu Ser Glu His Gly Ser Glu Pro Asp Phe	
1131 1136 1141 1146	
tta cac aat cct cag atg cag atc tct tgg tta ggc cag ccg aag tta	3986
Leu His Asn Pro Gln Met Gln Ile Ser Trp Leu Gly Gln Pro Lys Leu	
1147 1152 1157 1162	
gaa gac tta aat cgg aag gac aga aca gga atg aac tac atg aaa gtg	4034
Glu Asp Leu Asn Arg Lys Asp Arg Thr Gly Met Asn Tyr Met Lys Val	
1163 1168 1173 1178	
aga act gga gtg agg cat gct gtt cgg ggt cta atg gag gaa gat gct	4082
Arg Thr Gly Val Arg His Ala Val Arg Gly Leu Met Glu Glu Asp Ala	
1179 1184 1189 1194	
gag ccc atc ttt gaa gat gtg atg atg tca tcc cga agc cag tta gaa	4130

<222> (65)..(1303)

<400> 4

cacgaggtgc cgcaccggcc gcgggcgag ggagtattat gggctgtggg tgccgctgag 60

caag atg gag ctg tct gca gtg ggc gag cgg gtc ttc gcg gcc gaa tcc 109
Met Glu Leu Ser Ala Val Gly Glu Arg Val Phe Ala Ala Glu Ser
1 5 10

atc atc aaa cgg cgg atc cga aag gga cgc atc gag tac ctg gtg aaa 157
Ile Ile Lys Arg Arg Ile Arg Lys Gly Arg Ile Glu Tyr Leu Val Lys
16 21 26 31

tgg aag ggg tgg gcg atc aag tac agc act tgg gag^a ccc gag gag aac 205
Trp Lys Gly Trp Ala Ile Lys Tyr Ser Thr Trp Glu Pro Glu Glu Asn
32 37 42 47

atc ctg gac tcg cgg ctc att gca gcc ttc gaa caa aag gag agg gag 253
Ile Leu Asp Ser Arg Leu Ile Ala Ala Phe Glu Gln Lys Glu Arg Glu
48 53 58 63

cgt gag ctg tat ggg ccc aag aag agg gga ccc aaa ccc aaa act ttc 301
Arg Glu Leu Tyr Gly Pro Lys Lys Arg Gly Pro Lys Pro Lys Thr Phe
64 69 74 79

ctc ctg aag gcg cgg gcc cag gcc gag gcc^{*} ctc cgc atc agt gat gtg 349
Leu Leu Lys Ala Arg Ala Gln Ala Glu Ala Leu Arg Ile Ser Asp Val
80 85 90 95

cat ttc tct gtc aag ccg agc gcc agt gcc tcc tcg ccc aag ctg cac 397
His Phe Ser Val Lys Pro Ser Ala Ser Ala Ser Ser Pro Lys Leu His
96 101 106 111

tcc agc gca gcc gtg cac cgg ctc aag aag gac atc cgc cgc tgc cac 445
Ser Ser Ala Ala Val His Arg Leu Lys Lys Asp Ile Arg Arg Cys His
112 117 122 127

cgt atg tcc cgc cgt ccc ctg ccc cgc ccg gac ccg cag ggg ggc agc 493
Arg Met Ser Arg Arg Pro Leu Pro Arg Pro Asp Pro Gln Gly Gly Ser
128 133 138 143

ccc gga ctg cgc ccg ccc att tcg ccc ttc tcg gag acg gtg cgc atc 541
Pro Gly Leu Arg Pro Pro Ile Ser Pro Phe Ser Glu Thr Val Arg Ile
144 149 154 159

atc aac cgc aag gtg aag ccg cgg gag ccc aag cgg aac cgc atc atc 589
Ile Asn Arg Lys Val Lys Pro Arg Glu Pro Lys Arg Asn Arg Ile Ile
160 165 170 175

ctg aac ctg aag gtg atc gac aag ggc gct ggc ggc ggg ggc gcc ggg 637
Leu Asn Leu Lys Val Ile Asp Lys Gly Ala Gly Gly Gly Gly Ala Gly
176 181 186 191

cag ggg gcc[!] ggg gcg ctg gcc cgc ccc aaa gtc ccc tcg cgg aac cgc 685
Gln Gly Ala Gly Ala Leu Ala Arg Pro Lys Val Pro Ser Arg Asn Arg
192 197 202 207

gtt ata ggc aag agc aag aag ttc agc gag agc gtc ctg cgt aca cag	733
Val Ile Gly Lys Ser Lys Lys Phe Ser Glu Ser Val Leu Arg Thr Gln	
208 213 218 223	
atc cgc cac atg aag ttc ggc gcc ttt gcg ctg tac aag cct ccg ccc	781
Ile Arg His Met Lys Phe Gly Ala Phe Ala Leu Tyr Lys Pro Pro Pro	
224 229 234 239	
gcc ccc ctg gta gcc ccg tcc ccc ggc aag gct gag gcc tca gcc ccg	829
Ala Pro Leu Val Ala Pro Ser Pro Gly Lys Ala Glu Ala Ser Ala Pro	
240 245 250 255	
ggc cct ggg cta ctt ctg gcc gcc ccc gcc gcc ccg tac gac gcc cgc	877
Gly Pro Gly Leu Leu Leu Ala Ala Pro Ala Ala Pro Tyr Asp Ala Arg	
256 261 266 271	
agc tct ggc tcc tcc ggc tgc ccc tcg cct aca cca cag tcc tct gac	925
Ser Ser Gly Ser Ser Gly Cys Pro Ser Pro Thr Pro Gln Ser Ser Asp	
272 277 282 287	
ccc gac gac acg ccc ccc aag ctc ctc ccc gag acc gtg agc cca tcc	973
Pro Asp Asp Thr Pro Pro Lys Leu Leu Pro Glu Thr Val Ser Pro Ser	
288 293 298 303	
gcc ccc agc tgg cgc gag ccg gag gtg ctc gac ctg tcc ctc cct ccc	1021
Ala Pro Ser Trp Arg Glu Pro Glu Val Leu Asp Leu Ser Leu Pro Pro	
304 309 314 319	
gag tcg gca gcc acc agc aag cgg gca ccg cct gag gtc aca gct gct	1069
Glu Ser Ala Ala Thr Ser Lys Arg Ala Pro Pro Glu Val Thr Ala Ala	
320 325 330 335	
gcc ggc ccg gca cct ccc acg gcc cct gac ccc gcc ggt gcc tcc tcc	1117
Ala Gly Pro Ala Pro Pro Thr Ala Pro Asp Pro Ala Gly Ala Ser Ser	
336 341 346 351	
gag ccc gag gct ggg gac tgg cgc ccc gag atg tca ccc tgc tcc aat	1165
Glu Pro Glu Ala Gly Asp Trp Arg Pro Glu Met Ser Pro Cys Ser Asn	
352 357 362 367	
gtg gtc gtc acc gat gtc acc agc aac ctc ctg acg gtc aca atc aag	1213
Val Val Val Thr Asp Val Thr Ser Asn Leu Leu Thr Val Thr Ile Lys	
368 373 378 383	
gaa ttc tgc aac cct gag gat ttc gag aag gtg gct gct ggg gta gca	1261
Glu Phe Cys Asn Pro Glu Asp Phe Glu Lys Val Ala Ala Gly Val Ala	
384 389 394 399	
ggc gcc gct ggg ggc ggt ggc agc att ggg gcg agc aag tga gggggct	1310
Gly Ala Ala Gly Gly Gly Ser Ile Gly Ala Ser Lys *	
400 405 410	
ccaccaagga ggggggcttg gggggggccct cctgcccgaa gtcatactct tgctcccacc	1370
ccacccttg ccccgccct ctctccctgt gctttgcttg tctcaaatgg ctcggtgttg	1430
accagggat ggggctgggt agttggggtc ccagaaagcc gggggtaggg gccaccctgg	1490

aatggggcag gggaagggca cccccctgc ccatgcatgg tagccactg ggtggtttct 1550
ggaaagccct agaaactagg gtccctctgc ccctccaca tcccacctgt ctctctagct 1610
tgcttctctgc tctcctgtgc ggcgtctgat ttctcgggtgc taacctggca gctgtggggc 1670
ccttaggagc cccccaccga ggggtggacac agtccctttc cttcctgcag atgcctaggc 1730
aggaggaggg cttcctgcct gtttggcaaa gtcccaggca gaggccaagg atgaggcctg 1790
actcggctcc tccctccaca tcagccaggg catcagaagt tgggccaggg cggggtcttc 1850
cctgctcgat tttggaagag gctaagtag acccctatg ccttgccca gccctggctc 1910
tttctaacc cctcaacgg tgggaggaac tggcagaggg tgcgcctggc cacagcctcc 1970
ccgcatctaa agggcccttc agttcttgac caaagggtgt acgagaacct gccgtggaaa 2030
cttcagttg tgctctgcc ccactcgtg tgtttgtccg tgggttcata catgcattgg 2090
gtgctaggcc ccaggctgcc ggggtggacc ctttacagtt cctttgaaca ggggcattga 2150
aggcctggac tgctctctgc ctcaagtag ctggggacca ggcttgggtc tggaggtttg 2210
ctgtggaagt caccaggcct cccctcctgg ccagggtgtg ctgggggcac cgtgcccccc 2270
acccccctgc cctcctcagg gtggtcagcc caacctgtcg gaccttact tcacatcatg 2330
gtggggaccg agatagagag ggagaccoca ttccaagctc cctcttctc cgggtgtttg 2390
gggaggatgc tgaagaatcc attcccagg gctcccggc ttgtcccagc cctcttttg 2450
cttctgacca cggaggcttt ctacagccc agcctgcctg aagcaaagga ggctcccgtg 2510
tcctgggcag cttctgtttc cctctgctgc ctgggagctg aggcacccgt gccagtggca 2570
gaggccacag cccagcctt aggcaggcc ctgggagggc aggcaggcaa aggggagacc 2630
agagggtctg tgttctccag gagaatgagg gtgttggtcc cagaattggg accggggccc 2690
cgctggccag cctggggcca cttcccgggt cttcattgtg cgtgggtggc gtgttccagg 2750
cgtggctgga gctggcttcc tggctgtgt gccatgggc cctccctcag aagcacgttg 2810
gcaggaggcc gatcagaacc ctagcgctt tggctcctaag aatgggaggc tgccttctt 2870
cccaatctcc ctgccagggc ccacagcgtg gccctagccc tcccctccc gggatgtaga 2930
acggggaccc tcgcagggtt ggggcggggg ctgatactcc tcggccctc cctaccctgc 2990
cctgtgtgtt ggctttgtgg cgtccaagt gccaatggc ttttcgcca aataagggt 3050
ggatattctc ctctgtcctt ggagggtgatt tcccctgac cccctcccc aggtgagtga 3110
ccacctgggt gccagttaca ggtgtttcca gagaccatag aaatgtgttt tcctgagagt 3170

tcgtgtcatt cgtgactttt ttgtaaagaa gttgtgtttt cagaggtgat tttatgacag 3230
gaaagtgaaa gaattagttt tgcaaaaaaa caaaaaaaa aaaa 3274

<210> 5
<211> 1941
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (138)..(773)

<400> 5
gcacgaggag aagtggggcc gagatcgcgc cgtccagcc cgcccgccgg cgtctgcgct 60
gctccggcgc ccttaccctt gctggccctt gcaaggcgcg accggcggcc atgcagcccc 120
ggggctgagg ccgcccc atg gca aag cct ggc ggt ccc ggc gaa cga cgg 170
Met Ala Lys Pro Gly Gly Pro Gly Glu Arg Arg
1 5
cgc atg gag aac ttc cgt aag gtg cgc tcc gaa gag gcg cca cgg gga 218
Arg Met Glu Asn Phe Arg Lys Val Arg Ser Glu Glu Ala Pro Arg Gly
12 17 22 27
tgc ggg gcc gag gga ggc ggc ccg ggc tcc ggc ccg ttc gca gac ctg 266
Cys Gly Ala Glu Gly Gly Gly Pro Gly Ser Gly Pro Phe Ala Asp Leu
28 33 38 43
gcg ccg ggc gcg gtg cac atg ccg gtc aag gaa ggc agc aag atc cgg 314
Ala Pro Gly Ala Val His Met Arg Val Lys Glu Gly Ser Lys Ile Arg
44 49 54 59
aac ctg atg gcc ttc gcc acc gcc agc atg gcg cag cca gcc acg cgc 362
Asn Leu Met Ala Phe Ala Thr Ala Ser Met Ala Gln Pro Ala Thr Arg
60 65 70 75
gcc atc gtc ttc agc ggc tgc ggc ccg gcc acc acc aaa acc gtc acg 410
Ala Ile Val Phe Ser Gly Cys Gly Arg Ala Thr Thr Lys Thr Val Thr
76 81 86 91
tgc gcc gag atc ctc aag cgc cgc ctg gcg ggc ctg cac cag gtc acg 458
Cys Ala Glu Ile Leu Lys Arg Arg Leu Ala Gly Leu His Gln Val Thr
92 97 102 107
cgg ctg cgc tac ccg agc gta cgc gag gtg tgg cag agc ctc ccg cct 506
Arg Leu Arg Tyr Arg Ser Val Arg Glu Val Trp Gln Ser Leu Pro Pro
108 113 118 123
ggg ccc acg cag ggt cag acg cct ggc gag ccg gcc gct agt ctc agc 554
Gly Pro Thr Gln Gly Gln Thr Pro Gly Glu Pro Ala Ala Ser Leu Ser
124 129 134 139

gta ctt aag aac gtg ccc ggc ctc gcc atc cta ctt tcc aag gac gcg	602
Val Leu Lys Asn Val Pro Gly Leu Ala Ile Leu Leu Ser Lys Asp Ala	
140 145 150 155	
ctg gat ccg cga cag ccc ggc tac cag ccc ccg aat ccc cat cct ggt	650
Leu Asp Pro Arg Gln Pro Gly Tyr Gln Pro Pro Asn Pro His Pro Gly	
156 161 166 171	
ccc tcg tcc ccg cca gcc gcg cca gcg tcc aag agg agc cta ggg gaa	698
Pro Ser Ser Pro Pro Ala Ala Pro Ala Ser Lys Arg Ser Leu Gly Glu	
172 177 182 187	
ccc gca gct gga gaa ggc tcc gcg aag cga tcg caa ccc gag cca ggg	746
Pro Ala Ala Gly Glu Gly Ser Ala Lys Arg Ser Gln Pro Glu Pro Gly	
188 193 198 203	
gtt gcg gac gag gat cag acg gcc tga aactc cggactgtgg gccacctagt	798
Val Ala Asp Glu Asp Gln Thr Ala *	
204 209	
ccggcaggat cttccgccag cgcctccacc ttcagatgta cctccagcct ttcactcctc	858
ggctctccgg agcccacaac ctggacacag ctctcaaga caggtagcat ggaccttaag	918
gcgacaagag aggggccccca ggagtggcag gagaggatcc ccgaccaccc tagggaaact	978
tcgtgcgata attgctgctt atgcccgtgt tgcgtgaaga cacggaactt caccttttct	1038
gggaccttct ttgggggaga atgggtggaca gtgggattct ggaaacttgt ttgggacccc	1098
caagggttaa agccaccacag cattcacgaa gagcacctga agtatggaag ctgagaagag	1158
ttattggaat cccccccacc gttgacagag gaaggcaggg ggtgagaatt aactgcttga	1218
gggtaggaga gtctgagatg tgggggccct attccgctcc ccgccctggg acagttttcc	1278
tttctagttt tttttccct gcttcagagg agcatctctg agggttctag ctcttttaac	1338
acctttttc cccctgctgg ccagagggga gaccaggac tgaactctcc aggcctctc	1398
ccctgagccc tgcagctggc tggagtcttg cttccaataa aacaagcaca aaaatggctg	1458
tgtcccccatt ttttttcta accaccgcc tgtgcagaga cagctctcgc ctggccctt	1518
gtgtctcccc tcccctccag ccttgctcc tgagtcttg gagtcttcag ggtcaggcac	1578
agagactgaa cagcttcaaa atgggtcaag ggactgccca gtccctgggt tcttcctctc	1638
ttctttcccc actccgccct ccgggtggg cctgggcttc agagggtgtt tgcaaatggg	1698
ggggccctgg taacctttaa cattggtcat taaggggaaa gggagcggga cattgtttt	1758
ttggggaggg ggaaggaagg gagttggaaa gacaacattc gtggaatctt tgggggggtc	1818
aatggaaaag ggtggaagac ccgtttaggg tctcgaattt tgaggtttca gacaataaat	1878
gtaactttac cagaaggttg ggaaaaaggc ccatttttgg gtagggtttt ccttaatttc	1938

ttc

1941

<210> 6
<211> 1663
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (413)..(1420)

<400> 6

tcggtaccgg cccggaattc ccgggtcgac ccacgcgtgc gccacgcgt ccgcgttgtg	60
ccagatgcac agcacattgt gtgacactga cttaagattc taactctgtg caagagggaa	120
aaaaacagtg gagaaggctg ggctggacca cgggaaagag ataggaaaac ggatacgaat	180
gtaaggcaca gagttggctc ggcgccctg gcagtttaga agacagggtcc ctggaggggc	240
cttggcgggt ctccgctcgc gggagttccg cgggtgtctt cccagtgcta tctgcaggct	300
ggccagcttc ctctgcgctc cggaaagctg cggcccagcg cggactagtg aggacctcca	360
cagctcctga cattgccagg agtcctgtcg gcgttttctc ccagcctccg cc atg	415
	Met
	1
ccg gcg gtg ctg ggt ttt gaa ggc agc gcc aat aag att ggc gtg ggc	463
Pro Ala Val Leu Gly Phe Glu Gly Ser Ala Asn Lys Ile Gly Val Gly	
2 7 12 17	
gtg gtg cgg gat ggc aag gtg ctg gcg aac ccg cgg cgg act tac gtc	511
Val Val Arg Asp Gly Lys Val Leu Ala Asn Pro Arg Arg Thr Tyr Val	
18 23 28 33	
acg cct cct ggc aca gga ttc ctt cca ggt gat aca gcc agg cat cac	559
Thr Pro Pro Gly Thr Gly Phe Leu Pro Gly Asp Thr Ala Arg His His	
34 39 44 49	
cga gct gtt atc cta gac ctg ctg cag gag gca cta aca gag tct gga	607
Arg Ala Val Ile Leu Asp Leu Leu Gln Glu Ala Leu Thr Glu Ser Gly	
50 55 60 65	
tta acc tcc cag gat atc gac tgc att gca tac acc aag ggc cct ggc	655
Leu Thr Ser Gln Asp Ile Asp Cys Ile Ala Tyr Thr Lys Gly Pro Gly	
66 71 76 81	
atg ggt gcc cca ctg gtt tct gtg gct gtt gtg gcc cgt act gtg gcc	703
Met Gly Ala Pro Leu Val Ser Val Ala Val Val Ala Arg Thr Val Ala	
82 87 92 97	
cag ctg tgg aat aag cca ttg gtg ggt gtg aac cac tgt ata ggc cac	751

Gln	Leu	Trp	Asn	Lys	Pro	Leu	Val	Gly	Val	Asn	His	Cys	Ile	Gly	His		
98					103					108					113		
att	gag	atg	ggc	cgc	ctc	atc	act	gga	gcc	acc	agc	cca	acc	gtg	ttg	799	
Ile	Glu	Met	Gly	Arg	Leu	Ile	Thr	Gly	Ala	Thr	Ser	Pro	Thr	Val	Leu		
114					119					124					129		
tat	gtg	agt	gga	gga	aat	acg	cag	gtg	att	gca	tac	tcg	gaa	cat	cgt	847	
Tyr	Val	Ser	Gly	Gly	Asn	Thr	Gln	Val	Ile	Ala	Tyr	Ser	Glu	His	Arg		
130					135					140					145		
tac	cgt	atc	ttt	ggg	gaa	acc	atc	gat	att	gca	gtg	ggg	aat	tgt	ctg	895	
Tyr	Arg	Ile	Phe	Gly	Glu	Thr	Ile	Asp	Ile	Ala	Val	Gly	Asn	Cys	Leu		
146					151					156					161		
gat	cgt	ttt	gct	cga	gtg	ctg	aag	att	tct	aac	gac	cca	agt	cca	gga	943	
Asp	Arg	Phe	Ala	Arg	Val	Leu	Lys	Ile	Ser	Asn	Asp	Pro	Ser	Pro	Gly		
162					167					172					177		
tac	aac	att	gaa	cag	atg	gca	aag	cga	ggc	aag	aag	ctg	gtt	gag	ctg	991	
Tyr	Asn	Ile	Glu	Gln	Met	Ala	Lys	Arg	Gly	Lys	Lys	Leu	Val	Glu	Leu		
178					183					188					193		
cca	tac	act	gta	aag	ggg	atg	gac	gtc	tca	ttc	tca	ggg	atc	ctg	tct	1039	
Pro	Tyr	Thr	Val	Lys	Gly	Met	Asp	Val	Ser	Phe	Ser	Gly	Ile	Leu	Ser		
194					199					204					209		
ttc	att	gag	gat	gta	gcc	cat	cgg	atg	ctg	gcc	aca	ggc	gag	tgt	act	1087	
Phe	Ile	Glu	Asp	Val	Ala	His	Arg	Met	Leu	Ala	Thr	Gly	Glu	Cys	Thr		
210					215					220					225		
oct	gag	gat	ctg	tgt	ttc	tcc	ctg	cag	gaa	act	gtg	ttt	gca	atg	ctg	1135	
Pro	Glu	Asp	Leu	Cys	Phe	Ser	Leu	Gln	Glu	Thr	Val	Phe	Ala	Met	Leu		
226					231					236					241		
gta	gag	atc	aca	gag	cga	gcc	atg	gca	cat	tgt	ggc	tcc	cag	gag	gcc	1183	
Val	Glu	Ile	Thr	Glu	Arg	Ala	Met	Ala	His	Cys	Gly	Ser	Gln	Glu	Ala		
242					247					252					257		
ctc	att	gtg	gga	gga	gtg	ggg	tgt	aat	gtg	agg	cta	cag	gag	atg	atg	1231	
Leu	Ile	Val	Gly	Gly	Val	Gly	Cys	Asn	Val	Arg	Leu	Gln	Glu	Met	Met		
258					263					268					273		
gca	aca	atg	tgc	cag	gaa	cgt	gga	gcc	cgg	ctt	ttt	gct	aca	gat	gag	1279	
Ala	Thr	Met	Cys	Gln	Glu	Arg	Gly	Ala	Arg	Leu	Phe	Ala	Thr	Asp	Glu		
274					279					284					289		
aga	ttc	tgt	att	gac	aat	gga	gcg	atg	ata	gcc	cag	gct	ggc	tgg	gag	1327	
Arg	Phe	Cys	Ile	Asp	Asn	Gly	Ala	Met	Ile	Ala	Gln	Ala	Gly	Trp	Glu		
290					295					300					305		
atg	ttt	cgg	gct	gga	cac	agg	acc	cca	ctc	agt	gat	tct	ggg	gtt	aca	1375	
Met	Phe	Arg	Ala	Gly	His	Arg	Thr	Pro	Leu	Ser	Asp	Ser	Gly	Val	Thr		
306					311					316					321		
cag	agg	tat	cgg	aca	gat	gaa	gta	gag	gtg	acc	tgg	agg	gac	taa	taa	1423	
Gln	Arg	Tyr	Arg	Thr	Asp	Glu	Val	Glu	Val	Thr	Trp	Arg	Asp	*			

322

327

332

gatcaacaga atcagagtag atagttcctt aatcggaacc caaaggaccc cgtgcctcaa 1483
 tctctatcct gatgtcatgg gaggcttagc aaagctatag actccaagca aggcttgggg 1543
 tcctttatgg aaccccagga tgactcagcc tcagaacaac gacagcggcc gctctagagg 1603
 atccaagctt acgtacgcgt gcatgcgacg tcatagctct tctatagtgt cacctaaatt 1663

<210> 7

<211> 1920

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (120)..(1394)

<400> 7

gaccgtcccg gaattcccgg gtcgaccac ggcgcggga agataaggcg ggcgcgggaag 60
 aggacacagg gtgggctgga gctcaaactc aactggactc tcgctcctgc tggctggac 119
 atg gag gat ttg gag gaa gat gta agg ttt att gtg gat gag acc ttg 167
 Met Glu Asp Leu Glu Glu Asp Val Arg Phe Ile Val Asp Glu Thr Leu
 1 5 10 15
 gac ttt ggg ggg ctg tca cca tct gac agc cgt gag gag gaa gac ata 215
 Asp Phe Gly Gly Leu Ser Pro Ser Asp Ser Arg Glu Glu Glu Asp Ile
 17 22 27 32
 aca gtg ttg gtg act cca gag aaa cca ctt cga cgg tgc ctc tcc cac 263
 Thr Val Leu Val Thr Pro Glu Lys Pro Leu Arg Arg Cys Leu Ser His
 33 38 43 48
 cga agt gac cca aat gca gtg gca cct gcc ccc cag ggt gtg agg ctc 311
 Arg Ser Asp Pro Asn Ala Val Ala Pro Ala Pro Gln Gly Val Arg Leu
 49 54 59 64
 agc cta tgc ccc ctc agt cca gag aag ctg gag gag atc ctc gat gag 359
 Ser Leu Cys Pro Leu Ser Pro Glu Lys Leu Glu Glu Ile Leu Asp Glu
 65 70 75 80
 gcc aac cgg ctg gcc gct cag ctg gag cag tgt gcc ctg cag gat cgg 407
 Ala Asn Arg Leu Ala Ala Gln Leu Glu Gln Cys Ala Leu Gln Asp Arg
 81 86 91 96
 gag agc gca ggc gag ggc ctg ggg cct cgc cga gtg aag ccc agt cct 455
 Glu Ser Ala Gly Glu Gly Leu Gly Pro Arg Arg Val Lys Pro Ser Pro
 97 102 107 112
 cgg cgg gag acc ttt gtg ctg aag gat agt cct gtc cga gac ctg ctg 503
 Arg Arg Glu Thr Phe Val Leu Lys Asp Ser Pro Val Arg Asp Leu Leu
 113 118 123 128

ccc act gtg aac tct ttg acg cgg agc acc ccc tcc cca agc agc ctg	551
Pro Thr Val Asn Ser Leu Thr Arg Ser Thr Pro Ser Pro Ser Ser Leu	
129 134 139 144	
acg cct cga ctc cgg agt aat gat agg aag ggg tca gtc agg gct ctc	599
Thr Pro Arg Leu Arg Ser Asn Asp Arg Lys Gly Ser Val Arg Ala Leu	
145 150 155 160	
cgg gct aca tct gga aag agg ccc tcc aac atg aag agg gag tca ccc	647
Arg Ala Thr Ser Gly Lys Arg Pro Ser Asn Met Lys Arg Glu Ser Pro	
161 166 171 176	
act tgc aat ctg ttc cct gca tcc aaa agc cca gca tct tct cct ctt	695
Thr Cys Asn Leu Phe Pro Ala Ser Lys Ser Pro Ala Ser Ser Pro Leu	
177 182 187 192	
acc cga tcg act ccc cca gtc cgg ggg aga gcc ggg ccc agt ggg aga	743
Thr Arg Ser Thr Pro Pro Val Arg Gly Arg Ala Gly Pro Ser Gly Arg	
193 198 203 208	
gca gca gcc agt gag gag acc aga gca gcc aag ttg cgg gga gca gct	791
Ala Ala Ala Ser Glu Glu Thr Arg Ala Ala Lys Leu Arg Gly Ala Ala	
209 214 219 224	
gct aaa tct tcc agt caa ctg ccc att ccc tcg gcc atc ccc agg cct	839
Ala Lys Ser Ser Ser Gln Leu Pro Ile Pro Ser Ala Ile Pro Arg Pro	
225 230 235 240	
gcc agc cga atg cca ctc acc agc cgg agt gtg cca cct ggc aga ggt	887
Ala Ser Arg Met Pro Leu Thr Ser Arg Ser Val Pro Pro Gly Arg Gly	
241 246 251 256	
gcc cta cct cgg gat tct ctg tca act cga aaa ggg ctt cca aga cca	935
Ala Leu Pro Pro Asp Ser Leu Ser Thr Arg Lys Gly Leu Pro Arg Pro	
257 262 267 272	
agc act gca gga cac aga gtg cgg gaa agt gga cac aag gtt cct gtt	983
Ser Thr Ala Gly His Arg Val Arg Glu Ser Gly His Lys Val Pro Val	
273 278 283 288	
tcc cag cga cta aat ctt cct gtc atg ggt gcc act cgc agc aat ctg	1031
Ser Gln Arg Leu Asn Leu Pro Val Met Gly Ala Thr Arg Ser Asn Leu	
289 294 299 304	
cag ccc ccc agg aaa gtg gca gtc cca gga cct acc agg tca gtc tgg	1079
Gln Pro Pro Arg Lys Val Ala Val Pro Gly Pro Thr Arg Ser Val Trp	
305 310 315 320	
tcc tcc ctt gcc cat cct gtc tcc cta ccc cgc cat cat ctg gga ttc	1127
Ser Ser Leu Ala His Pro Val Ser Leu Pro Arg His His Leu Gly Phe	
321 326 331 336	
caa gct gtt atg cac atc agc cct gaa ttt tgt atg gaa aga tgg aga	1175
Gln Ala Val Met His Ile Ser Pro Glu Phe Cys Met Glu Arg Trp Arg	
337 342 347 352	

gag gag ggg agc ctg ggg cag ggg aag ggg gat ccc att tct tcc cac	1223
Glu Glu Gly Ser Leu Gly Gln Gly Lys Gly Asp Pro Ile Ser Ser His	
353 358 363 368	
cct gag gag ctt gaa ttc tgc tgg gtg aca aat ggg ctt gag gaa gaa	1271
Pro Glu Glu Leu Glu Phe Cys Trp Val Thr Asn Gly Leu Glu Glu Glu	
369 374 379 384	
ggg cat ttt aaa gca gtt att cct tct att tct tta ggt aaa gag atc	1319
Gly His Phe Lys Ala Val Ile Pro Ser Ile Ser Leu Gly Lys Glu Ile	
385 390 395 400	
agg aca gca agc aag act tca gta gca aac act aca gtc agg tac ctg	1367
Arg Thr Ala Ser Lys Thr Ser Val Ala Asn Thr Thr Val Arg Tyr Leu	
401 406 411 416	
gac tcg cct cta ccc agc aga ccc tga ctcca gcagattctg gcccgaggac	1419
Asp Ser Pro Leu Pro Ser Arg Pro *	
417 422	
aggaggaaga gatgccacca gggctgggtct cccaggagta gagaccatgg gaaatggggg	1479
ggattaggat tgagctggag gagacttaaa ctctctgggt tgaaagaaga ttaggggaaa	1539
agaggtcacc ttccagcagt gaaatgaaca aatagaagat gagaagtaca ggcaagtgg	1599
ttgtctttat ccacccccac tgttgtgggc agccccagag aattttatct tcttccttgg	1659
cattggttca ctggacattt ccacgtgagc ggctctcgta gtaacctcc ctgccctctg	1719
aggagccatc ttctgaatc gcattctcta ctggactctg gcctgcttgg agaggtggca	1779
gcaggcacct ggtcttcaga aattggttcc tgtgaattct gtgactccta ataggccagt	1839
ttgtgataag ctactctat gagtcttcat tttctaaaa taaagtgaat gtatttttat	1899
attctctgta aaaaaaaaaa a	1920

<210> 8
 <211> 1609
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (309)..(1202)

<400> 8	
ctagttcgag atctcgcgcg gcctcgggag ctgccccggcg gccccggacc gaggcagccc	60
tccccctttaa aagaagcgga ggacaggatt gggatccttg aaacccgaaa cccagaaaca	120
gcacgcggagc ggaaaccaga ggggaaacct tgaactcctc cagacaattg cttccgggga	180

gttgcgaggg agcgaggggg aataaaggac ccgcgaggaa gggcccgcg atggcgcgtc 240

cctgaggggtc gtggcgagtt cgcgagcggt ggggaaggagc ggaccctgct ctccccgggc 300

tgcggggcc atg gcc acg gcg gag cgg aga gcc ctc ggc atc ggc ttc cag 350
Met Ala Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln
1 5 10

tgg ctc tct ttg gcc act ctg gtg ctc atc tgc gcc ggg caa ggg gga 398
Trp Leu Ser Leu Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly
15 20 25 30

cgc agg gag gat ggg ggt cca gcc tgc tac ggc gga ttt gac ctg tac 446
Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr
31 36 41 46

ttc att ttg gac aaa tca gga agt gtg ctg cac cac tgg aat gaa atc 494
Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile
47 52 57 62

tat tac ttt gtg gaa cag ttg gct cac aaa ttc atc agc cca cag ttg 542
Tyr Tyr Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu
63 68 73 78

aga atg tcc ttt att gtt ttc tcc acc cga gga aca acc tta atg aaa 590
Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys
79 84 89 94

ctg aca gaa gac aga gaa caa atc cgt caa ggc cta gaa gaa ctc cag 638
Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln
95 100 105 110

aaa gtt ctg cca gga gga gac act tac atg cat gaa gga ttt gaa agg 686
Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg
111 116 121 126

gcc agt gag cag att tat tat gaa aac aga caa ggg tac agg aca gcc 734
Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala
127 132 137 142

agc gtc atc att gct ttg act gat gga gaa ctc cat gaa gat ctc ttt 782
Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe
143 148 153 158

ttc tat tca gag agg gag gct aat agg tct cga gat ctt ggt gca att 830
Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile
159 164 169 174

gtt tac tgt gtt ggt gtg aaa gat ttc aat gag aca cag ctg gcc cgg 878
Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg
175 180 185 190

att gcg gac agt aag gat cat gtg ttt ccc gtg aat gac ggc ttt cag 926
Ile Ala Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln
191 196 201 206

gct ctg caa ggc atc atc cac tca att ttg aag aag tcc tgc atc gaa 974

[illegible]

```
<220>
<221> CDS
<222> (587) .. (2683)
```

<400> 9

60

ccccctcctg ccagtgcagc gcgagtaaga gcgcccagg gaccacagct ggcatcccag 120
gggttaattt cggagcagcc caggtaggagg tcgagcccc aaccccgtcg gcacctccag 180
gcttccgagg ccaccggaac ggaggaggct tcggtggctc tttgtctacc tgctctgggt 240
gttaaagagc ccgctcgcag cctgcatcgc cggggctcgg gacagaagtc agcggcgggg 300
aatgggggt ctgtcacttt aagtacagct ggagccctgg gatgaaagca gctccatcag 360
tagtggactc agcgatgcct cagacaatct cagttcagaa gaattcaatg ccagctcctc 420
actcaactcc ctcccaagta ctcccactgc ttctcgcagg aactcaacaa tagtgctacg 480
cacagactca tagaagcgct cactggcaga aagtgggctg agctgggttta gtgaatcaga 540
ggagaaagcc cctaaaaaac tggagtacga cagtggtagc ctgaag atg gaa cct 595
Met Glu Pro
1
ggg act tct aag tgg cgg agg gag cgg cct gag agc tgt gat gat tca 643
Gly Thr Ser Lys Trp Arg Arg Glu Arg Pro Glu Ser Cys Asp Asp Ser
4 9 14 19
tcc aag ggt gga gaa ctg aaa aag ccc atc agc ctg ggc cac cct ggt 691
Ser Lys Gly Gly Glu Leu Lys Lys Pro Ile Ser Leu Gly His Pro Gly
20 25 30 35
tcc ctg aag aag ggc aag acc cca cct gtg gct gta act tcc ccc atc 739
Ser Leu Lys Lys Gly Lys Thr Pro Pro Val Ala Val Thr Ser Pro Ile
36 41 46 51
act cac aca gcc cag agt gcc ctc aaa gtc gca ggc aaa cct gag ggc 787
Thr His Thr Ala Gln Ser Ala Leu Lys Val Ala Gly Lys Pro Glu Gly
52 57 62 67
aaa gct aca gac aag ggt aag ctt gca gtg aag aat act ggg ctc caa 835
Lys Ala Thr Asp Lys Gly Lys Leu Ala Val Lys Asn Thr Gly Leu Gln
68 73 78 83
cgc tcc tcc tct gat gct ggt cgg gac cgc ctg agt gat gct aag aag 883
Arg Ser Ser Ser Asp Ala Gly Arg Asp Arg Leu Ser Asp Ala Lys Lys
84 89 94 99
ccc ccc tcg ggc att gct cgc ccc tcc act tcg gga tcc ttt ggc tac 931
Pro Pro Ser Gly Ile Ala Arg Pro Ser Thr Ser Gly Ser Phe Gly Tyr
100 105 110 115
aag aag cct cct cct gcc aca ggc aca gcc act gtc atg caa act ggt 979
Lys Lys Pro Pro Pro Ala Thr Gly Thr Ala Thr Val Met Gln Thr Gly
116 121 126 131
ggg tca gcc act ctc agc aag atc cag aag tcc tca ggc atc cct gtc 1027
Gly Ser Ala Thr Leu Ser Lys Ile Gln Lys Ser Ser Gly Ile Pro Val
132 137 142 147
aag cca gta aat ggg cgc aag act agc tta gat gtt tcc aac agt gca 1075

Lys Pro Val Asn Gly Arg Lys Thr Ser Leu Asp Val Ser Asn Ser Ala	
148 153 158 163	
gag cca gga ttc ctg gct cct gga gcc cgt tct aac atc cag tac cgc	1123
Glu Pro Gly Phe Leu Ala Pro Gly Ala Arg Ser Asn Ile Gln Tyr Arg	
164 169 174 179	
agc ctg ccc cgg cca gcc aag tca agt tct atg agc gtg acc ggc ggg	1171
Ser Leu Pro Arg Pro Ala Lys Ser Ser Ser Met Ser Val Thr Gly Gly	
180 185 190 195	
cgg ggt gga cct cgc cct gtg agc agc agc att gac ccc agt ctc ctc	1219
Arg Gly Gly Pro Arg Pro Val Ser Ser Ser Ile Asp Pro Ser Leu Leu	
196 201 206 211	
agc acc aag cag gga ggc ctt acg cct tcc aga ctg aag gag cct acc	1267
Ser Thr Lys Gln Gly Gly Leu Thr Pro Ser Arg Leu Lys Glu Pro Thr	
212 217 222 227	
aag gta gcc agt ggg cgg acc act cca gcc cct gtc aat cag aca gat	1315
Lys Val Ala Ser Gly Arg Thr Thr Pro Ala Pro Val Asn Gln Thr Asp	
228 233 238 243	
cgg gaa aag gag aag gcc aaa gcc aag gca gtg gcc ttg gac tca gac	1363
Arg Glu Lys Glu Lys Ala Lys Ala Lys Ala Val Ala Leu Asp Ser Asp	
244 249 254 259	
aac atc tcc ttg aag agt att ggc tcc cca gaa agt act ccc aag aac	1411
Asn Ile Ser Leu Lys Ser Ile Gly Ser Pro Glu Ser Thr Pro Lys Asn	
260 265 270 275	
caa gca agc cac ccc aca gcc acc aag ctg gca gag ctg cca cca acc	1459
Gln Ala Ser His Pro Thr Ala Thr Lys Leu Ala Glu Leu Pro Pro Thr	
276 281 286 291	
cct ctc agg gcc aca gcg aag agc ttt gtc aaa cca ccc tca cta gcc	1507
Pro Leu Arg Ala Thr Ala Lys Ser Phe Val Lys Pro Pro Ser Leu Ala	
292 297 302 307	
aat ctt gac aag gtc aac tcc aac agt ctg gat cta cca tca tcc agt	1555
Asn Leu Asp Lys Val Asn Ser Asn Ser Leu Asp Leu Pro Ser Ser Ser	
308 313 318 323	
gat acc acc cat gct tca aag gtc cca gat ctg cat gct aca agc tca	1603
Asp Thr Thr His Ala Ser Lys Val Pro Asp Leu His Ala Thr Ser Ser	
324 329 334 339	
gca tct ggg ggc cct ctc cct tcc tgc ttc acc ccc agt ccg gca ccc	1651
Ala Ser Gly Gly Pro Leu Pro Ser Cys Phe Thr Pro Ser Pro Ala Pro	
340 345 350 355	
atc ctc aat att aac tca gcc agc ttc tcc cag ggc ctg gag cta atg	1699
Ile Leu Asn Ile Asn Ser Ala Ser Phe Ser Gln Gly Leu Glu Leu Met	
356 361 366 371	
agt ggt ttc agt gtg cca aaa gag acc cgc atg tac ccc aaa ctc tca	1747
Ser Gly Phe Ser Val Pro Lys Glu Thr Arg Met Tyr Pro Lys Leu Ser	

372	377	382	387	
ggc ctg cac agg agc atg gag tcc ctc cag atg cca atg agc ctc ccc				1795
Gly Leu His Arg Ser Met Glu Ser Leu Gln Met Pro Met Ser Leu Pro				
388	393	398	403	
agt gcc ttc ccc agc agt act ccc gtc ccc acc cca cct gct ccc cct				1843
Ser Ala Phe Pro Ser Ser Thr Pro Val Pro Thr Pro Pro Ala Pro Pro				
404	409	414	419	
gct gct ccc aca gaa gaa gag acg gaa gag ctg act tgg agt gga agc				1891
Ala Ala Pro Thr Glu Glu Glu Thr Glu Glu Thr Trp Ser Gly Ser				
420	425	430	435	
ccc aga gct ggg caa ctg gac agt aat cag cgg gat cgg aac act ctt				1939
Pro Arg Ala Gly Gln Leu Asp Ser Asn Gln Arg Asp Arg Asn Thr Leu				
436	441	446	451	
ccc aag aaa ggg ctc agg tac cag ctt cag tcc cag gag gag acc aag				1987
Pro Lys Lys Gly Leu Arg Tyr Gln Leu Gln Ser Gln Glu Glu Thr Lys				
452	457	462	467	
gag agg cga cat tcc cat acc att ggt ggg ctg cct gaa tcc gat gac				2035
Glu Arg Arg His Ser His Thr Ile Gly Gly Leu Pro Glu Ser Asp Asp				
468	473	478	483	
cag tca gag ctg cct tct ccc cct gca ctt ccc atg tct ctg agt gca				2083
Gln Ser Glu Leu Pro Ser Pro Pro Ala Leu Pro Met Ser Leu Ser Ala				
484	489	494	499	
aag ggc caa ctt acc aac ata gtg agt ccc act gcg gcc acc acg cca				2131
Lys Gly Gln Leu Thr Asn Ile Val Ser Pro Thr Ala Ala Thr Thr Pro				
500	505	510	515	
aga atc acc cgc tcc aac agc atc ccc acc cac gag gcg gcc ttc gag				2179
Arg Ile Thr Arg Ser Asn Ser Ile Pro Thr His Glu Ala Ala Phe Glu				
516	521	526	531	
ctg tac agc ggc tcc caa atg ggg agc acc ctg tcc ctg gcc gag aga				2227
Leu Tyr Ser Gly Ser Gln Met Gly Ser Thr Leu Ser Leu Ala Glu Arg				
532	537	542	547	
ccc aag gga atg att cgg tca gga tcc ttc cga gac ccc acg gac gat				2275
Pro Lys Gly Met Ile Arg Ser Gly Ser Phe Arg Asp Pro Thr Asp Asp				
548	553	558	563	
gtt cac ggc tca gtg ctg tcc ctg gcc tcc agt gcc tcc tcc acc tac				2323
Val His Gly Ser Val Leu Ser Leu Ala Ser Ser Ala Ser Ser Thr Tyr				
564	569	574	579	
tcc tca caa atc cgg aag ctt cgt agg gaa ctg gaa tca tcc cag gaa				2371
Ser Ser Gln Ile Arg Lys Leu Arg Arg Glu Leu Glu Ser Ser Gln Glu				
580	585	590	595	
aaa gtg gcc acc ttg acg tct cag ctt tct gcc aat gct aat ctg gtg				2419
Lys Val Ala Thr Leu Thr Ser Gln Leu Ser Ala Asn Ala Asn Leu Val				
596	601	606	611	

ccccctcctg ccagtgcagc gcgagtaaga gcgcccgaagg gaccacagct ggcatcccag	120
gggttaattt cggagcagcc caggtggagg tcgagcccc aaccccgctc gcacctccag	180
gcttccgagg ccaccggaac ggaggagget tcggtggctc tttgtctacc tgctctgggt	240
gttaaagagc ccgctcgcag cctgcatcgc cggggctcgg gacagaagtc agcggcgggg	300
aaatggggct ctgtcacttt aagtacagct ggagccctgg gatgaaagca gctccatcag	360
tagtggactc agcgatgcct cagacaatct cagttcagaa gaattcaatg ccagctcctc	420
actcaactcc ctcccaagta ctcccactgc ttctcgcagg aactcaacaa tagtgctacg	480
cacagactca tagaagcgct cactggcaga aagtgggctg agctgggtta gtgaatcaga	540
ggagaaaagcc cctaaaaaac tggagtacga cagtggtagc ctgaag atg gaa cct	595
Met Glu Pro	
1	
ggg act tct aag tgg cgg agg gag cgg cct gag agc tgt gat gat tca	643
Gly Thr Ser Lys Trp Arg Arg Glu Arg Pro Glu Ser Cys Asp Asp Ser	
4 9 14 19	
tcc aag ggt gga gaa ctg aaa aag ccc atc agc ctg ggc cac cct ggt	691
Ser Lys Gly Gly Glu Leu Lys Lys Pro Ile Ser Leu Gly His Pro Gly	
20 25 30 35	
tcc ctg aag aag ggc aag acc cca cct gtg gct gta act tcc ccc atc	739
Ser Leu Lys Lys Gly Lys Thr Pro Pro Val Ala Val Thr Ser Pro Ile	
36 41 46 51	
act cac aca gcc cag agt gcc ctc aaa gtc gca ggc aaa cct gag ggc	787
Thr His Thr Ala Gln Ser Ala Leu Lys Val Ala Gly Lys Pro Glu Gly	
52 57 62 67	
aaa gct aca gac aag ggt aag ctt gca gtg aag aat act ggg ctc caa	835
Lys Ala Thr Asp Lys Gly Lys Leu Ala Val Lys Asn Thr Gly Leu Gln	
68 73 78 83	
cgc tcc tcc tct gat gct ggt cgg gac cgc ctg agt gat gct aag aag	883
Arg Ser Ser Ser Asp Ala Gly Arg Asp Arg Leu Ser Asp Ala Lys Lys	
84 89 94 99	
ccc ccc tcg ggc att gct cgc ccc tcc act tcg gga tcc ttt ggc tac	931
Pro Pro Ser Gly Ile Ala Arg Pro Ser Thr Ser Gly Ser Phe Gly Tyr	
100 105 110 115	
aag aag cct cct cct gcc aca ggc aca gcc act gtc atg caa act ggt	979
Lys Lys Pro Pro Pro Ala Thr Gly Thr Ala Thr Val Met Gln Thr Gly	
116 121 126 131	
ggt tca gcc act ctc agc aag atc cag aag tcc tca ggc atc cct gtc	1027
Gly Ser Ala Thr Leu Ser Lys Ile Gln Lys Ser Ser Gly Ile Pro Val	
132 137 142 147	
aag cca gta aat ggg cgc aag act agc tta gat gtt tcc aac agt gca	1075

Lys	Pro	Val	Asn	Gly	Arg	Lys	Thr	Ser	Leu	Asp	Val	Ser	Asn	Ser	Ala		
148					153					158					163		
gag	cca	gga	ttc	ctg	gct	cct	gga	gcc	cgt	tct	aac	atc	cag	tac	cgc		1123
Glu	Pro	Gly	Phe	Leu	Ala	Pro	Gly	Ala	Arg	Ser	Asn	Ile	Gln	Tyr	Arg		
164					169					174					179		
agc	ctg	ccc	cgg	cca	gcc	aag	tca	agt	tct	atg	agc	gtg	acc	ggc	ggg		1171
Ser	Leu	Pro	Arg	Pro	Ala	Lys	Ser	Ser	Ser	Met	Ser	Val	Thr	Gly	Gly		
180					185					190					195		
cgg	ggt	gga	cct	cgc	cct	gtg	agc	agc	agc	att	gac	ccc	agt	ctc	ctc		1219
Arg	Gly	Gly	Pro	Arg	Pro	Val	Ser	Ser	Ser	Ile	Asp	Pro	Ser	Leu	Leu		
196					201					206					211		
agc	acc	aag	cag	gga	ggc	ctt	acg	cct	tcc	aga	ctg	aag	gag	cct	acc		1267
Ser	Thr	Lys	Gln	Gly	Gly	Leu	Thr	Pro	Ser	Arg	Leu	Lys	Glu	Pro	Thr		
212					217					222					227		
aag	gta	gcc	agt	ggg	cgg	acc	act	cca	gcc	cct	gtc	aat	cag	aca	gat		1315
Lys	Val	Ala	Ser	Gly	Arg	Thr	Thr	Pro	Ala	Pro	Val	Asn	Gln	Thr	Asp		
228					233					238					243		
cgg	gaa	aag	gag	aag	gcc	aaa	gcc	aag	gca	gtg	gcc	ttg	gac	tca	gac		1363
Arg	Glu	Lys	Glu	Lys	Ala	Lys	Ala	Lys	Ala	Val	Ala	Leu	Asp	Ser	Asp		
244					249					254					259		
aac	atc	tcc	ttg	aag	agt	att	ggc	tcc	cca	gaa	agt	act	ccc	aag	aac		1411
Asn	Ile	Ser	Leu	Lys	Ser	Ile	Gly	Ser	Pro	Glu	Ser	Thr	Pro	Lys	Asn		
260					265					270					275		
caa	gca	agc	cac	ccc	aca	gcc	acc	aag	ctg	gca	gag	ctg	cca	cca	acc		1459
Gln	Ala	Ser	His	Pro	Thr	Ala	Thr	Lys	Leu	Ala	Glu	Leu	Pro	Pro	Thr		
276					281					286					291		
cct	ctc	agg	gcc	aca	gcg	aag	agc	ttt	gtc	aaa	cca	ccc	tca	cta	gcc		1507
Pro	Leu	Arg	Ala	Thr	Ala	Lys	Ser	Phe	Val	Lys	Pro	Pro	Ser	Leu	Ala		
292					297					302					307		
aat	ctt	gac	aag	gtc	aac	tcc	aac	agt	ctg	gat	cta	cca	tca	tcc	agt		1555
Asn	Leu	Asp	Lys	Val	Asn	Ser	Asn	Ser	Leu	Asp	Leu	Pro	Ser	Ser	Ser		
308					313					318					323		
gat	acc	acc	cat	gct	tca	aag	gtc	cca	gat	ctg	cat	gct	aca	agc	tca		1603
Asp	Thr	Thr	His	Ala	Ser	Lys	Val	Pro	Asp	Leu	His	Ala	Thr	Ser	Ser		
324					329					334					339		
gca	tct	ggg	ggc	cct	ctc	cct	tcc	tgc	ttc	acc	ccc	agt	ccg	gca	ccc		1651
Ala	Ser	Gly	Gly	Pro	Leu	Pro	Ser	Cys	Phe	Thr	Pro	Ser	Pro	Ala	Pro		
340					345					350					355		
atc	ctc	aat	att	aac	tca	gcc	agc	ttc	tcc	cag	ggc	ctg	gag	cta	atg		1699
Ile	Leu	Asn	Ile	Asn	Ser	Ala	Ser	Phe	Ser	Gln	Gly	Leu	Glu	Leu	Met		
356					361					366					371		
agt	ggt	ttc	agt	gtg	cca	aaa	gag	acc	cgc	atg	tac	ccc	aaa	ctc	tca		1747
Ser	Gly	Phe	Ser	Val	Pro	Lys	Glu	Thr	Arg	Met	Tyr	Pro	Lys	Leu	Ser		

372	377	382	387	
ggc ctg cac agg agc atg gag tcc ctc cag atg cca atg agc ctc ccc				1795
Gly Leu His Arg Ser Met Glu Ser Leu Gln Met Pro Met Ser Leu Pro				
388	393	398	403	
agt gcc ttc ccc agc agt act ccc gtc ccc acc cca cct gct ccc cct				1843
Ser Ala Phe Pro Ser Ser Thr Pro Val Pro Thr Pro Pro Ala Pro Pro				
404	409	414	419	
gct gct ccc aca gaa gaa gag acg gaa gag ctg act tgg agt gga agc				1891
Ala Ala Pro Thr Glu Glu Glu Thr Glu Glu Leu Thr Trp Ser Gly Ser				
420	425	430	435	
ccc aga gct ggg caa ctg gac agt aat cag cgg gat cgg aac act ctt				1939
Pro Arg Ala Gly Gln Leu Asp Ser Asn Gln Arg Asp Arg Asn Thr Leu				
436	441	446	451	
ccc aag aaa ggg ctc agg tac cag ctt cag tcc cag gag gag acc aag				1987
Pro Lys Lys Gly Leu Arg Tyr Gln Leu Gln Ser Gln Glu Glu Thr Lys				
452	457	462	467	
gag agg cga cat tcc cat acc att ggt ggg ctg cct gaa tcc gat gac				2035
Glu Arg Arg His Ser His Thr Ile Gly Gly Leu Pro Glu Ser Asp Asp				
468	473	478	483	
cag tca gag ctg cct tct ccc cct gca ctt ccc atg tct ctg agt gca				2083
Gln Ser Glu Leu Pro Ser Pro Pro Ala Leu Pro Met Ser Leu Ser Ala				
484	489	494	499	
aag ggc caa ctt acc aac ata gtt cac ggc tca gtg ctg tcc ctg gcc				2131
Lys Gly Gln Leu Thr Asn Ile Val His Gly Ser Val Leu Ser Leu Ala				
500	505	510	515	
tcc agt gcc tcc tcc acc tac tcc tca caa atc cgg aag ctt cgt agg				2179
Ser Ser Ala Ser Ser Thr Tyr Ser Ser Gln Ile Arg Lys Leu Arg Arg				
516	521	526	531	
gaa ctg gaa tca tcc cag gaa aaa gtg gcc acc ttg acg tct cag ctt				2227
Glu Leu Glu Ser Ser Gln Glu Lys Val Ala Thr Leu Thr Ser Gln Leu				
532	537	542	547	
tct gcc aat gct aat ctg gtg gct gct ttt gag cag agc ctg gtg aat				2275
Ser Ala Asn Ala Asn Leu Val Ala Ala Phe Glu Gln Ser Leu Val Asn				
548	553	558	563	
atg aca tcc cgc ctg cga cac ctg gca gag acg gcc gag gag aag gac				2323
Met Thr Ser Arg Leu Arg His Leu Ala Glu Thr Ala Glu Glu Lys Asp				
564	569	574	579	
act gag ctg ctg gat ttg cga gaa acc ata gac ttt ctg aag aaa aag				2371
Thr Glu Leu Leu Asp Leu Arg Glu Thr Ile Asp Phe Leu Lys Lys Lys				
580	585	590	595	
aac tct gag gcc cag gca gtc att cag gga gcc ctt aat gcc tca gaa				2419
Asn Ser Glu Ala Gln Ala Val Ile Gln Gly Ala Leu Asn Ala Ser Glu				
596	601	606	611	

ggagaaagcc cctaaaaaac tggagtacga cagtggtagc ctgaag	atg gaa cct	595
	Met Glu Pro	
	1	
ggg act tct aag tgg cgg agg gag cgg cct gag agc tgt gat gat tca		643
Gly Thr Ser Lys Trp Arg Arg Glu Arg Pro Glu Ser Cys Asp Asp Ser		
4 9 14 19		
tcc aag ggt gga gaa ctg aaa aag ccc atc agc ctg ggc cac cct ggt		691
Ser Lys Gly Gly Glu Leu Lys Lys Pro Ile Ser Leu Gly His Pro Gly		
20 25 30 35		
tcc ctg aag aag ggc aag acc cca cct gtg gct gta act tcc ccc atc		739
Ser Leu Lys Lys Gly Lys Thr Pro Pro Val Ala Val Thr Ser Pro Ile		
36 41 46 51		
act cac aca gcc cag agt gcc ctc aaa gtc gca ggc aaa cct gag ggc		787
Thr His Thr Ala Gln Ser Ala Leu Lys Val Ala Gly Lys Pro Glu Gly		
52 57 62 67		
aaa gct aca gac aag ggt aag ctt gca gtg aag aat act ggg ctc caa		835
Lys Ala Thr Asp Lys Gly Lys Leu Ala Val Lys Asn Thr Gly Leu Gln		
68 73 78 83		
cgc tcc tcc tct gat gct ggt cgg gac cgc ctg agt gat gct aag aag		883
Arg Ser Ser Ser Asp Ala Gly Arg Asp Arg Leu Ser Asp Ala Lys Lys		
84 89 94 99		
ccc ccc tcg ggc att gct cgc ccc tcc act tcg gga tcc ttt ggc tac		931
Pro Pro Ser Gly Ile Ala Arg Pro Ser Thr Ser Gly Ser Phe Gly Tyr		
100 105 110 115		
aag aag cct cct cct gcc aca ggc aca gcc act gtc atg caa act ggt		979
Lys Lys Pro Pro Pro Ala Thr Gly Thr Ala Thr Val Met Gln Thr Gly		
116 121 126 131		
ggt tca gcc act ctc agc aag atc cag aag tcc tca ggc atc cct gtc		1027
Gly Ser Ala Thr Leu Ser Lys Ile Gln Lys Ser Ser Gly Ile Pro Val		
132 137 142 147		
aag cca gta aat ggg cgc aag act agc tta gat gtt tcc aac agt gca		1075
Lys Pro Val Asn Gly Arg Lys Thr Ser Leu Asp Val Ser Asn Ser Ala		
148 153 158 163		
gag cca gga ttc ctg gct cct gga gcc cgt tct aac atc cag tac cgc		1123
Glu Pro Gly Phe Leu Ala Pro Gly Ala Arg Ser Asn Ile Gln Tyr Arg		
164 169 174 179		
agc ctg ccc cgg cca gcc aag tca agt tct atg agc gtg acc ggc ggg		1171
Ser Leu Pro Arg Pro Ala Lys Ser Ser Ser Met Ser Val Thr Gly Gly		
180 185 190 195		
cgg ggt gga cct cgc cct gtg agc agc agc att gac ccc agt ctc ctc		1219
Arg Gly Gly Pro Arg Pro Val Ser Ser Ser Ile Asp Pro Ser Leu Leu		
196 201 206 211		
agc acc aag cag gga ggc ctt acg cct tcc aga ctg aag gag cct acc		1267

Ser Thr Lys Gln Gly Gly Leu Thr Pro Ser Arg Leu Lys Glu Pro Thr	
212 217 222 227	
aag gta gcc agt ggg cgg acc act cca gcc cct gtc aat cag aca gat	1315
Lys Val Ala Ser Gly Arg Thr Thr Pro Ala Pro Val Asn Gln Thr Asp	
228 233 238 243	
cgg gaa aag gag aag gcc aaa gcc aag gca gtg gcc ttg gac tca gac	1363
Arg Glu Lys Glu Lys Ala Lys Ala Lys Ala Val Ala Leu Asp Ser Asp	
244 249 254 259	
aac atc tcc ttg aag agt att ggc tcc cca gaa agt act ccc aag aac	1411
Asn Ile Ser Leu Lys Ser Ile Gly Ser Pro Glu Ser Thr Pro Lys Asn	
260 265 270 275	
caa gca agc cac ccc aca gcc acc aag ctg gca gag ctg cca cca acc	1459
Gln Ala Ser His Pro Thr Ala Thr Lys Leu Ala Glu Leu Pro Pro Thr	
276 281 286 291	
cct ctc agg gcc aca gcg aag agc ttt gtc aaa cca ccc tca cta gcc	1507
Pro Leu Arg Ala Thr Ala Lys Ser Phe Val Lys Pro Pro Ser Leu Ala	
292 297 302 307	
aat ctt gac aag gtc aac tcc aac agt ctg gat cta cca tca tcc agt	1555
Asn Leu Asp Lys Val Asn Ser Asn Ser Leu Asp Leu Pro Ser Ser Ser	
308 313 318 323	
gat acc acc cat gct tca aag gtc cca gat ctg cat gct aca agc tca	1603
Asp Thr Thr His Ala Ser Lys Val Pro Asp Leu His Ala Thr Ser Ser	
324 329 334 339	
gca tct ggg ggc cct ctc cct tcc tgc ttc acc ccc agt ccg gca ccc	1651
Ala Ser Gly Gly Pro Leu Pro Ser Cys Phe Thr Pro Ser Pro Ala Pro	
340 345 350 355	
atc ctc aat att aac tca gcc agc ttc tcc cag ggc ctg gag cta atg	1699
Ile Leu Asn Ile Asn Ser Ala Ser Phe Ser Gln Gly Leu Glu Leu Met	
356 361 366 371	
agt ggt ttc agt gtg cca aaa gag acc cgc atg tac ccc aaa ctc tca	1747
Ser Gly Phe Ser Val Pro Lys Glu Thr Arg Met Tyr Pro Lys Leu Ser	
372 377 382 387	
ggc ctg cac agg agc atg gag tcc ctc cag atg cca atg agc ctc ccc	1795
Gly Leu His Arg Ser Met Glu Ser Leu Gln Met Pro Met Ser Leu Pro	
388 393 398 403	
agt gcc ttc ccc agc agt act ccc gtc ccc acc cca cct gct ccc cct	1843
Ser Ala Phe Pro Ser Ser Thr Pro Val Pro Thr Pro Pro Ala Pro Pro	
404 409 414 419	
gct gct ccc aca gaa gaa gag acg gaa gag ctg act tgg agt gga agc	1891
Ala Ala Pro Thr Glu Glu Glu Thr Glu Glu Leu Thr Trp Ser Gly Ser	
420 425 430 435	
ccc aga gct ggg caa ctg gac agt aat cag cgg gat cgg aac act ctt	1939
Pro Arg Ala Gly Gln Leu Asp Ser Asn Gln Arg Asp Arg Asn Thr Leu	

436	441	446	451	
ccc aag aaa ggg ctc agg tac cag ctt cag tcc cag gag gag acc aag				1987
Pro Lys Lys Gly Leu Arg Tyr Gln Leu Gln Ser Gln Glu Glu Thr Lys				
452	457	462	467	
gag agg cga cat tcc cat acc att ggt ggg ctg cct gaa tcc gat gac				2035
Glu Arg Arg His Ser His Thr Ile Gly Gly Leu Pro Glu Ser Asp Asp				
468	473	478	483	
cag tca gag ctg cct tct ccc cct gca ctt ccc atg tct ctg agt gca				2083
Gln Ser Glu Leu Pro Ser Pro Pro Ala Leu Pro Met Ser Leu Ser Ala				
484	489	494	499	
aag ggc caa ctt acc aac ata gtg agt ccc act gcg gcc acc acg cca				2131
Lys Gly Gln Leu Thr Asn Ile Val Ser Pro Thr Ala Ala Thr Thr Pro				
500	505	510	515	
aga atc acc cgc tcc aac agc atc ccc acc cac gag gcg gcc ttc gag				2179
Arg Ile Thr Arg Ser Asn Ser Ile Pro Thr His Glu Ala Ala Phe Glu				
516	521	526	531	
ctg tac agc ggc tcc caa atg ggg agc acc ctg tcc ctg gcc gag aga				2227
Leu Tyr Ser Gly Ser Gln Met Gly Ser Thr Leu Ser Leu Ala Glu Arg				
532	537	542	547	
ccc aag gga atg att cgg tca gga tcc ttc cga gac ccc acg gac gat				2275
Pro Lys Gly Met Ile Arg Ser Gly Ser Phe Arg Asp Pro Thr Asp Asp				
548	553	558	563	
gtt cac ggc tca gtg ctg tcc ctg gcc tcc agt gcc tcc tcc acc tac				2323
Val His Gly Ser Val Leu Ser Leu Ala Ser Ser Ala Ser Ser Thr Tyr				
564	569	574	579	
tcc tca gct gag gag agg atg caa tct gag caa atc cgg aag ctt cgt				2371
Ser Ser Ala Glu Glu Arg Met Gln Ser Glu Gln Ile Arg Lys Leu Arg				
580	585	590	595	
agg gaa ctg gaa tca tcc cag gaa aaa gtg gcc acc ttg acg tct cag				2419
Arg Glu Leu Glu Ser Ser Gln Glu Lys Val Ala Thr Leu Thr Ser Gln				
596	601	606	611	
ctt tct gcc aat gct aat ctg gtg gct gct ttt gag cag agc ctg gtg				2467
Leu Ser Ala Asn Ala Asn Leu Val Ala Ala Phe Glu Gln Ser Leu Val				
612	617	622	627	
aat atg aca tcc cgc ctg cga cac ctg gca gag acg gcc gag gag aag				2515
Asn Met Thr Ser Arg Leu Arg His Leu Ala Glu Thr Ala Glu Glu Lys				
628	633	638	643	
gac act gag ctg ctg gat ttg cga gaa acc ata gac ttt ctg aag aaa				2563
Asp Thr Glu Leu Leu Asp Leu Arg Glu Thr Ile Asp Phe Leu Lys Lys				
644	649	654	659	
aag aac tct gag gcc cag gca gtc att cag gga gcc ctt aat gcc tca				2611
Lys Asn Ser Glu Ala Gln Ala Val Ile Gln Gly Ala Leu Asn Ala Ser				
660	665	670	675	

gaa acc aca ccc aaa ggt agg aca tcc agc cac aga ttg aga ggg aac 2659
 Glu Thr Thr Pro Lys Gly Arg Thr Ser Ser His Arg Leu Arg Gly Asn
 676 681 686 691
 agg gag cag gaa agt aag agt att aca gat ttt tat ctg ggc cca tag 2707
 Arg Glu Gln Glu Ser Lys Ser Ile Thr Asp Phe Tyr Leu Gly Pro *
 692 697 702 707
 tattccaagt cctatatcaa gtctctagaa ggtgagggcc tttagatacc ctttagtgtg 2767
 atgtctggac tgggtcagtga ggagtaccag gggcatgacc ccagcttcct agggcatgaa 2827
 ggcaagcaga ggagacctgt aagccccagg ggtcctctcc ttaaccttta cctcacggcc 2887
 aaagagccat caaagaccat cgtaaata gccctttaca ttnttatgca aatgtgttgt 2947
 gtgtccacac acacacaaac aatcttattt gatcctcact ttagttctcc aactactctt 3007
 ccaatganac aaccaagct cacatagggt atatggtgct gaaatggcaa gttagcoctg 3067
 ag 3069

<210> 12
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (216)..(2129)

<220>
 <221> misc_feature
 <222> (1)...(2243)
 <223> n = a,t,c or g

<400> 12
 aaggccatta acaatgacac tcgtccctat ttaggtgaca ctatagaaca agtttgtaca 60
 aaaaagcagg ctggtaccgg tccggaattc ctgggatatc gtcgaccac gcgtccgccc 120
 acgcgtccgc ggacgcgtgg gccgccctga agaagctggt ggggtcggac caggccccgg 180
 gccgggacaa gaacatcccc gccgggctgc agtcc atg aac cag gcg ttg cag 233
 Met Asn Gln Ala Leu Gln
 1
 agg cgc ttc gcc aag ggg gtg cag tac aac atg aag ata gtg atc cgg 281
 Arg Arg Phe Ala Lys Gly Val Gln Tyr Asn Met Lys Ile Val Ile Arg
 7 12 17 22
 gga gac agg aac acg ggc aag aca gcg ctg tgg cac cgc ctg cag ggc 329
 Gly Asp Arg Asn Thr Gly Lys Thr Ala Leu Trp His Arg Leu Gln Gly

23	28	33	38	
cgg ccg ttc gtg gag gag tac atc ccc aca cag gag atc cag gtc acc				377
Arg Pro Phe Val Glu Glu Tyr Ile Pro Thr Gln Glu Ile Gln Val Thr				
39	44	49	54	
agc atc cac tgg agc tac aag acc acg gat gac atc gtg aag gtt gaa				425
Ser Ile His Trp Ser Tyr Lys Thr Thr Asp Asp Ile Val Lys Val Glu				
55	60	65	70	
gtc tgg gat gta gta gac aaa gga aaa tgc aaa aag cga ggc gac ggc				473
Val Trp Asp Val Val Asp Lys Gly Lys Cys Lys Lys Arg Gly Asp Gly				
71	76	81	86	
tta aag atg gag aac gac ccc cag gag gcg gag tct gaa atg gcc ctg				521
Leu Lys Met Glu Asn Asp Pro Gln Glu Ala Glu Ser Glu Met Ala Leu				
87	92	97	102	
gat gct gag ttc ctg gac gtg tac aag aac tgc aac ggg gtg gtc atg				569
Asp Ala Glu Phe Leu Asp Val Tyr Lys Asn Cys Asn Gly Val Val Met				
103	108	113	118	
atg ttc gac att acc aag cag tgg acc ttc aat tac att ctc cgg gag				617
Met Phe Asp Ile Thr Lys Gln Trp Thr Phe Asn Tyr Ile Leu Arg Glu				
119	124	129	134	
ctt cca aaa gtg ccc acc cac gtg cca gtg tgc gtg ctg ggg aac tac				665
Leu Pro Lys Val Pro Thr His Val Pro Val Cys Val Leu Gly Asn Tyr				
135	140	145	150	
cgg gac atg ggc gag cac cga gtc atc ctg ccg gac gac gtg cgt gac				713
Arg Asp Met Gly Glu His Arg Val Ile Leu Pro Asp Asp Val Arg Asp				
151	156	161	166	
ttc atc gac aac ctg gac aga cct cca ggt tcc tcc tac ttc cgc tat				761
Phe Ile Asp Asn Leu Asp Arg Pro Pro Gly Ser Ser Tyr Phe Arg Tyr				
167	172	177	182	
gct gag tct tcc atg aag aac agc ttc ggc cta aag tac ctt cat aag				809
Ala Glu Ser Ser Met Lys Asn Ser Phe Gly Leu Lys Tyr Leu His Lys				
183	188	193	198	
ttc ttc aat atc cca ttt ttg cag ott cag agg gag acg ctg ttg cgg				857
Phe Phe Asn Ile Pro Phe Leu Gln Leu Gln Arg Glu Thr Leu Leu Arg				
199	204	209	214	
cag ctg gag acg aac cag ctg gac atg gac gcc acg ctg gag gag ctg				905
Gln Leu Glu Thr Asn Gln Leu Asp Met Asp Ala Thr Leu Glu Glu Leu				
215	220	225	230	
tcg gtg cag cag gag agg gag gac cag aac tac ggc atc ttc ctg gag				953
Ser Val Gln Gln Glu Arg Glu Asp Gln Asn Tyr Gly Ile Phe Leu Glu				
231	236	241	246	
atg atg gag gct cgc agc cgt ggc cat gcg tcc cca ctg gcg gcc aac				1001
Met Met Glu Ala Arg Ser Arg Gly His Ala Ser Pro Leu Ala Ala Asn				
247	252	257	262	

ggg cag agc cca tcc ccg ggc tcc cag tca cca gtg gtg cct gca ggc	1049
Gly Gln Ser Pro Ser Pro Gly Ser Gln Ser Pro Val Val Pro Ala Gly	
263 268 273 278	
gct gtg tcc acg ggg agc tcc agc ccc ggc aca ccc cag ccc gcc cca	1097
Ala Val Ser Thr Gly Ser Ser Ser Pro Gly Thr Pro Gln Pro Ala Pro	
279 284 289 294	
cag ctg ccc ctc aat gct gcc cca cca tcc tct gtg ccc cct gta cca	1145
Gln Leu Pro Leu Asn Ala Ala Pro Pro Ser Ser Val Pro Pro Val Pro	
295 300 305 310	
ccc tca gag gcc ctg ccc cca cct gcg tgc ccc tca gcc ccc gcc cca	1193
Pro Ser Glu Ala Leu Pro Pro Ala Cys Pro Ser Ala Pro Ala Pro	
311 316 321 326	
cgg cgc agc atc atc tct agg ctg ttt ggg acg tca cct gcc acc gag	1241
Arg Arg Ser Ile Ile Ser Arg Leu Phe Gly Thr Ser Pro Ala Thr Glu	
327 332 337 342	
gca gcc cct cca cct cca gag cca gtc ccg gcc gca cag ggc cca gca	1289
Ala Ala Pro Pro Pro Pro Glu Pro Val Pro Ala Ala Gln Gly Pro Ala	
343 348 353 358	
acg gtc cag agt gtg gag gac ttt gtt cct gac gac cgc ctg gac cgc	1337
Thr Val Gln Ser Val Glu Asp Phe Val Pro Asp Asp Arg Leu Asp Arg	
359 364 369 374	
agc ttc ctg gaa gac aca acc ccc gcc agg gac gag aag aag gtg ggg	1385
Ser Phe Leu Glu Asp Thr Thr Pro Ala Arg Asp Glu Lys Lys Val Gly	
375 380 385 390	
gcc aag gct gcc cag cag gac agc gac agt gat ggg gag gcc ctg ggc	1433
Ala Lys Ala Ala Gln Gln Asp Ser Asp Ser Asp Gly Glu Ala Leu Gly	
391 396 401 406	
ggc aac ccg atg gtg gca ggg ttc cag gac gat gtg gac ctc gaa gac	1481
Gly Asn Pro Met Val Ala Gly Phe Gln Asp Asp Val Asp Leu Glu Asp	
407 412 417 422	
cag cca cgt ggg agt ccc ccg ctg cct gca ggc ccc gtc ccc agt caa	1529
Gln Pro Arg Gly Ser Pro Pro Leu Pro Ala Gly Pro Val Pro Ser Gln	
423 428 433 438	
gac atc act ctt tcg agt gag gag gaa gca gaa gtg gca gct ccc aca	1577
Asp Ile Thr Leu Ser Ser Glu Glu Glu Ala Glu Val Ala Ala Pro Thr	
439 444 449 454	
aaa ggc cct gcc cca gct ccc cag cag tgc tca gag cca gag acc aag	1625
Lys Gly Pro Ala Pro Ala Pro Gln Gln Cys Ser Glu Pro Glu Thr Lys	
455 460 465 470	
tgg tcc tcc ata cca gct tcg aag cca cgg agg ggg aca gct ccc acg	1673
Trp Ser Ser Ile Pro Ala Ser Lys Pro Arg Arg Gly Thr Ala Pro Thr	
471 476 481 486	

agg acc gca gca ccc ccc tgg cca ggc ggt gtc tct gtt cgc aca ggt	1721
Arg Thr Ala Ala Pro Pro Trp Pro Gly Gly Val Ser Val Arg Thr Gly	
487 492 497 502	
ccg gag aag cgc agc agc acc agg ccc cct gct gag atg gag ccg ggg	1769
Pro Glu Lys Arg Ser Ser Thr Arg Pro Pro Ala Glu Met Glu Pro Gly	
503 508 513 518	
aag ggt gag cag gcc tcc tcg tcg gag agt gac ccc gag gga ccc att	1817
Lys Gly Glu Gln Ala Ser Ser Ser Glu Ser Asp Pro Glu Gly Pro Ile	
519 524 529 534	
gct gca caa atg ctg tcc ttc gtc atg gat gac ccc gac ttt gag agc	1865
Ala Ala Gln Met Leu Ser Phe Val Met Asp Asp Pro Asp Phe Glu Ser	
535 540 545 550	
gag gga tca gac aca cag cgc agg gcg gat gac ttt ccc gtg cga gat	1913
Glu Gly Ser Asp Thr Gln Arg Arg Ala Asp Asp Phe Pro Val Arg Asp	
551 556 561 566	
gac ccc tcc gat gtg act gac gag gat gag ggc cct gcc gag ccg ccc	1961
Asp Pro Ser Asp Val Thr Asp Glu Asp Glu Gly Pro Ala Glu Pro Pro	
567 572 577 582	
cca ccc ccc aag ctc cct ctc ccc gcc ttc aga ctg aag aat gac tcg	2009
Pro Pro Pro Lys Leu Pro Leu Pro Ala Phe Arg Leu Lys Asn Asp Ser	
583 588 593 598	
gac ctc ttc ggg ctg ggg ctg gag gag gcc gga ccc aag gag agc agt	2057
Asp Leu Phe Gly Leu Gly Leu Glu Glu Ala Gly Pro Lys Glu Ser Ser	
599 604 609 614	
gag gaa ggt aag gag ggc aaa acc ccc tct aag gag aag aag aaa aaa	2105
Glu Glu Gly Lys Glu Gly Lys Thr Pro Ser Lys Glu Lys Lys Lys Lys	
615 620 625 630	
aaa aaa aaa ggg cgg ccg ctc tag agtatccctc gaggggccca agcttacgcg	2159
Lys Lys Lys Gly Arg Pro Leu *	
631 636	
taccagcgtt tcttgtacaa agtggtccct atagtgagtc gtatataagc tagggactgg	2219
tcgagtgtaa tcaatnttac accc	2243

<210> 13
 <211> 2042
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (141)..(1646)

<400> 13

attgtgcct gtcgattcgg caccaggcga cagcaatccc gccccggcct gtcgggagcg 60

gtggggcaga ggctgaggag cccaggagg atctgcctcc gctttcacag tcctccagat 120

ttttccaaga gcagcagaaa atg aat aaa tcc ctg ggg cca gtg tca ttc 170
Met Asn Lys Ser Leu Gly Pro Val Ser Phe
1 5

aag gac gtg gct gtg gac ttc acc cag gag gaa tgg cag cag ctg gat 218
Lys Asp Val Ala Val Asp Phe Thr Gln Glu Glu Trp Gln Gln Leu Asp
11 16 21 26

cct gag cag aag ata act tac agg gat gtg atg ctg gag aac tac agc 266
Pro Glu Gln Lys Ile Thr Tyr Arg Asp Val Met Leu Glu Asn Tyr Ser
27 32 37 42

aat cta gtt tct gtg ggg tat cac att atc aaa ccg gat gtt atc agc 314
Asn Leu Val Ser Val Gly Tyr His Ile Ile Lys Pro Asp Val Ile Ser
43 48 53 58

aag ttg gag caa gga gaa gag cca tgg ata gta gaa gga gaa ttc cta 362
Lys Leu Glu Gln Gly Glu Glu Pro Trp Ile Val Glu Gly Glu Phe Leu
59 64 69 74

ctt cag agc tat cca gat gaa gtc tgg caa act gat gac cta ata gag 410
Leu Gln Ser Tyr Pro Asp Glu Val Trp Gln Thr Asp Asp Leu Ile Glu
75 80 85 90

aga atc cag gaa gag gaa aat aaa cct tca agg caa act gtg ttc att 458
Arg Ile Gln Glu Glu Glu Asn Lys Pro Ser Arg Gln Thr Val Phe Ile
91 96 101 106

gag acc ctg att gaa gag aga ggt aat gtt cct ggt aaa act ttt gat 506
Glu Thr Leu Ile Glu Glu Arg Gly Asn Val Pro Gly Lys Thr Phe Asp
107 112 117 122

gta gaa acg aac cct gtt cct tca aga aaa ata gcc tat aaa aat agc 554
Val Glu Thr Asn Pro Val Pro Ser Arg Lys Ile Ala Tyr Lys Asn Ser
123 128 133 138

ctc tgt gac tca tgt gaa aag tgt tta acg tct gtt tca gaa tat att 602
Leu Cys Asp Ser Cys Glu Lys Cys Leu Thr Ser Val Ser Glu Tyr Ile
139 144 149 154

agt agt gat gga agc tat gca aga atg aaa gct gat gaa tgt agt gga 650
Ser Ser Asp Gly Ser Tyr Ala Arg Met Lys Ala Asp Glu Cys Ser Gly
155 160 165 170

tgt ggg aaa tca ctc ctc cat att aag ctt gag aaa act cat cca gga 698
Cys Gly Lys Ser Leu Leu His Ile Lys Leu Glu Lys Thr His Pro Gly
171 176 181 186

gat caa gct tat gaa ttt aat caa aat ggg gaa cct tat act cta aat 746
Asp Gln Ala Tyr Glu Phe Asn Gln Asn Gly Glu Pro Tyr Thr Leu Asn
187 192 197 202

gaa gaa agt ctt tat cag aaa att cgt att ttg gag aaa cct ttt gaa 794

Glu Glu Ser Leu Tyr Gln Lys Ile Arg Ile Leu Glu Lys Pro Phe Glu	
203 208 213 218	
tat att gaa tgc cag aaa gcc ttc caa aag gac act gtt ttt gtt aat	842
Tyr Ile Glu Cys Gln Lys Ala Phe Gln Lys Asp Thr Val Phe Val Asn	
219 224 229 234	
cac atg gaa gaa aag ccc tat aag tgg aat gga tct gaa ata gcc ttt	890
His Met Glu Glu Lys Pro Tyr Lys Trp Asn Gly Ser Glu Ile Ala Phe	
235 240 245 250	
ctc cag atg tgc gac ctc act gta cat cag aca tct cat atg gaa atg	938
Leu Gln Met Ser Asp Leu Thr Val His Gln Thr Ser His Met Glu Met	
251 256 261 266	
aag ccc tat gaa tgc agt gaa tgt ggg aaa tcc ttc tgt aaa aag tca	986
Lys Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ser Phe Cys Lys Lys Ser	
267 272 277 282	
aaa ttt att ata cat cag agg act cac aca gga gag aaa cct tac gaa	1034
Lys Phe Ile Ile His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu	
283 288 293 298	
tgt aat cag tgt ggg aaa tcc ttc tgc cag aag gga acc ctt act gtg	1082
Cys Asn Gln Cys Gly Lys Ser Phe Cys Gln Lys Gly Thr Leu Thr Val	
299 304 309 314	
cat cag aga aca cac aca ggg gag aag ccc tat gaa tgt aat gaa tgt	1130
His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys	
315 320 325 330	
ggg aag aac ttt tac cag aag tta cac ctc att cag cat cag aga act	1178
Gly Lys Asn Phe Tyr Gln Lys Leu His Leu Ile Gln His Gln Arg Thr	
331 336 341 346	
cac tca gga gag aag ccc tat gaa tgt agt tat tgt gga aaa tcc ttt	1226
His Ser Gly Glu Lys Pro Tyr Glu Cys Ser Tyr Cys Gly Lys Ser Phe	
347 352 357 362	
tgc cag aag aca cac ctc aca caa cat cag aga aca cat tca gga gag	1274
Cys Gln Lys Thr His Leu Thr Gln His Gln Arg Thr His Ser Gly Glu	
363 368 373 378	
aga cct tat gtt tgt cat gac tgt ggg aaa acc ttc tgc cag aag tca	1322
Arg Pro Tyr Val Cys His Asp Cys Gly Lys Thr Phe Ser Gln Lys Ser	
379 384 389 394	
gca ctt aat gac cat cag aaa att cac aca ggt gtg aaa ctc tac aag	1370
Ala Leu Asn Asp His Gln Lys Ile His Thr Gly Val Lys Leu Tyr Lys	
395 400 405 410	
tgt agt gaa tgt ggg aaa tgc ttc tgc cgc aag tct act ctc acg acc	1418
Cys Ser Glu Cys Gly Lys Cys Phe Cys Arg Lys Ser Thr Leu Thr Thr	
411 416 421 426	
cac ctg agg acc cac aca gga gag aaa ccg tat gaa tgt aat gag tgt	1466
His Leu Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys	

427	432	437	442	
gga aaa gcc ttc tct cgg atg tca tac ctc act gta cat tat aga act				1514
Gly Lys Ala Phe Ser Arg Met Ser Tyr Leu Thr Val His Tyr Arg Thr				
443	448	453	458	
cat tca gga gag aaa ccc tat gag tgt act gaa tgt gga aaa aaa ttc				1562
His Ser Gly Glu Lys Pro Tyr Glu Cys Thr Glu Cys Gly Lys Lys Phe				
459	464	469	474	
tac cac aaa tca gca ttc aac agc cat cag aga att cat agg aga ggc				1610
Tyr His Lys Ser Ala Phe Asn Ser His Gln Arg Ile His Arg Arg Gly				
475	480	485	490	
aat atg aat gta ata gat gtg gga agg ctt ctc tga agtc agacctcatt				1660
Asn Met Asn Val Ile Asp Val Gly Arg Leu Leu *				
491	496	501		
ttatatcaga gaaccctttc agtatagtga atcagaaaact cctgcctgaa gtcaaacacc				1720
ttgtacatca gagagttcac acaggttagt gtggacatcc ccttgtgtgt tggactcata				1780
atctgaagac tcacagaatg gaaaccatga ttataacaag accacatggt ataacaatac				1840
tagactatag acaagtaaaa atttataaat attaagaaatg tatatacatg tcaccatgga				1900
ttggaactgt tttgcatatc agggaaatca tagccaaggg gaaatctatc agtataagga				1960
atgtggaaga cataatcctt tggaaactgt taataactaaa agatatgttt ctgatacaat				2020
agcaaaacttg aaaaaaaaaa aa				2042

<210> 14
 <211> 1392
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (164)..(520)

<400> 14	
caggagggtg taggaataga ccatgggatc tccgcctatt taggtgacac tatagaacaa	60
gtttgtacaa aaaagcaggc tggatccggt ccggaattcc cgggatatcg tcgacccacg	120
cgtcgggtcg tcgacgctgg gctttcgggt cccgcgccca gag atg ggc tcc aag	175
	Met Gly Ser Lys
	1

gca aag aag cgc gtg ctg ctg ccc acc cgc cca gcg ccc ccc acg' gtg	223
Ala Lys Lys Arg Val Leu Leu Pro Thr Arg Pro Ala Pro Pro Thr Val	
5 10 15 20	

gag cag atc ctg gag gat gtg cgg ggt gcg ccg gca gag gat cca gtg	271
Glu Gln Ile Leu Glu Asp Val Arg Gly Ala Pro Ala Glu Asp Pro Val	
21 26 31 36	
ttc acc atc ctg gcc ccg gaa gac ccc cca gtt ccc ttc agg atg atg	319
Phe Thr Ile Leu Ala Pro Glu Asp Pro Pro Val Pro Phe Arg Met Met	
37 42 47 52	
gag gat gcg gag gcc ccg gga gag cag ctc tac cag caa agc cgg gcc	367
Glu Asp Ala Glu Ala Pro Gly Glu Gln Leu Tyr Gln Gln Ser Arg Ala	
53 58 63 68	
tac gtg gct gcc aac cag cgg ctg cag cag gcg ggc aac gtg ctg agg	415
Tyr Val Ala Ala Asn Gln Arg Leu Gln Gln Ala Gly Asn Val Leu Arg	
69 74 79 84	
cag agg tgt gag ctc ctg cag cga gcc ggc gag gac ctg gag cgg gag	463
Gln Arg Cys Glu Leu Leu Gln Arg Ala Gly Glu Asp Leu Glu Arg Glu	
85 90 95 100	
gtg gcc cag atg aag cag gca gca tta ccg gca gcc gag gct gcc tcc	511
Val Ala Gln Met Lys Gln Ala Ala Leu Pro Ala Ala Glu Ala Ala Ser	
101 106 111 116	
tca ggc tga cctctcg gggcctgcag gcttgggcag cgcacaaggt ggcctgcacc	567
Ser Gly *	
117	
caggetttcc ctgggggtcc gtgcggccca gactggcatt cacgggggtcc cagcccacgt	627
gggtgttgac acaggcgccc ctccctgatgc tggggctgcg gttcatccgt cgtctcattc	687
atgccgagtt ggtgggaccc acccagctgg ctccgtcctg cgtgacctga gggccccact	747
ggggttcttg aagaggatag ggacattatt gctgtactgt gattctgtcg tcagctcaca	807
gtggccgtgc tctgcagtgg ggccccctggg agcagggtgcc acctccttcc tctcccgggg	867
caggcactcg cctgtccact totgagtcca ggtgttggga tcgaggtggt aactgtgatt	927
ccatccagcg agtggccacc caatgtcaga gcagcccgag ggccagcctg agcccctgac	987
cccacttctt tctgggcccc gggctcctcc cacaagccac gttgatcttc acaacgaccc	1047
tgggcccgtg gggtcaccca agagaagcag ccctgagacc cagccaggct gggcctagct	1107
ccacggcacg ggtgtctccc agccactgcc cttgctggag gaccgctgtg agtcactggc	1167
caggagccca ggggtgtcctg agtctcatag ccacctgcc agctgcagca ggtcctgggc	1227
ctgcttccct gcgggttctg gccctggggg agggggcggt agtgccggcg aggggtcttg	1287
caaaggcctt tcatcctaaa tagcaacttg agtggaaacc tgggcaaggc ggcccagagg	1347
ctggggccctg cacataaagc tttcgtgtgt gtcaaaaaaa aaaaa	1392

<210> 15
 <211> 2242
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (156)..(1649)

<400> 15

ctgcaggtac cgctccggaa ttcccgggtc gacgatttcg tgcgggtgggg acgcgctgtg	60
ttctcgcagc tcagaggcgg gtctgaggct cgggtggcggc gcccaggggtg gcccgggccc	120
tttcctcggt cgttgtotca ccgccacagg ctccg atg gcg gcg gcc gcc ctg	173
Met Ala Ala Ala Ala Leu	
1	
agg gac ccc gct cag ggc tat gtg acc ttt gag gat gtg gct gtc tac	221
Arg Asp Pro Ala Gln Gly Tyr Val Thr Phe Glu Asp Val Ala Val Tyr	
7 12 17 22	
ttc tcc cag gag gaa tgg aga ttg ctt gat gac gct cag agg ctc ctc	269
Phe Ser Gln Glu Glu Trp Arg Leu Leu Asp Asp Ala Gln Arg Leu Leu	
23 28 33 38	
tac cgc aat gtg atg ctg gag aac ttt aca ctt ctg gcc tct ctg gga	317
Tyr Arg Asn Val Met Leu Glu Asn Phe Thr Leu Leu Ala Ser Leu Gly	
39 44 49 54	
ctt gcg tct tcc aag acc cat gaa ata acc cag ctg gag tca tgg gag	365
Leu Ala Ser Ser Lys Thr His Glu Ile Thr Gln Leu Glu Ser Trp Glu	
55 60 65 70	
gag ccc ttc atg cct gct tgg gaa gtt gtg act tca gcc ata ccg aga	413
Glu Pro Phe Met Pro Ala Trp Glu Val Val Thr Ser Ala Ile Pro Arg	
71 76 81 86	
ggg tgt tgg cat gga gcc gag gct gag gag gct cct gag cag att gct	461
Gly Cys Trp His Gly Ala Glu Ala Glu Glu Ala Pro Glu Gln Ile Ala	
87 92 97 102	
tct gta gga ctg ctc agt tca aac att cag caa cac cag aag cag cac	509
Ser Val Gly Leu Leu Ser Ser Asn Ile Gln Gln His Gln Lys Gln His	
103 108 113 118	
tgt gga gag aaa ccc tta aaa aga caa cag ggc agg gtc cca gtt ttg	557
Cys Gly Glu Lys Pro Leu Lys Arg Gln Gln Gly Arg Val Pro Val Leu	
119 124 129 134	
agg agt tgc aaa gtt cac cta tca gag aag tcc ttg caa agc agg gag	605
Arg Ser Cys Lys Val His Leu Ser Glu Lys Ser Leu Gln Ser Arg Glu	
135 140 145 150	
gtt ggg aag gcc ctc ctg atc agc tca ggt gtt ctc aag cac cag gtg	653

Val	Gly	Lys	Ala	Leu	Leu	Ile	Ser	Ser	Gly	Val	Leu	Lys	His	Gln	Val	
151					156					161					166	
act	cac	aca	gga	gag	aag	tca	cat	agg	agc	tcc	aaa	agt	agg	gag	gcc	701
Thr	His	Thr	Gly	Glu	Lys	Ser	His	Arg	Ser	Ser	Lys	Ser	Arg	Glu	Ala	
167					172					177					182	
ttt	cat	gct	gga	aaa	agg	cat	tac	aaa	tgc	agt	gaa	tgt	ggg	aaa	gcc	749
Phe	His	Ala	Gly	Lys	Arg	His	Tyr	Lys	Cys	Ser	Glu	Cys	Gly	Lys	Ala	
183					188					193					198	
ttt	ggt	cag	aaa	tat	tta	ctt	gtt	cag	cac	cag	aga	cta	cat	gct	ggg	797
Phe	Gly	Gln	Lys	Tyr	Leu	Leu	Val	Gln	His	Gln	Arg	Leu	His	Ala	Gly	
199					204					209					214	
aaa	aag	acg	tat	gaa	tgc	agt	gaa	tgt	ggg	aag	tta	ttt	aga	gat	atg	845
Lys	Lys	Thr	Tyr	Glu	Cys	Ser	Glu	Cys	Gly	Lys	Leu	Phe	Arg	Asp	Met	
215					220					225					230	
tcc	aac	ctt	ttt	ata	cac	caa	ata	gtt	cac	act	gga	gaa	agg	cct	tac	893
Ser	Asn	Leu	Phe	Ile	His	Gln	Ile	Val	His	Thr	Gly	Glu	Arg	Pro	Tyr	
231					236					241					246	
ggg	tgt	agt	aac	tgt	gga	aaa	tcc	ttt	agc	cgt	aat	gct	cac	ctc	att	941
Gly	Cys	Ser	Asn	Cys	Gly	Lys	Ser	Phe	Ser	Arg	Asn	Ala	His	Leu	Ile	
247					252					257					262	
gaa	cac	cag	aga	gtt	cac	act	gga	gaa	aag	cct	ttt	aca	tgc	agt	gaa	989
Glu	His	Gln	Arg	Val	His	Thr	Gly	Glu	Lys	Pro	Phe	Thr	Cys	Ser	Glu	
263					268					273					278	
tgt	gga	aaa	gct	ttc	agg	cat	aat	tcc	aca	ctt	gtt	cag	cat	cac	aaa	1037
Cys	Gly	Lys	Ala	Phe	Arg	His	Asn	Ser	Thr	Leu	Val	Gln	His	His	Lys	
279					284					289					294	
atc	cac	act	gga	gta	agg	cct	tat	gag	tgc	agt	gaa	tgt	gga	aaa	ttg	1085
Ile	His	Thr	Gly	Val	Arg	Pro	Tyr	Glu	Cys	Ser	Glu	Cys	Gly	Lys	Leu	
295					300					305					310	
ttt	agt	ttc	aac	tcc	agc	ctc	atg	aaa	cat	cag	aga	att	cac	act	gga	1133
Phe	Ser	Phe	Asn	Ser	Ser	Leu	Met	Lys	His	Gln	Arg	Ile	His	Thr	Gly	
311					316					321					326	
gaa	aga	cct	tat	aag	tgc	agt	gaa	tgt	gga	aaa	ttc	tat	agc	cac	aag	1181
Glu	Arg	Pro	Tyr	Lys	Cys	Ser	Glu	Cys	Gly	Lys	Phe	Tyr	Ser	His	Lys	
327					332					337					342	
tcc	aac	ctt	atc	aaa	cat	tgg	cgt	gtt	cat	act	gga	gaa	agg	cct	tac	1229
Ser	Asn	Leu	Ile	Lys	His	Trp	Arg	Val	His	Thr	Gly	Glu	Arg	Pro	Tyr	
343					348					353					358	
aag	tgc	agc	gac	tgt	ggg	aaa	ttt	ttt	acc	caa	tgc	tca	agc	ctc	atg	1277
Lys	Cys	Ser	Asp	Cys	Gly	Lys	Phe	Phe	Thr	Gln	Cys	Ser	Ser	Leu	Met	
359					364					369					374	
caa	cat	caa	aaa	gtt	cac	act	gga	gaa	aag	cct	ttt	aag	tgc	aat	gaa	1325
Gln	His	Gln	Lys	Val	His	Thr	Gly	Glu	Lys	Pro	Phe	Lys	Cys	Asn	Glu	

375	380	385	390	
tgt ggg aga ttc ttt aga gag aat tcc acc cta gtt aga cat cag agg				1373
Cys Gly Arg Phe Phe Arg Glu Asn Ser Thr Leu Val Arg His Gln Arg				
391	396	401	406	
gtt cac act gga gca aag cct tat gag tgc agg gaa tgt ggg aaa ttt				1421
Val His Thr Gly Ala Lys Pro Tyr Glu Cys Arg Glu Cys Gly Lys Phe				
407	412	417	422	
ttt agc caa agc tca acc ctc atg caa cat cga aaa gtt cac att gga				1469
Phe Ser Gln Ser Ser Thr Leu Met Gln His Arg Lys Val His Ile Gly				
423	428	433	438	
gaa aag cct ttt aag tgc aat gaa tgt ggg aga ttg ttt aga gag aat				1517
Glu Lys Pro Phe Lys Cys Asn Glu Cys Gly Arg Leu Phe Arg Glu Asn				
439	444	449	454	
tcc agc ctt gtt aaa cat cag agg gtt cac act gga gca aag cct tat				1565
Ser Ser Leu Val Lys His Gln Arg Val His Thr Gly Ala Lys Pro Tyr				
455	460	465	470	
gag tgc agg gaa tgt ggg aag ttt ttt cgc cac aac tcc agt ctt ttt				1613
Glu Cys Arg Glu Cys Gly Lys Phe Phe Arg His Asn Ser Ser Leu Phe				
471	476	481	486	
aaa cat cga agg att cac act gga gaa atg cag tga ttgt gtgaaatcct				1663
Lys His Arg Arg Ile His Thr Gly Glu Met Gln *				
487	492	497		
ttagccagcg tttcaacctc attcaacacc agaaagtcca cagtggaaaa aatcttgaag				1723
gtaacagatg gaaatccgtt agccacacct ccagtctcat tcaacactgg acagtttaca				1783
atgtggacaa tgtagtgaat atggaaaaag gtttcagcca aaggcctaac cctattcaac				1843
accagaaagt ttagaatgga gaaaggcctt agggtgacag gttatgtact gtctctgaat				1903
caatatgacc tcacttaaaa cagaaactct gaggatggcc tttatgaggg agctggcaat				1963
tgaacatcat tcatctaaat atgcacactg gaggcaagat gagaattcct gacagattgt				2023
ccttcttgag aagacagccc tctgccttgg agctccagag agagggagcc ctgtattctt				2083
ggctgtaccc gtcgaatgga gttttgatct cgctgagttt ggagttgggg gaggaaagga				2143
gtggtcttgg ttcaaagtgt actcactttt gctgttcttg tgaatgttag atcttcttta				2203
ataaatatattt atttcccata cacccttaaa aaaaaaaaaa				2242

<210> 16
 <211> 753
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (258)..(593)

<400> 16

```

aactgagttg cctatgtata tacctatcta ttcgatgatg aagatacccc accaaaccca      60
aaaaaagaga tctctcgagg atccgaattc gcggcgcggt cgaccggggt ttcccatgt      120
tggccaggat ggtctcgctc tcctgacctt gtaatccgcc tgccctcggtc tccaaggtg      180
ctggaattac aggcttgagc caccatgccc ccaagtgttt tcatccagtg atcaggactg      240
aacacagagg actcacc      atg gag ttt ggg ctg agc tgg ctt ttc ctt gct      290
                        Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Ala
                        1              5

gct ttt ttt aaa ggt gtt cag tgc gag gtg cag ctg gtg gag tct ggg      338
Ala Phe Phe Lys Gly Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly
12              17              22              27

ggg ggc ttg gtt aag gcg ggg ggg tcc cta aga ctc tcc tgt gca gcg      386
Gly Gly Leu Val Lys Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
28              33              38              43

tct gga ttc agg tcc act tct gcc tcg atg agc tgg gtc cgc caa cgt      434
Ser Gly Phe Arg Ser Thr Ser Ala Ser Met Ser Trp Val Arg Gln Arg
44              49              54              59

cca ggg aag ggg ctg gag tgg ctt ggc cat att aaa agt aaa gat gac      482
Pro Gly Lys Gly Leu Glu Trp Leu Gly His Ile Lys Ser Lys Asp Asp
60              65              70              75

gat ggg acg aca gac tac gct gca ccc gtg aaa ggc aga ttc acc atc      530
Asp Gly Thr Thr Asp Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile
76              81              86              91

tca aga gat gat tcg gaa aac acg ggt cga cgc ggc cgc gaa ttc cag      578
Ser Arg Asp Asp Ser Glu Asn Thr Gly Arg Arg Gly Arg Glu Phe Gln
92              97              102              107

atc tat gaa tcg tag atactgaaaa accccgcaag ttcaattcaa ctgtgcatcg      633
Ile Tyr Glu Ser *
108

tgcaccatct caatttcttt catttataca tcgttttgcc ttcttttatg taactatact      693

cctctaagtt tcaatcttgg ccatgtaacc tctgatctat agaatttttt aaatgactag      753

```

<210> 17
 <211> 2097
 <212> DNA
 <213> Homo sapiens

<222> (141) .. (1757)

agcagcggtg gccggctagg atg ggc tgt ctc tgg ggt ctg gct ctg ccc 170
Met Gly Cys Leu Trp Gly Leu Ala Leu Pro
 1 5

ctt ttc ttc ttc tgc tgg gag gtt ggg gtc tct ggg agc tct gca ggc 218
Leu Phe Phe Phe Cys Trp Glu Val Gly Val Ser Gly Ser Ser Ala Gly
11 16 21 26

ccc agc acc cgc aga gca gac act gcg atg aca acg gac gac aca gaa 266
Pro Ser Thr Arg Arg Ala Asp Thr Ala Met Thr Thr Asp Asp Thr Glu
27 32 37 42

gtg	ccc	gct	atg	act	cta	gca	ccg	ggc	cac	gcc	gct	ctg	gaa	act	caa	314
Val	Pro	Ala	Met	Thr	Leu	Ala	Pro	Gly	His	Ala	Ala	Leu	Glu	Thr	Gln	
43					48					53					58	

acg ctg agc gct gag acc tct tct agg gcc tca acc cca gcc ggc ccc 362
Thr Leu Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro
59 64 69 74

att cca gaa gca gag acc agg gga gcc aag aga att tcc cct gca aga 410
Ile Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg
75 80 85 90

gag acc agg agt ttc aca aaa aca tct ccc aac ttc atg gtg ctg atc 458
Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met Val Leu Ile
91 96 101 106

gcc acc tcc gtg gag aca tca gcc gcc agt ggc agc ccc gag gga gct 506
Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro Glu Gly Ala
107 112 117 122

gga atg acc aca gtt cag acc atc aca ggc agt gat ccc gag gaa gcc 554
Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro Glu Glu Ala
123 128 133 138

atc ttt gac acc ctt tgc acc gat gac agc tct gaa gag gca aag aca 602
Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu Glu Ala Lys Thr
139 144 149 154

ctc aca atg gac ata ttg aca ttg gct cac acc tcc aca gaa gct aag 650
Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr Ser Thr Glu Ala Lys
155 160 165 170

ggc ctg tcc tca gag agc agt gcc tct tcc gac ggc ccc cat cca gtc 698
Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val
171 176 181 186

atc acc ccg tca cgg gcc tca gag agc agc gcc tct tcc gac ggc ccc	746
Ile Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro	
187 192 197 202	
cat cca gtc atc acc ccg tca cgg gcc tca gag agc agc gcc tct tcc	794
His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser	
203 208 213 218	
gac ggc ccc cat cca gtc atc acc ccc tca tgg tcc ccg gga tct gat	842
Asp Gly Pro His Pro Val Ile Thr Pro Ser Trp Ser Pro Gly Ser Asp	
219 224 229 234	
gtc act ctc ctc gct gaa gcc ctg gtg act gtc acc aac atc gag gtt	890
Val Thr Leu Leu Ala Glu Ala Leu Val Thr Val Thr Asn Ile Glu Val	
235 240 245 250	
att aat tgc agc atc acc gaa ata gaa acc acc act tcc agc atc cct	938
Ile Asn Cys Ser Ile Thr Glu Ile Glu Thr Thr Thr Ser Ser Ile Pro	
251 256 261 266	
ggg gcc tca gac ata gat ctc atc ccc acg gaa ggg gtg aag gcc tcg	986
Gly Ala Ser Asp Ile Asp Leu Ile Pro Thr Glu Gly Val Lys Ala Ser	
267 272 277 282	
tcc acc tcc gat cca cca gct ctg cct gac tcc act gaa gca aaa cca	1034
Ser Thr Ser Asp Pro Pro Ala Leu Pro Asp Ser Thr Glu Ala Lys Pro	
283 288 293 298	
cac atc act gag gtc acc gcc tct gcc gag acc ctg tcc acc gcc ggc	1082
His Ile Thr Glu Val Thr Ala Ser Ala Glu Thr Leu Ser Thr Ala Gly	
299 304 309 314	
acc acc gag tca gct gca cct gat gcc acg gtt ggg acc cca ctc ccc	1130
Thr Thr Glu Ser Ala Ala Pro Asp Ala Thr Val Gly Thr Pro Leu Pro	
315 320 325 330	
act aac agc gcc acc gaa aga gaa gtg acc gca ccc ggg gcc acg acc	1178
Thr Asn Ser Ala Thr Glu Arg Glu Val Thr Ala Pro Gly Ala Thr Thr	
331 336 341 346	
ctc agt gga gct ctg gtc acc gtt agc agg aat ccc ctg gaa gaa acc	1226
Leu Ser Gly Ala Leu Val Thr Val Ser Arg Asn Pro Leu Glu Glu Thr	
347 352 357 362	
tca gcc ctc tct gtt gag acc cca agt tac gtc aaa gtc tca gga gca	1274
Ser Ala Leu Ser Val Glu Thr Pro Ser Tyr Val Lys Val Ser Gly Ala	
363 368 373 378	
gct ccg gtc tcc ata gag gct ggg tca gca gtg ggc aaa acc act tcc	1322
Ala Pro Val Ser Ile Glu Ala Gly Ser Ala Val Gly Lys Thr Thr Ser	
379 384 389 394	
ttt gct ggg agc tct gct tcc tcc tac agc ccc tcg gaa gcc gcc ctc	1370
Phe Ala Gly Ser Ser Ala Ser Ser Tyr Ser Pro Ser Glu Ala Ala Leu	
395 400 405 410	

aag aac ttc acc cct tca gag aca ctg acc atg gac atc caa cca agg	1418
Lys Asn Phe Thr Pro Ser Glu Thr Leu Thr Met Asp Ile Gln Pro Arg	
411 416 421 426	
ggg ccc ttc ccc acc agc agg gac cct ctt ctt tct gtc cct ccg act	1466
Gly Pro Phe Pro Thr Ser Arg Asp Pro Leu Leu Ser Val Pro Pro Thr	
427 432 437 442	
aca acc aac agc agc cga ggg acg aac agc act tta gcc aag atc aca	1514
Thr Thr Asn Ser Ser Arg Gly Thr Asn Ser Thr Leu Ala Lys Ile Thr	
443 448 453 458	
acc tca gcg aag acc acg atg aag ccc cca aca gcc acg ccc acg act	1562
Thr Ser Ala Lys Thr Thr Met Lys Pro Pro Thr Ala Thr Pro Thr Thr	
459 464 469 474	
gcc cgg acg agg ccg acc aca gac gtg agt gca ggt gaa aat gga ggt	1610
Ala Arg Thr Arg Pro Thr Thr Asp Val Ser Ala Gly Glu Asn Gly Gly	
475 480 485 490	
ttc ctc ctc ctg cgg ctg agt gtg gct tcc ccg gaa gac ctc act gac	1658
Phe Leu Leu Leu Arg Leu Ser Val Ala Ser Pro Glu Asp Leu Thr Asp	
491 496 501 506	
ccc aga gtg gca gaa agg ctg atg cag cag ctc cac cgg gaa ctc cac	1706
Pro Arg Val Ala Glu Arg Leu Met Gln Gln His Arg Glu Leu His	
507 512 517 522	
gcc cac gcg cct cac ttc cag gtc tcc tta ctg cgt gtc agg aga ggc	1754
Ala His Ala Pro His Phe Gln Val Ser Leu Leu Arg Val Arg Arg Gly	
523 528 533 538	
taa cgga catcagctgc agccaggcat gtcccgtatg ccaaaagagg gtgctgcccc	1811
*	
539	
tagcctgggc cccaccgac agactgcagc tgcgttactg tgctgagagg taccagaag	1871
gttcccatga agggcagcat gtccaagccc ctgaccccag atgtggcaac aggaccctcg	1931
ctcacatcca ccggagtgtg tgtgtgggga ggggcttcac ctgttcccag aggtgtcctt	1991
ggactcacct tggcacatgt tctgtgtttc agtaaagaga gacctgatca cccatctgtg	2051
tgtttccatc ctgcattaaa attcactcag tgtgaaaaaa aaaaaa	2097

<210> 18
 <211> 2743
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (719)..(1909)

<400> 18
 aagctcgtac gcctgcaggt accggtccgg aattccccggg tcgactacta ctactaaatt 60
 cgcgggccgcg tcgaccgtgc tttcccattt tgcacagcga ctgtttgatg acgtcccgcga 120
 ggtccggcggg gcggtggcct ccgtgggtggg cggctggctg ctgtgtctgc gtgaccgtta 180
 ctcctttcttc cacaagctca tccctctgct gctcagtagc ctcaacgacg aggtgcctga 240
 ggtcaggcag ctggctgccg gcctctggga ggacgttggc ctgcagtggc agaaggagaa 300
 tgaggaggac ctgaaggaca agctggactt tgccccctcc accccacccc attaccctcc 360
 acatgagcgc cgccctgtgc tgggctgccg ggagctcgtc ttcaggaacc tctccagatc 420
 ctccctgccc tgtgccacga catcaccgac tgggtgggtg ggacccgagt gaagtcggca 480
 cagctgctcc cagtgtgct gctgcatgcc gaggaccacg ccacgcagca cctggaggtc 540
 gtcctccgga ccctgttcca ggctgcacc gacgaggagg cagccgtggt ccaaagttgt 600
 accagatccg cagagctcgt cgggacgttt gtcagccctg aggtgtttct gaagctgatc 660
 ttatcgacgc tgaagaagac gccctctgcc tccggcctcc tgggtgctggc ctcccgcc 718
 atg cgg ggt tgc ccc cga gaa gcc ctc cag ccg cac ctg gca gcc atc 766
 Met Arg Gly Cys Pro Arg Glu Ala Leu Gln Pro His Leu Ala Ala Ile
 1 5 10 15
 gcc aca gag ctg gca cag gcc cac atc tgc cag gca tct gaa aac gac 814
 Ala Thr Glu Leu Ala Gln Ala His Ile Cys Gln Ala Ser Glu Asn Asp
 17 22 27 32
 ctc tac ctg gag cgc ctg ctg ctg tgt gtg cag gct ctg gtg tct gtg 862
 Leu Tyr Leu Glu Arg Leu Leu Leu Cys Val Gln Ala Leu Val Ser Val
 33 38 43 48
 tgt cat gag gac tgt ggc gtg gcc agc ctg cag ctc ttg gac gtg ctg 910
 Cys His Glu Asp Cys Gly Val Ala Ser Leu Gln Leu Leu Asp Val Leu
 49 54 59 64
 ctg aca ata gtg gcc ctc gca ggt gct acc ggc ctg agg gac aag gca 958
 Leu Thr Ile Val Ala Leu Ala Gly Ala Thr Gly Leu Arg Asp Lys Ala
 65 70 75 80
 cag gag acg atg gac tca ctg gcc atg gtg gag ggt gtc agc agc tgc 1006
 Gln Glu Thr Met Asp Ser Leu Ala Met Val Glu Gly Val Ser Ser Cys
 81 86 91 96
 cag gac ctc tac cgc aag cac att ggt ccc ctc ctg gag cgg gtg acc 1054
 Gln Asp Leu Tyr Arg Lys His Ile Gly Pro Leu Leu Glu Arg Val Thr
 97 102 107 112
 gcg tcg cac ctt gac tgg acc gca cac tcg ccg gag ctc ctg cag ttc 1102
 Ala Ser His Leu Asp Trp Thr Ala His Ser Pro Glu Leu Leu Gln Phe
 113 118 123 128

1150
 1198
 1246
 1294
 1342
 1390
 1438
 1486
 1534
 1582
 1630
 1678
 1726
 1774
 1822

agt gtc atc gtc gca cag tca ggc cct gcc ctg gga gaa gcc ctg cca	1150
Ser Val Ile Val Ala Gln Ser Gly Pro Ala Leu Gly Glu Ala Leu Pro	
129 134 139 144	
cac gtc gtg ccc acg ctg agg gcc tgt ctg cag ccc tcc caa gac ccg	1198
His Val Val Pro Thr Leu Arg Ala Cys Leu Gln Pro Ser Gln Asp Pro	
145 150 155 160	
cag atg cgc ctg aag ctg ttc tcc atc ctg tcc acc gtg ctg ctc aga	1246
Gln Met Arg Leu Lys Leu Phe Ser Ile Leu Ser Thr Val Leu Leu Arg	
161 166 171 176	
gcc acg gac acc atc aac tcc cag ggg cag ttt ccc agc tac ctc gag	1294
Ala Thr Asp Thr Ile Asn Ser Gln Gly Gln Phe Pro Ser Tyr Leu Glu	
177 182 187 192	
acg gtg aca aag gac atc ctg gcc ccc aat ctg cag tgg cat gcg ggg	1342
Thr Val Thr Lys Asp Ile Leu Ala Pro Asn Leu Gln Trp His Ala Gly	
193 198 203 208	
agg aca gcc gcg gcc atc cgc acg gct gcc gtg tcc tgc ctc tgg gcg	1390
Arg Thr Ala Ala Ala Ile Arg Thr Ala Ala Val Ser Cys Leu Trp Ala	
209 214 219 224	
ctc acc agc agc gag gtc ctg tgc gca gag cag ata cgg gac gtg cag	1438
Leu Thr Ser Ser Glu Val Leu Ser Ala Glu Gln Ile Arg Asp Val Gln	
225 230 235 240	
gaa aca ctg atg ccc cag gtc ctg acc acc ctg gag gag gat tgc aag	1486
Glu Thr Leu Met Pro Gln Val Leu Thr Thr Leu Glu Glu Asp Ser Lys	
241 246 251 256	
atg acg cga ctg atc tca tgc cgt att atc aac acg ttc tta aaa acc	1534
Met Thr Arg Leu Ile Ser Cys Arg Ile Ile Asn Thr Phe Leu Lys Thr	
257 262 267 272	
tgc ggc ggc atg acg gat cca gag aaa ctc atc agg att tat cct gaa	1582
Ser Gly Gly Met Thr Asp Pro Glu Lys Leu Ile Arg Ile Tyr Pro Glu	
273 278 283 288	
ctc tta aaa cgc cta gat gac gtg tcc aac gat gtg agg atg gca gcc	1630
Leu Leu Lys Arg Leu Asp Asp Val Ser Asn Asp Val Arg Met Ala Ala	
289 294 299 304	
gcc tcc acc ttg gtc acc tgg ctg cag tgt gtc aag ggt gcc aac gca	1678
Ala Ser Thr Leu Val Thr Trp Leu Gln Cys Val Lys Gly Ala Asn Ala	
305 310 315 320	
aaa tcc tac tat cag agc agt gtc cag tac ctg tac cga gag ttg ctg	1726
Lys Ser Tyr Tyr Gln Ser Ser Val Gln Tyr Leu Tyr Arg Glu Leu Leu	
321 326 331 336	
gtt cac ctt gac gat cca gag agg gcc atc cag gat gca att tta gag	1774
Val His Leu Asp Asp Pro Glu Arg Ala Ile Gln Asp Ala Ile Leu Glu	
337 342 347 352	
gtc ctc aaa gag gcc agc ggg ctg ttc cca gat ctc ctg gtg agg gag	1822

Val	Leu	Lys	Glu	Gly	Ser	Gly	Leu	Phe	Pro	Asp	Leu	Leu	Val	Arg	Glu	
353					358					363					368	
acg	gag	gcc	gtc	atc	cac	aag	cac	cgc	tcg	gcc	acc	tac	tgc	gag	cag	1870
Thr	Glu	Ala	Val	Ile	His	Lys	His	Arg	Ser	Ala	Thr	Tyr	Cys	Glu	Gln	
369					374					379					384	
ctc	ctg	cag	cat	gtg	cag	gcc	gtg	cca	gcc	aca	cag	tga	ccacgctgg			1919
Leu	Leu	Gln	His	Val	Gln	Ala	Val	Pro	Ala	Thr	Gln	*				
385					390					395						
ttcagccacg	gcacaccctt	gtccccacct	gagccagagt	ttgtggcctt	taaatctcat											1979
aaacaaggca	cctctgtgcc	agcagtgaga	ctgtgacagc	aagaatgtac	tcctcaggac											2039
acctgcccgc	tctttccctg	gaataacagc	ctctgagtgg	attctgcatg	ttatgtgatt											2099
tgtttctgttc	atcgagaggg	ctcccaaaca	tctgcagctg	atttgaaatt	aaaagtaagt											2159
cgcagccgct	cctcccgag	ccacttcagc	agcatcttag	attttaagcc	tcacgtgcgc											2219
agctggttca	tgaactattg	gctgcatcct	gcttaggtgc	ccaccaagaa	ggtttttacc											2279
tacttaacaa	aaaggaagga	gcccaaagtg	attagaaaga	aatgaaatct	ctttttgggt											2339
tctgtctact	gaaattta	atctcagtga	acagactaaa	aggaatttag	aatcctaaca											2399
acttaccaga	tttctcctgt	tttaaata	ctgggacttt	aaagggtata	tgtccgggtca											2459
cogtatgttt	taagtcgggtg	ttaatgctaa	cagtgttgaa	aacaatattt	catgagatct											2519
aattgtgggt	gccctatag	gtagcaggaa	agtaaagttg	catttccttc	tcgcacattc											2579
tacaccaag	tgctaaaag	atctcattgt	aagtgggtag	tgttaccgga	agccattgtg											2639
ttcacacggg	ggaaatgccg	tatatatttt	tcaacaaata	ttaacgttta	tactttcatg											2699
tttgaaaatt	taattaaaaa	tatttgtttt	aaaaaaaaaa	aaaa												2743

<210> 19
 <211> 2747
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (206)..(1618)

<400> 19																	
gtgccctgcc	gtaccgggtcc	ggaattcccg	ggcgcacgat	ttcgtgctgg	aggttcgcta												60
gccgaagcgg	ctgcatctgg	cgcgcgtct	gccccgcgtg	ctcggagcgg	attctgccccg												120
ccgtccccgg	agccctcggc	gccccgctga	gccccgcgatc	acttccctccc	tgtgaccaac												180

cggcgctgca ggtagagcc tggca	atg ccg ttt ggg tgt gtg act ctg ggc	232
	Met Pro Phe Gly Cys Val Thr Leu Gly	
	1 5	
gac aag aag aac tat aac cag cca tcg gag gtg act gac aga tat gat	280	
Asp Lys Lys Asn Tyr Asn Gln Pro Ser Glu Val Thr Asp Arg Tyr Asp		
10 15 20 25		
ttg gga cag gtc atc aag act gag gag ttt tgt gaa atc ttc cgg gcc	328	
Leu Gly Gln Val Ile Lys Thr Glu Glu Phe Cys Glu Ile Phe Arg Ala		
26 31 36 41		
aag gac aag acg aca ggc aag ctg cac acc tgc aag aag ttc cag aag	376	
Lys Asp Lys Thr Thr Gly Lys Leu His Thr Cys Lys Lys Phe Gln Lys		
42 47 52 57		
cgg gac ggc cgc aag gtg cgg aaa gct gcc aag aac gag ata ggc atc	424	
Arg Asp Gly Arg Lys Val Arg Lys Ala Ala Lys Asn Glu Ile Gly Ile		
58 63 68 73		
ctc aag atg gtg aag cat ccc aac atc cta cag ctg gtg gat gtg ttt	472	
Leu Lys Met Val Lys His Pro Asn Ile Leu Gln Leu Val Asp Val Phe		
74 79 84 89		
gtg acc cgc aag gag tac ttt atc ttc ctg gag ctg gcc acg ggg agg	520	
Val Thr Arg Lys Glu Tyr Phe Ile Phe Leu Glu Leu Ala Thr Gly Arg		
90 95 100 105		
gag gtg ttt gac tgg atc ctg gac cag ggc tac tac tcg gag cga gac	568	
Glu Val Phe Asp Trp Ile Leu Asp Gln Gly Tyr Tyr Ser Glu Arg Asp		
106 111 116 121		
aca agc aac gtg gta cgg caa gtc ctg gag gcc gtg gcc tat ttg cac	616	
Thr Ser Asn Val Val Arg Gln Val Leu Glu Ala Val Ala Tyr Leu His		
122 127 132 137		
tca ctc aag atc gtg cac agg aat ctc aag ctg gag aac ctg gtt tac	664	
Ser Leu Lys Ile Val His Arg Asn Leu Lys Leu Glu Asn Leu Val Tyr		
138 143 148 153		
tac aac cgg ctg aag aac tcg aag att gtc atc agt gac ttc cat ctg	712	
Tyr Asn Arg Leu Lys Asn Ser Lys Ile Val Ile Ser Asp Phe His Leu		
154 159 164 169		
gct aag cta gaa aat ggc ctc atc aag gag ccc tgt ggg acc ccc gag	760	
Ala Lys Leu Glu Asn Gly Leu Ile Lys Glu Pro Cys Gly Thr Pro Glu		
170 175 180 185		
tat ctg gcc cca gag gtg gta ggc cgg cag cgg tat gga cgc cct gtg	808	
Tyr Leu Ala Pro Glu Val Val Gly Arg Gln Arg Tyr Gly Arg Pro Val		
186 191 196 201		
gac tgc tgg gcc att gga gtc atc atg tac atc ctg ctt tca ggc aat	856	
Asp Cys Trp Ala Ile Gly Val Ile Met Tyr Ile Leu Leu Ser Gly Asn		
202 207 212 217		

cca cct ttc tat gag gag gtg gaa gaa gat gat tat gag aac cat gat	904
Pro Pro Phe Tyr Glu Glu Val Glu Glu Asp Asp Tyr Glu Asn His Asp	
218 223 228 233	
aag aat ctc ttc cgc aag atc ctg gct ggt gac tat gag ttt gac tct	952
Lys Asn Leu Phe Arg Lys Ile Leu Ala Gly Asp Tyr Glu Phe Asp Ser	
234 239 244 249	
cca tat tgg gat gat att tcg cag gca gcc aaa gac ctg gtc aca agg	1000
Pro Tyr Trp Asp Asp Ile Ser Gln Ala Ala Lys Asp Leu Val Thr Arg	
250 255 260 265	
ctg atg gag gtg gag caa gac cag cgg atc act gca gaa gag gcc atc	1048
Leu Met Glu Val Glu Gln Asp Gln Arg Ile Thr Ala Glu Glu Ala Ile	
266 271 276 281	
tcc cat gag tgg att tct ggc aat gct gct tct gat aag aac atc aag	1096
Ser His Glu Trp Ile Ser Gly Asn Ala Ala Ser Asp Lys Asn Ile Lys	
282 287 292 297	
gat ggt gtc tgt gcc cag att gaa aag aac ttt gcc agg gcc aag tgg	1144
Asp Gly Val Cys Ala Gln Ile Glu Lys Asn Phe Ala Arg Ala Lys Trp	
298 303 308 313	
aag aag gct gtc cga gtg acc acc ctc atg aaa cgg ctc cgg gca cca	1192
Lys Lys Ala Val Arg Val Thr Thr Leu Met Lys Arg Leu Arg Ala Pro	
314 319 324 329	
gag cag tcc agc acg gct gca gcc cag tcg gcc tca gcc aca gac act	1240
Glu Gln Ser Ser Thr Ala Ala Ala Gln Ser Ala Ser Ala Thr Asp Thr	
330 335 340 345	
gcc acc ccc ggg gct gca gac cgt agt gcc acc cca gcc aca gat gga	1288
Ala Thr Pro Gly Ala Ala Asp Arg Ser Ala Thr Pro Ala Thr Asp Gly	
346 351 356 361	
agt gcc acc cca gcc act gat ggc agt gtc acc cca gcc acc gat gga	1336
Ser Ala Thr Pro Ala Thr Asp Gly Ser Val Thr Pro Ala Thr Asp Gly	
362 367 372 377	
agc atc act cca gcc act gat ggg agt gtc acc cca gcc act gac agg	1384
Ser Ile Thr Pro Ala Thr Asp Gly Ser Val Thr Pro Ala Thr Asp Arg	
378 383 388 393	
agc gct act cca tcc act gat ggg ata gcc aca cca gcc aca gaa gag	1432
Ser Ala Thr Pro Ser Thr Asp Gly Ile Ala Thr Pro Ala Thr Glu Glu	
394 399 404 409	
agc act gtg ccc acc acc caa agc agt gcc atg ctg gcc acc aag gca	1480
Ser Thr Val Pro Thr Thr Gln Ser Ser Ala Met Leu Ala Thr Lys Ala	
410 415 420 425	
gct gcc acc cct gag ccg gct atg gcc cag ccg gac agc aca gcc cca	1528
Ala Ala Thr Pro Glu Pro Ala Met Ala Gln Pro Asp Ser Thr Ala Pro	
426 431 436 441	
gag ggc gcc aca ggc cag gct cca ccc tct agt aaa ggg gaa gag gct	1576

<400> 20

gtgcctgcc gtaccggtcc ggaattcccg ggtcgacgat ttcgtgctgg aggttcgcta 60

gccgaagcgg ctgcattctgg cgcgcgtct gcccgcgtg ctccgagcgg attctgcccg 120

ccgtccccgg agccctcggc gcccgcgtga gcccgcgac acttctctccc tgtgaccaac 180

cggcgctgca ggtagagacc tggca atg ccg ttt ggg tgt gtg act ctg ggc 232
Met Pro Phe Gly Cys Val Thr Leu Gly
1 5

gac aag aag aac tat aac cag cca tcg gag gtg act gac aga tat gat 280
Asp Lys Lys Asn Tyr Asn Gln Pro Ser Glu Val Thr Asp Arg Tyr Asp
10 15 20 25

ttg gga cag gtc atc aag act gag gag ttt tgt gaa atc ttc cgg gcc 328
Leu Gly Gln Val Ile Lys Thr Glu Glu Phe Cys Glu Ile Phe Arg Ala
26 31 36 41

aag gac aag acg aca ggc aag ctg cac acc tgc aag aag ttc cag aag 376
Lys Asp Lys Thr Thr Gly Lys Leu His Thr Cys Lys Lys Phe Gln Lys
42 47 52 57

cgg gac ggc cgc aag gtg cgg aaa gct gcc aag aac gag ata ggc atc 424
Arg Asp Gly Arg Lys Val Arg Lys Ala Ala Lys Asn Glu Ile Gly Ile
58 63 68 73

ctc aag atg gtg aag cat ccc aac atc cta cag ctg gtg gat gtg ttt 472
Leu Lys Met Val Lys His Pro Asn Ile Leu Gln Leu Val Asp Val Phe
74 79 84 89

gtg acc cgc aag gag tac ttt atc ttc ctg gag ctg gcc acg ggg agg 520
Val Thr Arg Lys Glu Tyr Phe Ile Phe Leu Glu Leu Ala Thr Gly Arg
90 95 100 105

gag gtg ttt gac tgg atc ctg gac cag ggc tac tac tcg gag cga gac 568
Glu Val Phe Asp Trp Ile Leu Asp Gln Gly Tyr Tyr Ser Glu Arg Asp
106 111 116 121

aca agc aac gtg gta cgg caa gtc ctg gag gcc gtg gcc tat ttg cac 616
Thr Ser Asn Val Val Arg Gln Val Leu Glu Ala Val Ala Tyr Leu His
122 127 132 137

tca ctc aag atc gtg cac agg aat ctc aag ctg gag aac ctg gtt tac 664
Ser Leu Lys Ile Val His Arg Asn Leu Lys Leu Glu Asn Leu Val Tyr
138 143 148 153

tac aac cgg ctg aag aac tcg aag att gtc atc agt gac ttc cat ctg 712
Tyr Asn Arg Leu Lys Asn Ser Lys Ile Val Ile Ser Asp Phe His Leu
154 159 164 169

gct aag cta gaa aat ggc ctc atc aag gag ccc tgt ggg acc ccc gag 760
Ala Lys Leu Glu Asn Gly Leu Ile Lys Glu Pro Cys Gly Thr Pro Glu
170 175 180 185

tat ctg gcc cca gag gtg gta ggc cgg cag cgg tat gga cgc cct gtg 808
Tyr Leu Ala Pro Glu Val Val Gly Arg Gln Arg Tyr Gly Arg Pro Val

186	191	196	201	
gac tgc tgg gcc att gga gtc atc atg tac atc ctg ctt tca ggc aat				856
Asp Cys Trp Ala Ile Gly Val Ile Met Tyr Ile Leu Leu Ser Gly Asn				
202	207	212	217	
cca cct ttc tat gag gag gtg gaa gaa gat gat tat gag aac cat gat				904
Pro Pro Phe Tyr Glu Glu Val Glu Glu Asp Asp Tyr Glu Asn His Asp				
218	223	228	233	
aag aat ctc ttc cgc aag atc ctg gct ggt gac tat gag ttt gac tct				952
Lys Asn Leu Phe Arg Lys Ile Leu Ala Gly Asp Tyr Glu Phe Asp Ser				
234	239	244	249	
cca tat tgg gat gat att tcg cag gca gcc aaa gac ctg gtc aca agg				1000
Pro Tyr Trp Asp Asp Ile Ser Gln Ala Ala Lys Asp Leu Val Thr Arg				
250	255	260	265	
ctg atg gag gtg gag caa gac cag cgg atc act gca gaa gag gcc atc				1048
Leu Met Glu Val Glu Gln Asp Gln Arg Ile Thr Ala Glu Glu Ala Ile				
266	271	276	281	
tcc cat gag tgg att tct ggc aat gct gct tct gat aag aac atc aag				1096
Ser His Glu Trp Ile Ser Gly Asn Ala Ala Ser Asp Lys Asn Ile Lys				
282	287	292	297	
gat ggt gtc tgt gcc cag att gaa aag aac ttt gcc agg gcc aag tgg				1144
Asp Gly Val Cys Ala Gln Ile Glu Lys Asn Phe Ala Arg Ala Lys Trp				
298	303	308	313	
aag aag gct gtc cga gtg acc acc ctc atg aaa cgg ctc cgg gca cca				1192
Lys Lys Ala Val Arg Val Thr Thr Leu Met Lys Arg Leu Arg Ala Pro				
314	319	324	329	
gag cag tcc agc acg gct gca gcc cag tcg gcc tca gcc aca gac act				1240
Glu Gln Ser Ser Thr Ala Ala Ala Gln Ser Ala Ser Ala Thr Asp Thr				
330	335	340	345	
gcc acc ccc ggg gct gca ggt ggg gcc aca gct gca gct gcg agt gga				1288
Ala Thr Pro Gly Ala Ala Gly Gly Ala Thr Ala Ala Ala Ala Ser Gly				
346	351	356	361	
gct acc tca gcc cct gag ggt gat gct gct cgt gct gca aag agt gat				1336
Ala Thr Ser Ala Pro Glu Gly Asp Ala Ala Arg Ala Ala Lys Ser Asp				
362	367	372	377	
aat gtg gcc ccc gca gac cgt agt gcc acc cca gcc aca gat gga agt				1384
Asn Val Ala Pro Ala Asp Arg Ser Ala Thr Pro Ala Thr Asp Gly Ser				
378	383	388	393	
gcc acc cca gcc act gat ggc agt gtc acc cca gcc acc gat gga agc				1432
Ala Thr Pro Ala Thr Asp Gly Ser Val Thr Pro Ala Thr Asp Gly Ser				
394	399	404	409	
atc act cca gcc act gat ggg agt gtc acc cca gcc act gac agg agc				1480
Ile Thr Pro Ala Thr Asp Gly Ser Val Thr Pro Ala Thr Asp Arg Ser				
410	415	420	425	

gct act cca tcc act gat ggg ata gcc aca cca gcc aca gaa gag agc	1528
Ala Thr Pro Ser Thr Asp Gly Ile Ala Thr Pro Ala Thr Glu Glu Ser	
426 431 436 441	
act gtg ccc acc acc caa agc agt gcc atg ctg gcc acc aag gca gct	1576
Thr Val Pro Thr Thr Gln Ser Ser Ala Met Leu Ala Thr Lys Ala Ala	
442 447 452 457	
gcc acc cct gag ccg gct atg gcc cag ccg gac agc aca gcc cca gag	1624
Ala Thr Pro Glu Pro Ala Met Ala Gln Pro Asp Ser Thr Ala Pro Glu	
458 463 468 473	
ggc gcc aca ggc cag gct cca ccc tct agt aaa ggg gaa gag gct gct	1672
Gly Ala Thr Gly Gln Ala Pro Pro Ser Ser Lys Gly Glu Glu Ala Ala	
474 479 484 489	
ggt tat gcc cag gag tct caa agg gag gag gcc agc tga gtaggcagcc	1721
Gly Tyr Ala Gln Glu Ser Gln Arg Glu Glu Ala Ser *	
490 495 500	
tggtgagggg gggcagggga tgggcaggag ggtgggagag tggatgaggg gcttctcact	1781
gtacatagag tcaactggcat gatgccctcg ctcccccatg cccccacatc ccagtggggc	1841
ataactaggg gtcacgggag agcagtctcg tctcctgtgt gtatgtgtgt gagtgggtggg	1901
caggccagtg gcagggccgg cccagcccc tgcattggatt ccttgtggct tttctgtctt	1961
ttgctagctt caccagtttc tgttccttgt gggatgctgc tctagggata ctcagggggc	2021
tctgtctctc cttccccctc ctttcttgcc tcaccattcc cctaggcagg ccctgcagg	2081
cccacactct cccaggccct aaacttgggc ggcttgccc tgagagctgg tcctccagcg	2141
aggccctgtc agcggcttta ggctcctgca catgaagggtg tgtgcctgtg gtgtgtgggc	2201
tgtcttagga gcagatacag gctggtatag aggatgcaga aaggtagggc agtatgttta	2261
agtcagact tggcacatgg ctagggatac tgctcactag ctgtggaggt cctcaggagt	2321
ggagagaatg agtaggaggg cagaagcttc catttttgtc cttcctaaga ccctgttatt	2381
tgtgttattt cctgccttcc cgagtcctgc agtgggctgc cctgtaccct gaacctcatg	2441
agcctctaag ggaaaggagg aacaattagg acgtggcaat gagacctggc agggcagagt	2501
acaagcccag caccagtggt cccagcctta ctgggtcctt accctggggc aaacagggag	2561
ggctgatacc tccttgcctt tcttagatgc ccacctcta caatctcagc ccacaagtcc	2621
tctccacct agggggcttg ctgcatggca ataactcata atctgatttg gaggtttgcc	2681
ctttacaggg gcagattttc tgctcagttc aacaatgaaa tgaagaggaa ctccctcttt	2741
ctacagctca cttctatcag agggccagggt gcctcagagc cacattgagt tgctttttct	2801

gggatgagga agtaggggta aactccccag tttcctgag

2840

<210> 21

<211> 1367

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (355) .. (1278)

<400> 21

tacgcacgct gtaccgggtcc ggaattcccc ggtcgaccca cgcgtccgct tgttcccaat 60

cagtttccag ccaacaccag ggtgtcctag tccgcagagg tgtgggggac aactccata 120

atctctactt ttctttttgt gcagctgagt catggagctt tcagccccag cacatggctc 180

ctccttaact gcgtctgctc aacctccctc agccctgtga acagcatccc cgcacacaga 240

cgcagagcag gactctctct gctgccactt caccttctct agagaggacc agcggccaga 300

gcctcagtga ctgccaccct ggaggacagg gcacaacaac cgtttctgga gaga atg 357
Met
1

gga gga ttc cag agg ggc aaa tat gga act atg gct gaa ggt aga tca 405
Gly Gly Phe Gln Arg Gly Lys Tyr Gly Thr Met Ala Glu Gly Arg Ser
2 7 12 17

gaa gat aac ttg tct gca aca cca ccg gca ttg agg att atc cta gtg 453
Glu Asp Asn Leu Ser Ala Thr Pro Pro Ala Leu Arg Ile Ile Leu Val
18 23 28 33

ggc aaa aca ggc tgc ggg aaa agt gcc aca ggg aac agc atc ctt ggc 501
Gly Lys Thr Gly Cys Gly Lys Ser Ala Thr Gly Asn Ser Ile Leu Gly
34 39 44 49

cag ccc gtg ttt gag tcc aag ctg agg gcc cag tca gtg acc agg acg 549
Gln Pro Val Phe Glu Ser Lys Leu Arg Ala Gln Ser Val Thr Arg Thr
50 55 60 65

tgc cag gtg aaa aca gga aca tgg aac ggg agg aaa gtc ctg gtg gtt 597
Cys Gln Val Lys Thr Gly Thr Trp Asn Gly Arg Lys Val Leu Val Val
66 71 76 81

gac acg ccc tcc atc ttt gag tca cag gct gat acc caa gag ctg tac 645
Asp Thr Pro Ser Ile Phe Glu Ser Gln Ala Asp Thr Gln Glu Leu Tyr
82 87 92 97

aag aac atc ggg gac tgc tac ctg ctc tct gcc ccg ggg ccc cac gtc 693
Lys Asn Ile Gly Asp Cys Tyr Leu Leu Ser Ala Pro Gly Pro His Val
98 103 108 113

ctg ctt ctg gtg atc cag ctg ggg cgt ttc act gct cag gac aca gtg Leu Leu Leu Val Ile Gln Leu Gly Arg Phe Thr Ala Gln Asp Thr Val 114 119 124 129	741
gcc atc agg aag gtg aaa gag gtc ttt ggg aca ggg gcc atg aga cat Ala Ile Arg Lys Val Lys Glu Val Phe Gly Thr Gly Ala Met Arg His 130 135 140 145	789
gtg gtc atc ctc ttc acc cac aaa gag gac tta ggg ggc cag gcc ctg Val Val Ile Leu Phe Thr His Lys Glu Asp Leu Gly Gly Gln Ala Leu 146 151 156 161	837
gat gac tat gta gca aac acg gac aac tgc agc ctg aaa gac ctg gtg Asp Asp Tyr Val Ala Asn Thr Asp Asn Cys Ser Leu Lys Asp Leu Val 162 167 172 177	885
cgg gag tgt gag aga agg tac tgt gcc ttc aac aac tgg ggc tct gtg Arg Glu Cys Glu Arg Arg Tyr Cys Ala Phe Asn Asn Trp Gly Ser Val 178 183 188 193	933
gag gag cag agg cag cag cag gca gag ctc ctg gct gtg att gag agg Glu Glu Gln Arg Gln Gln Ala Glu Leu Leu Ala Val Ile Glu Arg 194 199 204 209	981
ctg ggg atg gag cga gag ggc tcc ttc cac agc aat gac ctc ttc ttg Leu Gly Met Glu Arg Glu Gly Ser Phe His Ser Asn Asp Leu Phe Leu 210 215 220 225	1029
gat gcc cag ctg ctc caa aga act gga gtt ggg gcc tgc cag gaa gac Asp Ala Gln Leu Leu Gln Arg Thr Gly Val Gly Ala Cys Gln Glu Asp 226 231 236 241	1077
tac agg cag tac cag gcc aaa gtg gaa tgg cag gtg gag aag cac aag Tyr Arg Gln Tyr Gln Ala Lys Val Glu Trp Gln Val Glu Lys His Lys 242 247 252 257	1125
caa gag ctg agg gag aac gag agt aac tgg gca tac aag gcg ctc ctc Gln Glu Leu Arg Glu Asn Glu Ser Asn Trp Ala Tyr Lys Ala Leu Leu 258 263 268 273	1173
aga gtc aaa cac ttg atg ctt ttg cat tat gag att ttt gtt ttt cta Arg Val Lys His Leu Met Leu Leu His Tyr Glu Ile Phe Val Phe Leu 274 279 284 289	1221
ttg ttg tgc agc ata ctt ttt ttc att att ttt ctg ttc atc ttt cat Leu Leu Cys Ser Ile Leu Phe Phe Ile Ile Phe Leu Phe Ile Phe His 290 295 300 305	1269
tac att taa atctctg gaccctggag cacttctaata gtatcacccc atggagtcac Tyr Ile * 306	1325
tgttctaata atcaccaatt cagactcaaa aaaaaaaaaa aa	1367

<210> 22
 <211> 2615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (160)..(849)

```

<400> 22
ccgggactgg ggctgggcgc gctgcccggg agccccgcac ccacgcctgg accgcggaga      60
cgcccaggcc gaggaacccc cagcccaggg actagacacc accagggccg ggcggagcca      120
gagccagacg cgccggagcg ggcgcctcta cgccgctag  atg ttc gcc atc cag      174
                                         Met Phe Ala Ile Gln
                                         1

cca ggg cta gct gag ggg ggc caa ttc ctg ggg gac cca cct cct gga      222
Pro Gly Leu Ala Glu Gly Gly Gln Phe Leu Gly Asp Pro Pro Pro Gly
  6                      11                      16                      21

tta tgt cag ccc gag ctc caa cca gac agc aac tcc aac ttc atg gca      270
Leu Cys Gln Pro Glu Leu Gln Pro Asp Ser Asn Ser Asn Phe Met Ala
  22                      27                      32                      37

agt gcc aag gat gct aac gag aat tgg cat ggg atg cca ggc aga gtg      318
Ser Ala Lys Asp Ala Asn Glu Asn Trp His Gly Met Pro Gly Arg Val
  38                      43                      48                      53

gaa cct atc ctg agg agg agc tcc tct gag tca ccc tct gac aac caa      366
Glu Pro Ile Leu Arg Arg Ser Ser Ser Glu Ser Pro Ser Asp Asn Gln
  54                      59                      64                      69

gcc ttc cag gcc cct gga tcc cct gag gaa ggg gtg cgc agc ccc cca      414
Ala Phe Gln Ala Pro Gly Ser Pro Glu Glu Gly Val Arg Ser Pro Pro
  70                      75                      80                      85

gag ggg gca gag att ccc ggg gct gag cct gag aag atg ggt ggt gct      462
Glu Gly Ala Glu Ile Pro Gly Ala Glu Pro Glu Lys Met Gly Gly Ala
  86                      91                      96                      101

ggc aca gtc tgc tcc cct ctg gag gac aac ggc tat gcc agc agt tcc      510
Gly Thr Val Cys Ser Pro Leu Glu Asp Asn Gly Tyr Ala Ser Ser Ser
  102                      107                      112                      117

ctg agc att gac agc cgt agc agc agt cct gag cct gcc tgt ggg acc      558
Leu Ser Ile Asp Ser Arg Ser Ser Ser Pro Glu Pro Ala Cys Gly Thr
  118                      123                      128                      133

ccg cga ggc cct ggc cct ccc gat ccc ctt ctg ccc tca gtg gcc cag      606
Pro Arg Gly Pro Gly Pro Pro Asp Pro Leu Leu Pro Ser Val Ala Gln
  134                      139                      144                      149

gct gtg cag cac tta caa gtc cag gag cgc tac aaa gag cag gag aag      654
Ala Val Gln His Leu Gln Val Gln Glu Arg Tyr Lys Glu Gln Glu Lys
  150                      155                      160                      165

```

gaa aag cac cac gtg cac ttg gtg atg tac cgt cgc ctg gca ctg ctc	702
Glu Lys His His Val His Leu Val Met Tyr Arg Arg Leu Ala Leu Leu	
166 171 176 181	
cag tgg atc cgg ggc ctg cag cat cag ttg att gac cag cag gcc cga	750
Gln Trp Ile Arg Gly Leu Gln His Gln Leu Ile Asp Gln Gln Ala Arg	
182 187 192 197	
ctg cag gag agc ttc gac acc atc cta gac aac cgg aag gag ctt att	798
Leu Gln Glu Ser Phe Asp Thr Ile Leu Asp Asn Arg Lys Glu Leu Ile	
198 203 208 213	
cgc tgt ctc cag cag agg gca gca cca tcc agg ccc cag gac cag gcc	846
Arg Cys Leu Gln Gln Arg Ala Ala Pro Ser Arg Pro Gln Asp Gln Ala	
214 219 224 229	
taa ggggt gtgcctccac aagtgtgcaa gggatatgt atatatttgc aggcattgtgt	903
*	
230	
gaggcgact agtaagtaca taatttgctg gcatgattgc aggtaggcat gagtgtgtat	963
gtgctaacat gtaggctgggt gtgtgttaggc atgtgtgaat aagcatgtat aaatgagctt	1023
aagtgtgctg tgtgcacatg tgtacacaca gctaatttat ctgcagacct atatgtgagc	1083
atgtaagagt gaacatatgt gtgtgtgtgt agtatgtaag aatgaggaac tcggtatgtg	1143
catgtgtaga caggtagcca gcagtgtgtg tatatgcgca tgagttagga tgtataggca	1203
gaagatgtgt gtgtctatga gtgagtttga gtgtgcaggc ttgtattagg tgtatgtgag	1263
gaagcccttg tgtgtgcagg ggtgcacatg tttggccaca ggcattggag gtgtatgtta	1323
ggagcatgtg tgtttgtagg cagactcatg agcaggtgtg tgcaaataca tatccagctg	1383
cactgtgggt gtccaccac acctgtgtgt cctcatggcc taccagacc tttcttctcc	1443
actgggtccc actgttccct ggagacagag ggctagcatg ctgtcattta tctgaagggt	1503
gtggctgacc cattctcctg ggatttccca ggccacctct cctttccctt tccctcactt	1563
aaccagact tgctcagctg aggcatttgt ccctgatgtt ggctttactt gtaggaggtt	1623
tagtggctgc tctggcctgc catggaattt tggctgcaat tttggcagtg tgtggagaac	1683
tggatcagg aaagggaacc aggagtagtg atgaagatga tgggtgggat ggggacagag	1743
gacatagggg actgtccctc ttgaactctg cctttgggca catgggagat ggggacagga	1803
aagatgataa cagtgaacc ctgtgaagaa taggagaatg ggaattctaa aataccagtt	1863
cccaaacaaa ccatctctcc attggaaaag gagctgttgc aaaccgtgtt catttaagct	1923
tctgatgaaa agcaatgtat gtttataagc ttgcaagtaa cagacaagat gttccaaggc	1983

ctg ctt ctg gtg atc cag ctg ggg cgt ttc act gct cag gac aca gtg	741
Leu Leu Leu Val Ile Gln Leu Gly Arg Phe Thr Ala Gln Asp Thr Val	
114 119 124 129	
gcc atc agg aag gtg aaa gag gtc ttt ggg aca ggg gcc atg aga cat	789
Ala Ile Arg Lys Val Lys Glu Val Phe Gly Thr Gly Ala Met Arg His	
130 135 140 145	
gtg gtc atc ctc ttc acc cac aaa gag gac tta ggg ggc cag gcc ctg	837
Val Val Ile Leu Phe Thr His Lys Glu Asp Leu Gly Gly Gln Ala Leu	
146 151 156 161	
gat gac tat gta gca aac acg gac aac tgc agc ctg aaa gac ctg gtg	885
Asp Asp Tyr Val Ala Asn Thr Asp Asn Cys Ser Leu Lys Asp Leu Val	
162 167 172 177	
cgg gag tgt gag aga agg tac tgt gcc ttc aac aac tgg ggc tct gtg	933
Arg Glu Cys Glu Arg Arg Tyr Cys Ala Phe Asn Asn Trp Gly Ser Val	
178 183 188 193	
gag gag cag agg cag cag cag gca gag ctc ctg gct gtg att gag agg	981
Glu Glu Gln Arg Gln Gln Gln Ala Glu Leu Leu Ala Val Ile Glu Arg	
194 199 204 209	
ctg ggg atg gag cga gag ggc tcc ttc cac agc aat gac ctc ttc ttg	1029
Leu Gly Met Glu Arg Glu Gly Ser Phe His Ser Asn Asp Leu Phe Leu	
210 215 220 225	
gat gcc cag ctg ctc caa aga act gga gtt ggg gcc tgc cag gaa gac	1077
Asp Ala Gln Leu Leu Gln Arg Thr Gly Val Gly Ala Cys Gln Glu Asp	
226 231 236 241	
tac agg cag tac cag gcc aaa gtg gaa tgg cag gtg gag aag cac aag	1125
Tyr Arg Gln Tyr Gln Ala Lys Val Glu Trp Gln Val Glu Lys His Lys	
242 247 252 257	
caa gag ctg agg gag aac gag agt aac tgg gca tac aag gcg ctc ctc	1173
Gln Glu Leu Arg Glu Asn Glu Ser Asn Trp Ala Tyr Lys Ala Leu Leu	
258 263 268 273	
aga gtc aaa cac ttg atg ctt ttg cat tat gag att ttt gtt ttt cta	1221
Arg Val Lys His Leu Met Leu Leu His Tyr Glu Ile Phe Val Phe Leu	
274 279 284 289	
ttg ttg tgc agc ata ctt ttt ttc att att ttt ctg ttc atc ttt cat	1269
Leu Leu Cys Ser Ile Leu Phe Phe Ile Ile Phe Leu Phe Ile Phe His	
290 295 300 305	
tac att taa atctctg gaccctggag cacttctaata gtatcacccc atggagtcac	1325
Tyr Ile *	
306	
tgttctaata atcaccaatt cagactcaaa aaaaaaaaaa aa	1367

<210> 22
 <211> 2615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (160)..(849)

<400> 22

```

ccgggactgg ggctggggcgc gctgcccggg agccccgcac ccacgcctgg accgcggaga      60

cgcccaggcc gaggaacccc cagcccaggg actagacacc accagggccg ggcggagcca      120

gagccagacg cgccggagcg ggcgcctcta cgccgctag  atg ttc gcc atc cag      174
              Met Phe Ala Ile Gln
              1

cca ggg cta gct gag ggg ggc caa ttc ctg ggg gac cca cct cct gga      222
Pro Gly Leu Ala Glu Gly Gly Gln Phe Leu Gly Asp Pro Pro Pro Gly
  6              11              16              21

tta tgt cag ccc gag ctg caa cca gac agc aac tcc aac ttc atg gca      270
Leu Cys Gln Pro Glu Leu Gln Pro Asp Ser Asn Ser Asn Phe Met Ala
  22              27              32              37

agt gcc aag gat gct aac gag aat tgg cat ggg atg cca ggc aga gtg      318
Ser Ala Lys Asp Ala Asn Glu Asn Trp His Gly Met Pro Gly Arg Val
  38              43              48              53

gaa cct atc ctg agg agg agc tcc tct gag tca ccc tct gac aac caa      366
Glu Pro Ile Leu Arg Arg Ser Ser Ser Glu Ser Pro Ser Asp Asn Gln
  54              59              64              69

gcc ttc cag gcc cct gga tcc cct gag gaa ggg gtg cgc agc ccc cca      414
Ala Phe Gln Ala Pro Gly Ser Pro Glu Glu Gly Val Arg Ser Pro Pro
  70              75              80              85

gag ggg gca gag att ccc ggg gct gag cct gag aag atg ggt ggt gct      462
Glu Gly Ala Glu Ile Pro Gly Ala Glu Pro Glu Lys Met Gly Gly Ala
  86              91              96              101

ggc aca gtc tgc tcc cct ctg gag gac aac ggc tat gcc agc agt tcc      510
Gly Thr Val Cys Ser Pro Leu Glu Asp Asn Gly Tyr Ala Ser Ser Ser
  102              107              112              117

ctg agc att gac agc cgt agc agc agt cct gag cct gcc tgt ggg acc      558
Leu Ser Ile Asp Ser Arg Ser Ser Ser Pro Glu Pro Ala Cys Gly Thr
  118              123              128              133

ccg cga ggc cct ggc cct ccc gat ccc ctt ctg ccc tca gtg gcc cag      606
Pro Arg Gly Pro Gly Pro Pro Asp Pro Leu Leu Pro Ser Val Ala Gln
  134              139              144              149

gct gtg cag cac tta caa gtc cag gag cgc tac aaa gag cag gag aag      654
Ala Val Gln His Leu Gln Val Gln Glu Arg Tyr Lys Glu Gln Glu Lys
  150              155              160              165

```

gaa aag cac cac gtg cac ttg gtg atg tac cgt cgc ctg gca ctg ctc	702
Glu Lys His His Val His Leu Val Met Tyr Arg Arg Leu Ala Leu Leu	
166 171 176 181	
cag tgg atc cgg ggc ctg cag cat cag ttg att gac cag cag gcc cga	750
Gln Trp Ile Arg Gly Leu Gln His Gln Leu Ile Asp Gln Gln Ala Arg	
182 187 192 197	
ctg cag gag agc ttc gac acc atc cta gac aac cgg aag gag ctt att	798
Leu Gln Glu Ser Phe Asp Thr Ile Leu Asp Asn Arg Lys Glu Leu Ile	
198 203 208 213	
cgc tgt ctc cag cag agg gca gca cca tcc agg ccc cag gac cag gcc	846
Arg Cys Leu Gln Gln Arg Ala Ala Pro Ser Arg Pro Gln Asp Gln Ala	
214 219 224 229	
taa ggggt gtgcctccac aagtgtgcaa ggggtatatgt atatatttgc aggcattgtgt	903
*	
230	
gaggcgcact agtaagtaca taatttgctg gcatgattgc aggtaggcat gagtgtgtat	963
gtgctaacat gtaggctgggt gtgtgtaggc atgtgtgaat aagcatgtat aaatgagctt	1023
aagtgtgctg tgtgcacatg tgtacacaca gctaatttat ctgcagacct atatgtgagc	1083
atgtaagagt gaacatatgt gtgtgtgtgt agtatgtaag aatgaggaac tcggtatgtg	1143
catgtgtaga caggtaacca gcagtgtgtg tatatgcgca tgagtgagga tgtataggca	1203
gaagatgtgt gtgtctatga gtgagtttga gtgtgcaggc ttgtattagg tgtatgtgag	1263
gaagcccttg tgtgtgcagg ggtgcacatg tttggccaca ggcatgggag gtgtatgtta	1323
ggagcatgtg tgttttagg cagactcatg agcagggtgtg tgcaaataca tatccagctg	1383
cactgtgggt gtccaccac accttgtgtt cctcatggcc taccacagcc tttcttctcc	1443
actgggtccc actgttccct ggagacagag ggctagcatg ctgtcattta tctgaagggt	1503
gtggctgacc cattctcctg ggatttccca ggccacctct ctttccctt tccctcactt	1563
aaccagact tgctcagctg aggctattgt ccctgatgtt ggctttactt gtaggaggtt	1623
tagtggctgc tctggcctgc catggaattt tggtgcaat tttggcagtg tgtggagaac	1683
tggtatcagg aaagggaacc aggagtagtg atgaagatga tggtggggat ggggacagag	1743
gacatagggg actgtccctc ttgaactctg cctttgggca catgggagat ggggacagga	1803
aagatgataa cagtggaacc ctgtgaagaa taggagaatg ggaattctaa aataccagtt	1863
cccaaacaaa ccatctctcc attggaaaag gagctgttgc aaaccgtgtt catttaagct	1923
tctgatgaaa agcaatgtat gtttataagc ttgcaagtaa cagacaagat gttccaaggc	1983

cgatgaggaa aatatcgctt ccctgtctct gcctctacct tgctgtgcct ctctggcttt 2043
 agcagcattg gatgttgaat tgggttggtt catttctctg aagtcggact gtcaggagga 2103
 gccagagggt ggctttcttg gatgtgaagg ggacagtgtc agcctaagcc tctggagatg 2163
 cttaggatgc tgaattttaa ccccttcttt cactgcatgg cccttcaaac agggattggc 2223
 aggctccgag agttacagag tgggtgagtc ttggagagaa ccaacgacta aggtagctta 2283
 gctctctgct ttgttcttgg gagccaagag aatgcaagat cctggtgggt gagcagtgg 2343
 atgaagaggg gacactgggt ggtgaacagt ggcattggaag tcaactgatgc agcctctggc 2403
 cctcagtctc cctatcgga aagtgggggg ctcttccctat ctctaaagag tttcatccct 2463
 gacaggtgga tgggtgaaag atccagagag tgggggtgag ggggtgggccc tgaagacttt 2523
 ttgtctgtag ctcttgcata ttgagtgtat aaacccggct tctggaccaa cccaagatga 2583
 ataaactggg gcagaaaatt aaaaaaaaaa aa 2615

<210> 23
 <211> 1463
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (178)..(1002)

<400> 23
 aagtacacac cctccagcac gactcgggac aggcacgtgc gccctatta cctgctggag 60
 tccctcagga cacctggctg gagctgatgg gcatgggagg gtgtgtgcga gcatgagccc 120
 gcaggtctgt gagcttcgtc tccctttcct tcttcgcagt gtactaatgg tcaacttg 177
 atg tgc gct ggc tgt ttt atc cac cta cta gca gat gcc cgg ctg aag 225
 Met Cys Ala Gly Cys Phe Ile His Leu Leu Ala Asp Ala Arg Leu Lys
 1 5 10 15
 gag gag cag gcc acg tgc ccc aat tgt cgt tgt gag atc agt aag agc 273
 Glu Glu Gln Ala Thr Cys Pro Asn Cys Arg Cys Glu Ile Ser Lys Ser
 17 22 27 32
 ctc tgc tgc cgg aac ctg gcc gtg gag aaa gcc gtg agc gag ctg cct 321
 Leu Cys Cys Arg Asn Leu Ala Val Glu Lys Ala Val Ser Glu Leu Pro
 33 38 43 48
 tca gag tgt ggc ttc tgc ctg cgc cag ttt ccc cgc tcc ctc ctg gag 369
 Ser Glu Cys Gly Phe Cys Leu Arg Gln Phe Pro Arg Ser Leu Leu Glu
 49 54 59 64
 agg cac cag aaa gag gaa tgc cag gac agg gta acc cag tgc aag tac 417

Arg	His	Gln	Lys	Glu	Glu	Cys	Gln	Asp	Arg	Val	Thr	Gln	Cys	Lys	Tyr		
65					70					75					80		
aaa	cgc	atc	ggc	tgc	cca	tgg	cac	ggc	ccc	ttc	cat	gag	ctg	acg	gtg	465	
Lys	Arg	Ile	Gly	Cys	Pro	Trp	His	Gly	Pro	Phe	His	Glu	Leu	Thr	Val		
81					86					91					96		
cac	gag	gct	gcg	tgc	gcc	cac	ccg	acc	aag	aca	ggc	agt	gag	ctg	atg	513	
His	Glu	Ala	Ala	Cys	Ala	His	Pro	Thr	Lys	Thr	Gly	Ser	Glu	Leu	Met		
97					102					107					112		
gag	atc	ctg	gat	ggg	atg	gac	cag	agc	cac	cgc	aag	gag	atg	cag	ctg	561	
Glu	Ile	Leu	Asp	Gly	Met	Asp	Gln	Ser	His	Arg	Lys	Glu	Met	Gln	Leu		
113					118					123					128		
tac	aac	agc	atc	ttc	agc	ctg	ctc	agc	ttc	gag	aag	att	ggc	tac	aca	609	
Tyr	Asn	Ser	Ile	Phe	Ser	Leu	Leu	Ser	Phe	Glu	Lys	Ile	Gly	Tyr	Thr		
129					134					139					144		
gag	gtc	cag	ttc	cgg	ccg	tac	cgc	aca	gac	gac	ttc	atc	acg	cgc	ctg	657	
Glu	Val	Gln	Phe	Arg	Pro	Tyr	Arg	Thr	Asp	Asp	Phe	Ile	Thr	Arg	Leu		
145					150					155					160		
tac	tat	gag	acg	ccc	agg	ttc	aca	gtg	ctg	aac	cag	acg	tgg	gtc	ctg	705	
Tyr	Tyr	Glu	Thr	Pro	Arg	Phe	Thr	Val	Leu	Asn	Gln	Thr	Trp	Val	Leu		
161					166					171					176		
aag	gct	cga	gtc	aac	gac	tcg	gag	cgt	aac	ccc	aac	ctg	tcc	tgc	aag	753	
Lys	Ala	Arg	Val	Asn	Asp	Ser	Glu	Arg	Asn	Pro	Asn	Leu	Ser	Cys	Lys		
177					182					187					192		
cgt	acg	ctc	tcc	ttc	cag	ctc	ctc	ctc	aag	agc	aag	gtc	acg	gca	ccg	801	
Arg	Thr	Leu	Ser	Phe	Gln	Leu	Leu	Leu	Lys	Ser	Lys	Val	Thr	Ala	Pro		
193					198					203					208		
ctg	gag	tgc	tcc	ttc	ctg	ctg	ctc	aag	ggc	ccc	tac	gac	gac	gtg	agg	849	
Leu	Glu	Cys	Ser	Phe	Leu	Leu	Leu	Lys	Gly	Pro	Tyr	Asp	Asp	Val	Arg		
209					214					219					224		
atc	agc	ccc	gtc	atc	tac	cac	ttt	gtc	ttc	acc	aac	gag	agc	aac	gag	897	
Ile	Ser	Pro	Val	Ile	Tyr	His	Phe	Val	Phe	Thr	Asn	Glu	Ser	Asn	Glu		
225					230					235					240		
acg	gac	tac	gtg	cca	ctg	ccc	atc	att	gac	tcc	gtg	gag	tgc	aac	aag	945	
Thr	Asp	Tyr	Val	Pro	Leu	Pro	Ile	Ile	Asp	Ser	Val	Glu	Cys	Asn	Lys		
241					246					251					256		
ctg	ctg	gct	gcc	aag	aac	atc	aac	ctg	cgg	ctc	ttc	ctg	ttc	cag	ata	993	
Leu	Leu	Ala	Ala	Lys	Asn	Ile	Asn	Leu	Arg	Leu	Phe	Leu	Phe	Gln	Ile		
257					262					267					272		
cag	aag	tag	ggcgggg	cctcaggatg	tccgaggagc	ccacggggcgg	catcccagca									1049	
Gln	Lys	*															
273																	
ccgctgccct	gtccacctgg	ctggcagctg	cttcacagga	ctatctgatc	acttttagcaa											1109	

aggaggagaa caaacgaagc caacacaggg caagtctgca tgcgtgcgcg acggggcccc	1169
cgctccggc tcaccccccc gaccctgcc tcccctcctt ccgagggccg ccagaggctg	1229
ggctgacccg aagaggagac ggtgcaccag gcgccccgag gctaagagac ggtggcagca	1289
aggaggccga gaggcacagc gaccctgccc cagcccttct gtgcagtcag gcggcggtgc	1349
tgctccatcc ctgcgggttc cggcgggggcg cgggggcctt gctgacatca gacgggatat	1409
ccgaatatct gatagcaatt aaaaggcagc cttgtttcgt aaaaaaaaaa aaaa	1463

<210> 24
 <211> 2288
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (832)..(1752)

<400> 24	
gaggtaccgg tccggaattc ccgggtogac ccacgcgtcc ggatgaaaat ccccttggga	60
ccctgagagt gaggggaagg tcacggaagc cgagagatcc aggaatgtga ggtcagaggc	120
tgacctggtt gtccacgcgg atgttcgaaa ctcccaggat ggagagaaaa acagagcagg	180
aggaatgagg aagatgtgga cgagtgtgag gctggggacg tgtgtgacaa tggcatctgc	240
agcaacacgc caggatcttt ccagtgtcag tgccctctctg gctaccatct gtccagggac	300
cggagccact gcgaggacat tgatgagtgt gacttccctg cagcctgcat tgggggtgac	360
tgcatcaata ccaatggctc ctacagatgt ctttgccccc aggggcatcg gctggtgggt	420
ggcaggaaat gccaaagacat agatgagtgc agccaggacc cgagcctgtg cttccccat	480
ggggcctgca agaaccttca gggctcctat gtgtgtgtct gcgatgaggg cttcactccc	540
accaggacc agcacggttg tgaggaggtg gagcagcccc accacaagaa ggagtgttac	600
ctgaacttcg atgacacagt gttctgcgac agcgtattgg ccaccaacgt gaccagcag	660
gagtgtgct gctctctggg ggccggctgg ggcgaccact gcgaaatcta cccctgccca	720
gtctacagct cagccgagtt ccacagcctc tgcccagacg gaaagggcta caccaggac	780
aacaacatcg tcaactacgg catcccagcc caccgtgaca tcgacgagtg c atg ttg	837
	Met Leu

1

ttc ggg tcg gag att tgc aag gag ggc aag tgc gtg aac acg cag cct	885
Phe Gly Ser Glu Ile Cys Lys Glu Gly Lys Cys Val Asn Thr Gln Pro	

3	8	13	18	
ggc tac gag tgc tac tgc aag cag ggc ttc tac tac gac ggg aac ctg				933
Gly Tyr Glu Cys Tyr Cys Lys Gln Gly Phe Tyr Tyr Asp Gly Asn Leu				
19	24	29	34	
ctg gaa tgc gtg gac gtg gac gag tgc ctg gac gag tcc aac tgc cgg				981
Leu Glu Cys Val Asp Val Asp Glu Cys Leu Asp Glu Ser Asn Cys Arg				
35	40	45	50	
aac gga gtg tgt gag aac acg cgc ggc ggc tac cgc tgt gcc tgc acg				1029
Asn Gly Val Cys Glu Asn Thr Arg Gly Gly Tyr Arg Cys Ala Cys Thr				
51	56	61	66	
ccc cct gcc gag tac agt ccc gcg cag cgc cag tgc ctg agc ccg gaa				1077
Pro Pro Ala Glu Tyr Ser Pro Ala Gln Arg Gln Cys Leu Ser Pro Glu				
67	72	77	82	
gag atg gac gtg gac gag tgc cag gac ccg gca gcc tgc cgc cct ggc				1125
Glu Met Asp Val Asp Glu Cys Gln Asp Pro Ala Ala Cys Arg Pro Gly				
83	88	93	98	
cgc tgc gtc aac ctg ccg ggc tcc tac cgc tgc gag tgt cgc ccg ccc				1173
Arg Cys Val Asn Leu Pro Gly Ser Tyr Arg Cys Glu Cys Arg Pro Pro				
99	104	109	114	
tgg gtg ccc ggg ccc tcc ggc cgc gat tgc cag ctc ccc gag agc ccg				1221
Trp Val Pro Gly Pro Ser Gly Arg Asp Cys Gln Leu Pro Glu Ser Pro				
115	120	125	130	
gcc gag cgt gcc ccg gag cgg cgc gac gtg tgc tgg agc cag cgc gga				1269
Ala Glu Arg Ala Pro Glu Arg Arg Asp Val Cys Trp Ser Gln Arg Gly				
131	136	141	146	
gag gac ggc atg tgc gct ggc ccc ctg gcc ggg cct gcc ctc acc ttc				1317
Glu Asp Gly Met Cys Ala Gly Pro Leu Ala Gly Pro Ala Leu Thr Phe				
147	152	157	162	
gac gac tgc tgc tgc cgc cag ggc cgc ggc tgg ggc gcc caa tgc cga				1365
Asp Asp Cys Cys Cys Arg Gln Gly Arg Gly Trp Gly Ala Gln Cys Arg				
163	168	173	178	
ccg tgc ccg ccg cgc ggc gcg ggg tcc cat tgc ccg aca tcg cag agc				1413
Pro Cys Pro Pro Arg Gly Ala Gly Ser His Cys Pro Thr Ser Gln Ser				
179	184	189	194	
gag agc aat tcc ttc tgg gac aca agc ccc ctg ctg ttg ggg aag ccc				1461
Glu Ser Asn Ser Phe Trp Asp Thr Ser Pro Leu Leu Leu Gly Lys Pro				
195	200	205	210	
cca aga gat gag gac agt tca gag gag gat tca gac gag tgt cgc tgc				1509
Pro Arg Asp Glu Asp Ser Ser Glu Glu Asp Ser Asp Glu Cys Arg Cys				
211	216	221	226	
gtg agt ggc cgc tgc gtg ccg cgg ccg ggc ggc gcc gtg tgc gag tgt				1557
Val Ser Gly Arg Cys Val Pro Arg Pro Gly Gly Ala Val Cys Glu Cys				
227	232	237	242	

```

ccc ggc ggc ttc cag ctc gac gcc tcc cgc gcc cgc tgc gtg gat atc      1605
Pro Gly Gly Phe Gln Leu Asp Ala Ser Arg Ala Arg Cys Val Asp Ile
243                248                253                258

gac gag tgc cga gag ctg aac cag cgc ggc ctg ctg tgc aag agc gag      1653
Asp Glu Cys Arg Glu Leu Asn Gln Arg Gly Leu Leu Cys Lys Ser Glu
259                264                269                274

cgc tgc gtg aac acc agc ggc tcc ttc cgc tgc gtc tgc aaa gcc ggc      1701
Arg Cys Val Asn Thr Ser Gly Ser Phe Arg Cys Val Cys Lys Ala Gly
275                280                285                290

ttc gcg cgc agc cgc ccg cac ggc gcc tgc gtt ccc cag cgc cgc cgc      1749
Phe Ala Arg Ser Arg Pro His Gly Ala Cys Val Pro Gln Arg Arg Arg
291                296                301                306

tga cgcc gccgacgccg ccctcggccc agacctcggt gatcactgag ggatttcgc      1806
*
307

gagctcggcc tcactttctgc cccgacttgt ggctcggacc cagggacctt cagggcccgc      1866

agaccctccc ggcgccttga gacccgaggc gccctaccg gccccctcc ccggttagcg      1926

ggcggttgta aggtctccgg cgggcgctgc ctgccttcct cccagagggt gtttcctaga      1986

aactgataaa tcagatcgtg cctctttacc cttggctttc gaagcaaatt gatgttcacg      2046

tgtgacgtgg ggcgcgggctg cgcagggcgg cgccagacct caaccgcctc ccaggggcta      2106

gactgagccc ggcccaaggg gtgtgaaata gaatttattg tggctctgat tatgtacacg      2166

tgaaatggcc tggctgggccc ggccgggctc acatggtttg tacaataaat acatctgtgg      2226

ggcgggctct cccagccgg gaagggccccc cccccgggt cagtccaaaa aaaaaaaaaa      2286

aa                                                                2288

```

```

<210> 25
<211> 6435
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (192)..(5339)

```

```

<400> 25
atgtaccgct ccggaattcc cgggtcgacg atttcgtaga atatggccgc cgggtgtggt      60

gagggcgacg cgcttcgagt cgcggtctct tgcttccccg tcctctgaca tcgcctgcag      120

ccgagcgggc ccgttcgcc ggagctgagg accaggtatt caaataaagt taattgcagc      180

```

tttctgtgaa a atg tca gtt ttg ata tca cag agc gtc ata aat tat gta	230
Met Ser Val Leu Ile Ser Gln Ser Val Ile Asn Tyr Val	
1 5 10	
 gag gaa gaa aac att cct gct ctg aaa gct ctt ctt gaa aaa tgc aaa	278
Glu Glu Glu Asn Ile Pro Ala Leu Lys Ala Leu Leu Glu Lys Cys Lys	
14 19 24 29	
 gat gta gat gag aga aat gag tgt ggc cag act cca ctg atg ata gct	326
Asp Val Asp Glu Arg Asn Glu Cys Gly Gln Thr Pro Leu Met Ile Ala	
30 35 40 45	
 gcc gaa caa ggc aat ctg gaa ata gtg aag gaa tta att aag aat gga	374
Ala Glu Gln Gly Asn Leu Glu Ile Val Lys Glu Leu Ile Lys Asn Gly	
46 51 56 61	
 gct aac tgc aat ctg gaa gat ttg gat aat tgg aca gca ctt ata tct	422
Ala Asn Cys Asn Leu Glu Asp Leu Asp Asn Trp Thr Ala Leu Ile Ser	
62 67 72 77	
 gca tcg aaa gaa ggg cat gtg cac atc gta gag gaa cta ctg aaa tgt	470
Ala Ser Lys Glu Gly His Val His Ile Val Glu Glu Leu Leu Lys Cys	
78 83 88 93	
 ggg gtt aac ttg gag cac cgt gat atg gga gga tgg aca gct ctt atg	518
Gly Val Asn Leu Glu His Arg Asp Met Gly Gly Trp Thr Ala Leu Met	
94 99 104 109	
 tgg gca tgt tac aaa ggc cgt act gac gta gta gag ttg ctt ctt tct	566
Trp Ala Cys Tyr Lys Gly Arg Thr Asp Val Val Glu Leu Leu Leu Ser	
110 115 120 125	
 cat ggt gcc aat cca agt gtc act ggt ctg cag tac agt gtt tac cca	614
His Gly Ala Asn Pro Ser Val Thr Gly Leu Gln Tyr Ser Val Tyr Pro	
126 131 136 141	
 atc att tgg gca gca ggg aga ggc cat gca gat ata gtt cat ctt tta	662
Ile Ile Trp Ala Ala Gly Arg Gly His Ala Asp Ile Val His Leu Leu	
142 147 152 157	
 ctg caa aat ggt gct aaa gtc aac tgc tct gat aag tat gga acc acc	710
Leu Gln Asn Gly Ala Lys Val Asn Cys Ser Asp Lys Tyr Gly Thr Thr	
158 163 168 173	
 cct tta gtt tgg gct gca cga aag ggt cat ttg gaa tgt gtg aaa cat	758
Pro Leu Val Trp Ala Ala Arg Lys Gly His Leu Glu Cys Val Lys His	
174 179 184 189	
 tta ttg gcc atg gga gct gat gtg gat caa gaa gga gct aat tca atg	806
Leu Leu Ala Met Gly Ala Asp Val Asp Gln Glu Gly Ala Asn Ser Met	
190 195 200 205	
 act gca ctt att gtg gca gtg aaa gga ggt tac aca cag tca gta aaa	854
Thr Ala Leu Ile Val Ala Val Lys Gly Gly Tyr Thr Gln Ser Val Lys	
206 211 216 221	

gaa att ttg aag agg aat cca aat gta aac tta aca gat aaa gat gga	902
Glu Ile Leu Lys Arg Asn Pro Asn Val Asn Leu Thr Asp Lys Asp Gly	
222 227 232 237	
aat aca gct ttg atg att gca tca aag gag gga cat acg gag att gtg	950
Asn Thr Ala Leu Met Ile Ala Ser Lys Glu Gly His Thr Glu Ile Val	
238 243 248 253	
cag gat ctg ctc gac gct gga aca tat gtg aac ata cct gac agg agt	998
Gln Asp Leu Leu Asp Ala Gly Thr Tyr Val Asn Ile Pro Asp Arg Ser	
254 259 264 269	
ggg gat act gtg ttg att ggc gct gtc aga ggt ggt cat gtt gaa att	1046
Gly Asp Thr Val Leu Ile Gly Ala Val Arg Gly Gly His Val Glu Ile	
270 275 280 285	
gtt cga gcg ctt ctc caa aaa tat gct gat ata gac att aga gga cag	1094
Val Arg Ala Leu Leu Gln Lys Tyr Ala Asp Ile Asp Ile Arg Gly Gln	
286 291 296 301	
gat aat aaa act gct ttg tat tgg gct gtt gag aaa gga aat gca aca	1142
Asp Asn Lys Thr Ala Leu Tyr Trp Ala Val Glu Lys Gly Asn Ala Thr	
302 307 312 317	
atg gtg aga gat atc tta cag tgc aat cct gac act gaa ata tgc aca	1190
Met Val Arg Asp Ile Leu Gln Cys Asn Pro Asp Thr Glu Ile Cys Thr	
318 323 328 333	
aag gat ggt gaa acg cca ctt ata aag gct acc aag atg aga aac att	1238
Lys Asp Gly Glu Thr Pro Leu Ile Lys Ala Thr Lys Met Arg Asn Ile	
334 339 344 349	
gaa gtg gtg gag ctg ctg cta gat aaa ggt gct aaa gtg tct gct gta	1286
Glu Val Val Glu Leu Leu Leu Asp Lys Gly Ala Lys Val Ser Ala Val	
350 355 360 365	
gat aag aaa gga gat act ccc ttg cat att gct att cgt gga agg agc	1334
Asp Lys Lys Gly Asp Thr Pro Leu His Ile Ala Ile Arg Gly Arg Ser	
366 371 376 381	
cgg aaa ctg gca gaa ctg ctt tta aga aat ccc aaa gat ggg cga tta	1382
Arg Lys Leu Ala Glu Leu Leu Leu Arg Asn Pro Lys Asp Gly Arg Leu	
382 387 392 397	
ctt tat agg ccc aac aaa gca ggc gag act cct tat aat att gac tgt	1430
Leu Tyr Arg Pro Asn Lys Ala Gly Glu Thr Pro Tyr Asn Ile Asp Cys	
398 403 408 413	
agc cat cag aag agt att tta act caa ata ttt gga gcc aga cac ttg	1478
Ser His Gln Lys Ser Ile Leu Thr Gln Ile Phe Gly Ala Arg His Leu	
414 419 424 429	
tct cct act gaa aca gac ggt gac atg ctt gga tat gat tta tat agc	1526
Ser Pro Thr Glu Thr Asp Gly Asp Met Leu Gly Tyr Asp Leu Tyr Ser	
430 435 440 445	
agt gcc ctg gca gat att ctc agt gag cct acc atg cag cca ccc att	1574

Ser Ala Leu Ala Asp Ile Leu Ser Glu Pro Thr Met Gln Pro Pro Ile	
446 451 456 461	
tgt gtg ggg tta tat gca cag tgg gga agt ggg aaa tct ttc tta ctc	1622
Cys Val Gly Leu Tyr Ala Gln Trp Gly Ser Gly Lys Ser Phe Leu Leu	
462 467 472 477	
aag aaa cta gaa gac gaa atg aaa acc ttc gcc gga caa cag att gag	1670
Lys Lys Leu Glu Asp Glu Met Lys Thr Phe Ala Gly Gln Gln Ile Glu	
478 483 488 493	
cct ctc ttt cag ttc tca tgg ctc ata gtg ttt ctt acc ctg cta ctt	1718
Pro Leu Phe Gln Phe Ser Trp Leu Ile Val Phe Leu Thr Leu Leu Leu	
494 499 504 509	
tgt gga ggg ctt ggt tta ttg ttt gcc ttc acg gtc cac cca aat ctt	1766
Cys Gly Gly Leu Gly Leu Leu Phe Ala Phe Thr Val His Pro Asn Leu	
510 515 520 525	
gga ata gca gtg tca ctg agc ttc ttg gct ctc tta tat ata ttc ttt	1814
Gly Ile Ala Val Ser Leu Ser Phe Leu Ala Leu Leu Tyr Ile Phe Phe	
526 531 536 541	
att gtc att tac ttt ggt gga cga aga gaa gga gag agt tgg aat tgg	1862
Ile Val Ile Tyr Phe Gly Gly Arg Arg Glu Gly Glu Ser Trp Asn Trp	
542 547 552 557	
gcc tgg gtc ctc agc act aga ttg gca aga cat att gga tat ttg gaa	1910
Ala Trp Val Leu Ser Thr Arg Leu Ala Arg His Ile Gly Tyr Leu Glu	
558 563 568 573	
ctc ctc ctt aaa ttg atg ttt gtg aat cca cct gag ttg cca gag cag	1958
Leu Leu Leu Lys Leu Met Phe Val Asn Pro Pro Glu Leu Pro Glu Gln	
574 579 584 589	
act act aaa gct tta cct gtg agg ttt ttg ttt aca gat tac aat aga	2006
Thr Thr Lys Ala Leu Pro Val Arg Phe Leu Phe Thr Asp Tyr Asn Arg	
590 595 600 605	
ctg tcc agt gta ggt gga gaa act tct ctg gct gaa atg att gca acc	2054
Leu Ser Ser Val Gly Gly Glu Thr Ser Leu Ala Glu Met Ile Ala Thr	
606 611 616 621	
ctc tcg gat gct tgt gaa aga gag ttt ggc ttt ttg gca acc agg ctt	2102
Leu Ser Asp Ala Cys Glu Arg Glu Phe Gly Phe Leu Ala Thr Arg Leu	
622 627 632 637	
ttt cga gta ttc aag act gaa gat act cag ggt aaa aag aaa tgg aaa	2150
Phe Arg Val Phe Lys Thr Glu Asp Thr Gln Gly Lys Lys Lys Trp Lys	
638 643 648 653	
aaa aca tgt tgt ctc cca tct ttt gtc atc ttc ctt ttt atc att ggc	2198
Lys Thr Cys Cys Leu Pro Ser Phe Val Ile Phe Leu Phe Ile Ile Gly	
654 659 664 669	
tgc att ata tct gga att act ctt ctg gct ata ttt aga gtt gac cca	2246
Cys Ile Ile Ser Gly Ile Thr Leu Leu Ala Ile Phe Arg Val Asp Pro	

670	675	680	685	
aag cat ctg act gta	aat gct gtc ctc ata	tca atc gca tct gta	gtg	2294
Lys His Leu Thr Val	Asn Ala Val Leu Ile	Ser Ile Ala Ser Val	Val	
686	691	696	701	
gga ttg gcc ttt gtg	ttg aac tgt cgt aca	tgg tgg caa gtg ctg	gac	2342
Gly Leu Ala Phe Val	Leu Asn Cys Arg Thr	Trp Trp Gln Val Leu	Asp	
702	707	712	717	
tcg ctc ctg aat tcc	caa aga aaa cgc ctc	cat aat gca gcc tcc	aaa	2390
Ser Leu Leu Asn Ser	Gln Arg Lys Arg Leu	His Asn Ala Ala Ser	Lys	
718	723	728	733	
ctg cac aaa ttg aaa	agt gaa gga ttc atg	aaa gtt ctt aaa tgt	gaa	2438
Leu His Lys Leu Lys	Ser Glu Gly Phe Met	Lys Val Leu Lys Cys	Glu	
734	739	744	749	
gtg gaa ttg atg gcc	agg atg gca aaa acc	att gac agc ttc act	cag	2486
Val Glu Leu Met Ala	Arg Met Ala Lys Thr	Ile Asp Ser Phe Thr	Gln	
750	755	760	765	
aat cag aca agg ctg	gtg gtc atc atc gat	gga tta gat gcc tgt	gag	2534
Asn Gln Thr Arg Leu	Val Val Ile Ile Asp	Gly Leu Asp Ala Cys	Glu	
766	771	776	781	
cag gac aaa gtc ctt	cag atg ctg gac act	gtc cga gtt ctg ttt	tca	2582
Gln Asp Lys Val Leu	Gln Met Leu Asp Thr	Val Arg Val Leu Phe	Ser	
782	787	792	797	
aaa ggc ccg ttc att	gcc att ttt gca agt	gat cca cat att atc	ata	2630
Lys Gly Pro Phe Ile	Ala Ile Phe Ala Ser	Asp Pro His Ile Ile	Ile	
798	803	808	813	
aag gca att aac cag	aac ctc aat agt gtg	ctt cgg gat tca aat	ata	2678
Lys Ala Ile Asn Gln	Asn Leu Asn Ser Val	Leu Arg Asp Ser Asn	Ile	
814	819	824	829	
aat ggc cat gac tac	atg cgc aac ata gtc	cac ttg cct gtg ttc	ctt	2726
Asn Gly His Asp Tyr	Met Arg Asn Ile Val	His Leu Pro Val Phe	Leu	
830	835	840	845	
aat agt cgt gga cta	agc aat gca aga aaa	ttt ctc gta act tca	gca	2774
Asn Ser Arg Gly Leu	Ser Asn Ala Arg Lys	Phe Leu Val Thr Ser	Ala	
846	851	856	861	
aca aat gga gac gtt	cca tgc tca gat act	aca ggg ata cag gaa	gat	2822
Thr Asn Gly Asp Val	Pro Cys Ser Asp Thr	Thr Gly Ile Gln Glu	Asp	
862	867	872	877	
gct gac aga aga gtt	tca cag aac agc ctt	ggg gag atg aca aaa	ctt	2870
Ala Asp Arg Arg Val	Ser Gln Asn Ser Leu	Gly Glu Met Thr Lys	Leu	
878	883	888	893	
ggc agc aag aca gcc	ctc aat aga cgg gac	act tac cga aga agg	cag	2918
Gly Ser Lys Thr Ala	Leu Asn Arg Arg Asp	Thr Tyr Arg Arg Arg	Gln	
894	899	904	909	

atg cag agg acc atc act cgc cag atg tcc ttt gat ctt aca aaa ctg	2966
Met Gln Arg Thr Ile Thr Arg Gln Met Ser Phe Asp Leu Thr Lys Leu	
910 915 920 925	
ctg gtt acc gag gac tgg ttc agt gac atc agt ccc cag acc atg aga	3014
Leu Val Thr Glu Asp Trp Phe Ser Asp Ile Ser Pro Gln Thr Met Arg	
926 931 936 941	
aga tta ctt aat att gtt tct gtg aca gga cga tta ctg aga gcc aat	3062
Arg Leu Leu Asn Ile Val Ser Val Thr Gly Arg Leu Leu Arg Ala Asn	
942 947 952 957	
cag att agt ttc aac tgg gac agg ctt gct agc tgg atc aac ctt act	3110
Gln Ile Ser Phe Asn Trp Asp Arg Leu Ala Ser Trp Ile Asn Leu Thr	
958 963 968 973	
gag cag tgg cca tac cgg act tca tgg ctc ata tta tat ttg gaa gag	3158
Glu Gln Trp Pro Tyr Arg Thr Ser Trp Leu Ile Leu Tyr Leu Glu Glu	
974 979 984 989	
act gaa ggt att cca gat caa atg aca tta aaa acc atc tac gaa aga	3206
Thr Glu Gly Ile Pro Asp Gln Met Thr Leu Lys Thr Ile Tyr Glu Arg	
990 995 1000 1005	
ata tca aag aat att cca aca act aag gat gtt gag cca ctt ctt gaa	3254
Ile Ser Lys Asn Ile Pro Thr Thr Lys Asp Val Glu Pro Leu Leu Glu	
1006 1011 1016 1021	
att gat gga gat ata aga aat ttt gaa gtg ttt ttg tct tca agg acc	3302
Ile Asp Gly Asp Ile Arg Asn Phe Glu Val Phe Leu Ser Ser Arg Thr	
1022 1027 1032 1037	
cca gtt ctt gtg gct cga gat gta aaa gtc ttt ttg cca tgc act gta	3350
Pro Val Leu Val Ala Arg Asp Val Lys Val Phe Leu Pro Cys Thr Val	
1038 1043 1048 1053	
aac cta gat ccc aaa cta cgg gaa att att gca gat gtt cgt gct gcc	3398
Asn Leu Asp Pro Lys Leu Arg Glu Ile Ile Ala Asp Val Arg Ala Ala	
1054 1059 1064 1069	
aga gag cag atc agt att gga gga ctg gcg tac ccc ccg ctc cct cta	3446
Arg Glu Gln Ile Ser Ile Gly Gly Leu Ala Tyr Pro Pro Leu Pro Leu	
1070 1075 1080 1085	
cat gag ggt cct cct agg gcg cca tca ggg tac agc cag ccc cca tcc	3494
His Glu Gly Pro Pro Arg Ala Pro Ser Gly Tyr Ser Gln Pro Pro Ser	
1086 1091 1096 1101	
gtg tgc tct tcc acg tcc ttc aat ggg ccc ttc gca ggt gga gtg gtg	3542
Val Cys Ser Ser Thr Ser Phe Asn Gly Pro Phe Ala Gly Gly Val Val	
1102 1107 1112 1117	
tca cca cag cct cac agc agc tat tac agc ggc atg acg ggc cct cag	3590
Ser Pro Gln Pro His Ser Ser Tyr Tyr Ser Gly Met Thr Gly Pro Gln	
1118 1123 1128 1133	

cat ccc ttc tac aac agg ggg tca ggc cca gcc cca ggc cca gtg gta His Pro Phe Tyr Asn Arg Gly Ser Gly Pro Ala Pro Gly Pro Val Val 1134 1139 1144 1149	3638
tta ctg aat tca ctg aat gtg gat gca gta tgt gag aag ctg aaa caa Leu Leu Asn Ser Leu Asn Val Asp Ala Val Cys Glu Lys Leu Lys Gln 1150 1155 1160 1165	3686
ata gaa ggg ctg gac cag agt atg ctg cct cag tat tgt acc acg atc Ile Glu Gly Leu Asp Gln Ser Met Leu Pro Gln Tyr Cys Thr Thr Ile 1166 1171 1176 1181	3734
aaa aag gca aac ata aat ggc cgt gtg tta gct cag tgt aac att gat Lys Lys Ala Asn Ile Asn Gly Arg Val Leu Ala Gln Cys Asn Ile Asp 1182 1187 1192 1197	3782
gag ctg aag aaa gag atg aat atg aat ttt gga gac tgg cac ctt ttc Glu Leu Lys Lys Glu Met Asn Met Asn Phe Gly Asp Trp His Leu Phe 1198 1203 1208 1213	3830
aga agc aca gta cta gaa atg aga aac gca gaa agc cac gtg gtc cct Arg Ser Thr Val Leu Glu Met Arg Asn Ala Glu Ser His Val Val Pro 1214 1219 1224 1229	3878
gaa gac cca cgt ttc ctc agt gag agc agc agt ggc cca gcc ccg cac Glu Asp Pro Arg Phe Leu Ser Glu Ser Ser Ser Gly Pro Ala Pro His 1230 1235 1240 1245	3926
ggg gag cct gct cgc cgc gct tcc cac aac gag ctg cct cac acc gag Gly Glu Pro Ala Arg Arg Ala Ser His Asn Glu Leu Pro His Thr Glu 1246 1251 1256 1261	3974
ctc tcc agc cag acg ccc tac aca ctc aac ttc agc ttc gaa gag ctg Leu Ser Ser Gln Thr Pro Tyr Thr Leu Asn Phe Ser Phe Glu Glu Leu 1262 1267 1272 1277	4022
aac acg ctt ggc ctg gat gaa ggt gcc cct cgt cac agt aat cta agt Asn Thr Leu Gly Leu Asp Glu Gly Ala Pro Arg His Ser Asn Leu Ser 1278 1283 1288 1293	4070
tgg cag tca caa act cgc aga acc cca agt ctt tcg agt ctc aat tcc Trp Gln Ser Gln Thr Arg Arg Thr Pro Ser Leu Ser Ser Leu Asn Ser 1294 1299 1304 1309	4118
cag gat tcc agt att gaa att tca aag ctt act gat aag gtg cag gcc Gln Asp Ser Ser Ile Glu Ile Ser Lys Leu Thr Asp Lys Val Gln Ala 1310 1315 1320 1325	4166
gag tat aga gat gcc tat aga gaa tac att got cag atg tcc cag tta Glu Tyr Arg Asp Ala Tyr Arg Glu Tyr Ile Ala Gln Met Ser Gln Leu 1326 1331 1336 1341	4214
gaa ggg ggc ccc ggg tct aca acc att agt ggc aga tct tct cca cat Glu Gly Gly Pro Gly Ser Thr Thr Ile Ser Gly Arg Ser Ser Pro His 1342 1347 1352 1357	4262
agc aca tat tac atg ggt cag agt tca tca ggg ggc tct att cat tca	4310

Ser Thr Tyr Tyr Met Gly Gln Ser Ser Ser Gly Gly Ser Ile His Ser	
1358 1363 1368 1373	
aac cta gag caa gaa aag ggg aag gat agt gaa cca aag ccc gat gat	4358
Asn Leu Glu Gln Glu Lys Gly Lys Asp Ser Glu Pro Lys Pro Asp Asp	
1374 1379 1384 1389	
ggg agg aag tcc ttt cta atg aag agg gga gat gtt atc gat tat tca	4406
Gly Arg Lys Ser Phe Leu Met Lys Arg Gly Asp Val Ile Asp Tyr Ser	
1390 1395 1400 1405	
tca tca ggg gtt tcc acc aac gat gct tcc ccc ctg gat cct atc act	4454
Ser Ser Gly Val Ser Thr Asn Asp Ala Ser Pro Leu Asp Pro Ile Thr	
1406 1411 1416 1421	
gaa gaa gat gaa aaa tca gat cag tca ggc agt aag ctt ctc cca ggc	4502
Glu Glu Asp Glu Lys Ser Asp Gln Ser Gly Ser Lys Leu Leu Pro Gly	
1422 1427 1432 1437	
aag aaa tct tcc gaa agg tca agc ctc ttc cag aca gat ttg aag ctt	4550
Lys Lys Ser Ser Glu Arg Ser Ser Leu Phe Gln Thr Asp Leu Lys Leu	
1438 1443 1448 1453	
aag gga agt ggg ctg cgc tat caa aaa ctc cca agt gac gag gat gaa	4598
Lys Gly Ser Gly Leu Arg Tyr Gln Lys Leu Pro Ser Asp Glu Asp Glu	
1454 1459 1464 1469	
tct ggc aca gaa gaa tca gat aac act cca ctg ctc aaa gat gac aaa	4646
Ser Gly Thr Glu Glu Ser Asp Asn Thr Pro Leu Leu Lys Asp Asp Lys	
1470 1475 1480 1485	
gac aga aaa gcc gaa ggg aaa gta gag aga gtg ccg aag tct cca gaa	4694
Asp Arg Lys Ala Glu Gly Lys Val Glu Arg Val Pro Lys Ser Pro Glu	
1486 1491 1496 1501	
cac agt gct gag ccg atc aga acc ttc att aaa gcc aaa gag tat tta	4742
His Ser Ala Glu Pro Ile Arg Thr Phe Ile Lys Ala Lys Glu Tyr Leu	
1502 1507 1512 1517	
tcg gat gcg ctc ctt gac aaa aag gat tca tcg gat tca gga gtg aga	4790
Ser Asp Ala Leu Leu Asp Lys Lys Asp Ser Ser Asp Ser Gly Val Arg	
1518 1523 1528 1533	
tcc agt gaa agt tct ccc aat cac tct ctg cac aat gaa gtg gcg gat	4838
Ser Ser Glu Ser Ser Pro Asn His Ser Leu His Asn Glu Val Ala Asp	
1534 1539 1544 1549	
gac tcc cag ctt gaa aag gca aat ctc ata gag ctg gaa gat gac agt	4886
Asp Ser Gln Leu Glu Lys Ala Asn Leu Ile Glu Leu Glu Asp Asp Ser	
1550 1555 1560 1565	
cac agc gga aag cgg gga atc cca cat agc ctg agt ggc ctg caa gat	4934
His Ser Gly Lys Arg Gly Ile Pro His Ser Leu Ser Gly Leu Gln Asp	
1566 1571 1576 1581	
cca att ata gct cgg atg tcc att tgt tca gaa gac aag aaa agc cct	4982
Pro Ile Ile Ala Arg Met Ser Ile Cys Ser Glu Asp Lys Lys Ser Pro	

1582	1587	1592	1597	
tcc gaa tgc agc ttg ata gcc agc agc cct gaa gaa aac tgg cct gca				5030
Ser Glu Cys Ser Leu Ile Ala Ser Ser Pro Glu Glu Asn Trp Pro Ala				
1598	1603	1608	1613	
tgc cag aaa gcc tac aac ctg aac cga act ccc agc acc gtg act ctg				5078
Cys Gln Lys Ala Tyr Asn Leu Asn Arg Thr Pro Ser Thr Val Thr Leu				
1614	1619	1624	1629	
aac aac aat agt gct cca gcc aac aga gcc aat caa aat ttc gat gag				5126
Asn Asn Asn Ser Ala Pro Ala Asn Arg Ala Asn Gln Asn Phe Asp Glu				
1630	1635	1640	1645	
atg gag gga att agg gag act tct caa gtc att ttg agg cct agt tcc				5174
Met Glu Gly Ile Arg Glu Thr Ser Gln Val Ile Leu Arg Pro Ser Ser				
1646	1651	1656	1661	
agt ccc aac cca acc act att cag aat gag aat cta aaa agc atg aca				5222
Ser Pro Asn Pro Thr Thr Ile Gln Asn Glu Asn Leu Lys Ser Met Thr				
1662	1667	1672	1677	
cat aag cga agc caa cgt tca agt tac aca agg ctc tcc aaa gat cct				5270
His Lys Arg Ser Gln Arg Ser Ser Tyr Thr Arg Leu Ser Lys Asp Pro				
1678	1683	1688	1693	
ccg gag ctc cat gca gca gcc tct tct gag agc aca ggc ttt gga gaa				5318
Pro Glu Leu His Ala Ala Ala Ser Ser Glu Ser Thr Gly Phe Gly Glu				
1694	1699	1704	1709	
gaa aga gaa agc att ctt tga ga aaaacaagca aaggagaaga gtgttactgt				5371
Glu Arg Glu Ser Ile Leu *				
1710	1715			
acccttatga cagaattgtc ctggattttg actccatcca cgcccatcac ctttctacat				5431
tttgctgaca gataactaac cgatgatgag gccgaggtaa aagagacatc tgcagtgtga				5491
cagaagggag catgagaagc atggctcacc agccagcctc tgtgggtcttt gtaattagaa				5551
gcttcagaac tcactaatac tactgtacct ttcatgtggc cattacccca taaaactttt				5611
tgagacgagg tgagatctga gtataaagat aggtcagaag tatttttaaag ggcttaatgt				5671
gccaaaaaga aaaaaagcta gagacccttt ttgcaaacat ttggtgacca cacatttgag				5731
ggaagacgtg gcgttaggtg aagcagaagc aaaccctgct cttaggggct cacctaggtg				5791
agtgcacagc ctgtgacgct acaggagag gctgagtaaa ccgagatcca gcgttctgta				5851
tggcaggggt attgcttatac acagagggtc tgaagagtag gaagtacata atgaagaggg				5911
ctttaaaaat tgccaacaaa gtgagtcacc agggctggca gtagtgtgac ggggctgtcc				5971
tgagctgtta ggagagtaga tgcggggagg gctggtgacc tccgtgggtt tatatgtcgg				6031
aaactcttct ctccaaatcc caggcctggc ttccagcacc atccagctgt gcccaagaag				6091

ccaccctgggt ctgttctcca actcttttaa atgggtgcca acttttctaa gtgagcttag 6151
 caatgagaag aaaaaaaaaac atgaattctt tttctggaaa atcagggaga catgggtaat 6211
 aataggtact aataaatatt tatagatgag tgaatgagga aataattaca tcaaaaaggt 6271
 cagtgacaat tgataaatga caaggaaata tttaattagg taaaactaaa tcattgctct 6331
 ctatactagg atagacttta tctacttcat ctgttcctaa gtcagcatgt tagttctggg 6391
 gaaggatcat aagaaaggaa atacttttta aaaaaaaaaa aaaa 6435

<210> 26
 <211> 932
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (428)..(835)

<400> 26
 tgtattgggtg gtgtcacca agtgggtacag ccctaagcaa gtgaacacaa acacatttaa 60
 gtgtatttttg tctgattaga tgtagccag ttatgctatt tcattcaaat gtctgaaaaa 120
 atcaattgac tattcccttt tcctaaaggg cagagacaga taatctcact tccagagaaa 180
 tgacttggag aaaaaaaagt gttggtcttt ttgctctttt gtaattaaat ccggatgtac 240
 ctcaaaagac ttaagactgt ggtgataaga tgctttcttc agcagaaagg agggaaaaaa 300
 aacaactgga actcaaagct tgaaattctg tggcaaaaca tgagatgtcc aggattggag 360
 gttgaaaaga ttctactaca gtgttctgca atagttggag cagataactt tcagtgtagc 420
 cacagcc atg gac tcc aga ttt cca gat ttt caa gac ctg gac ctg gaa 469
 Met Asp Ser Arg Phe Pro Asp Phe Gln Asp Leu Asp Leu Glu
 1 5 10
 ccc gaa aga gct tgt cac gat gcg gca gga aca ctg gag gta gat ttt 517
 Pro Glu Arg Ala Cys His Asp Ala Ala Gly Thr Leu Glu Val Asp Phe
 15 20 25 30
 ttt tta ttt ttg aat ttt ggg act gtt gac ctt gct gtg aga aaa gag 565
 Phe Leu Phe Leu Asn Phe Gly Thr Val Asp Leu Ala Val Arg Lys Glu
 31 36 41 46
 aca acg act gag caa gca cta cca cca gca ctg tta ctg gga att aga 613
 Thr Thr Thr Glu Gln Ala Leu Pro Pro Ala Leu Leu Leu Gly Ile Arg
 47 52 57 62
 aga cct gag ttt ctg tcc aga ccc tca gtg caa act gag gat gct cca 661

Cys Lys Asp Ile Asn Asn Asp Tyr Leu Ala Glu Arg Ser Ile Glu Glu
42 47 52 57

gtg tat tac ctt tgg tgt ttg gct gga ggt gac ttg gag aaa gag ctt 483
Val Tyr Tyr Leu Trp Cys Leu Ala Gly Gly Asp Leu Glu Lys Glu Leu
58 63 68 73

gtc aac aag gaa atc att cga tcc aaa cca cct atc tgc aca ctc ccc 531
Val Asn Lys Glu Ile Ile Arg Ser Lys Pro Pro Ile Cys Thr Leu Pro
74 79 84 89

aat ttt ctc ttt gag gat ggt gaa agc ttt gga caa ggt cga gat aga 579
Asn Phe Leu Phe Glu Asp Gly Glu Ser Phe Gly Gln Gly Arg Asp Arg
90 95 100 105

agc tcg ctt tta gat gat acc act gtg aca ttg tcg tta tgc cag cta 627
Ser Ser Leu Leu Asp Asp Thr Thr Val Thr Leu Ser Leu Cys Gln Leu
106 111 116 121

aga aat aga ttg aaa gat gtt ggt gga gaa gca ttt tac cca tta ctt 675
Arg Asn Arg Leu Lys Asp Val Gly Gly Glu Ala Phe Tyr Pro Leu Leu
122 127 132 137

gaa gat gac cag tct aat tta cct cat tca aac agc aat aat gag ttg 723
Glu Asp Asp Gln Ser Asn Leu Pro His Ser Asn Ser Asn Asn Glu Leu
138 143 148 153

tct gca gct gcc acg ctc cct tta atc atc aga gag aag gat aca gag 771
Ser Ala Ala Ala Thr Leu Pro Leu Ile Ile Arg Glu Lys Asp Thr Glu
154 159 164 169

tac caa cta aat aga att att ctc ttc gac agg ctg cta aag gct tat 819
Tyr Gln Leu Asn Arg Ile Ile Leu Phe Asp Arg Leu Leu Lys Ala Tyr
170 175 180 185

cca tat aaa aaa aac caa atc tgg aaa gaa gca aga gtt gac att cct 867
Pro Tyr Lys Lys Asn Gln Ile Trp Lys Glu Ala Arg Val Asp Ile Pro
186 191 196 201

cct ctt atg aga ggt tta acc tgg gct gct ctt ctg gga gtt gag gga 915
Pro Leu Met Arg Gly Leu Thr Trp Ala Ala Leu Leu Gly Val Glu Gly
202 207 212 217

gct att cat gcc aag tac gat gca att gat aaa gac act cca att cct 963
Ala Ile His Ala Lys Tyr Asp Ala Ile Asp Lys Asp Thr Pro Ile Pro
218 223 228 233

aca gat aga caa att gaa gtg gat att cct cgc tgt cat cag tac gat 1011
Thr Asp Arg Gln Ile Glu Val Asp Ile Pro Arg Cys His Gln Tyr Asp
234 239 244 249

gaa ctg tta tca tca cca gaa ggt cat gca aaa ttt agg cgt gta tta 1059
Glu Leu Leu Ser Ser Pro Glu Gly His Ala Lys Phe Arg Arg Val Leu
250 255 260 265

aaa gcc tgg gta gtg tct cat cct gat ctt gtg tat tgg caa ggt ctt 1107
Lys Ala Trp Val Val Ser His Pro Asp Leu Val Tyr Trp Gln Gly Leu

266	271	276	281	
gac tca ctt tgt gct cca ttc cta tat cta aac ttc aat aat gaa gcc				1155
Asp Ser Leu Cys Ala Pro Phe Leu Tyr Leu Asn Phe Asn Asn Glu Ala				
282	287	292	297	
ttg gct tat gca tgt atg tct gct ttt att ccc aaa tac ctg tat aac				1203
Leu Ala Tyr Ala Cys Met Ser Ala Phe Ile Pro Lys Tyr Leu Tyr Asn				
298	303	308	313	
ttc ttc tta aaa gac aac tca cat gta ata caa gag tat ctg act gtc				1251
Phe Phe Leu Lys Asp Asn Ser His Val Ile Gln Glu Tyr Leu Thr Val				
314	319	324	329	
ttc tct cag atg att gca ttt cat gat cca gag ctg agt aat cat ctc				1299
Phe Ser Gln Met Ile Ala Phe His Asp Pro Glu Leu Ser Asn His Leu				
330	335	340	345	
aat gag att ggt ttc att cca gat ctc tat gcc atc cct tgg ttt ctt				1347
Asn Glu Ile Gly Phe Ile Pro Asp Leu Tyr Ala Ile Pro Trp Phe Leu				
346	351	356	361	
acc atg ttt act cat gta ttt cca cta cac aaa att ttc cac ctc tgg				1395
Thr Met Phe Thr His Val Phe Pro Leu His Lys Ile Phe His Leu Trp				
362	367	372	377	
gat acc tta cta ctt ggg aat tcc tct ttc cca ttc tgt att ggg agt				1443
Asp Thr Leu Leu Leu Gly Asn Ser Ser Phe Pro Phe Cys Ile Gly Ser				
378	383	388	393	
agc aat tct tca ggc agc tgc ggg acc ggc ttt tgg gct aat ggc ttt				1491
Ser Asn Ser Ser Gly Ser Cys Gly Thr Gly Phe Trp Ala Asn Gly Phe				
394	399	404	409	
aat gag tgt att ctt ctc ttc tcc gat tta cca gaa att gac att gaa				1539
Asn Glu Cys Ile Leu Leu Phe Ser Asp Leu Pro Glu Ile Asp Ile Glu				
410	415	420	425	
cgc tgt gtg aga gaa tct atc aac ctg ttt tgt tgg act cct aaa agt				1587
Arg Cys Val Arg Glu Ser Ile Asn Leu Phe Cys Trp Thr Pro Lys Ser				
426	431	436	441	
gct act tac aga cag cat gct caa cct cca aag cca tct tct gac agc				1635
Ala Thr Tyr Arg Gln His Ala Gln Pro Pro Lys Pro Ser Ser Asp Ser				
442	447	452	457	
agt gga ggc aga agt tgc gca cct tat ttc tct gct gag tgt cca gat				1683
Ser Gly Gly Arg Ser Ser Ala Pro Tyr Phe Ser Ala Glu Cys Pro Asp				
458	463	468	473	
cct cca aag aca gat ctg tca aga gaa tcc atc cca tta aat gac ctg				1731
Pro Pro Lys Thr Asp Leu Ser Arg Glu Ser Ile Pro Leu Asn Asp Leu				
474	479	484	489	
aag tca gaa gta tca cca cgg att tca gca gag gac ctg att gac ttg				1779
Lys Ser Glu Val Ser Pro Arg Ile Ser Ala Glu Asp Leu Ile Asp Leu				
490	495	500	505	

tgt gag ctc aca gtg aca ggc cac ttc aaa aca ccc agc aag aaa aca	1827
Cys Glu Leu Thr Val Thr Gly His Phe Lys Thr Pro Ser Lys Lys Thr	
506 511 516 521	
aag tcc agt aaa cca aag ctc ctg gtg gtt gac atc cgg aat agt gaa	1875
Lys Ser Ser Lys Pro Lys Leu Leu Val Val Asp Ile Arg Asn Ser Glu	
522 527 532 537	
gac ttt att cgt ggt cac att tca gga agc atc aac att cca ttc agt	1923
Asp Phe Ile Arg Gly His Ile Ser Gly Ser Ile Asn Ile Pro Phe Ser	
538 543 548 553	
gct gcc ttc act gca gaa ggg gag ctt acc cag ggc cct tac act gct	1971
Ala Ala Phe Thr Ala Glu Gly Glu Leu Thr Gln Gly Pro Tyr Thr Ala	
554 559 564 569	
atg ctc cag aac ttc aaa ggg aag gtc att gtc atc gtg ggg cat gtg	2019
Met Leu Gln Asn Phe Lys Gly Lys Val Ile Val Ile Val Gly His Val	
570 575 580 585	
gca aaa cac aca gct gag ttt gca gct cac ctt gtg aag atg aaa tat	2067
Ala Lys His Thr Ala Glu Phe Ala Ala His Leu Val Lys Met Lys Tyr	
586 591 596 601	
cca aga atc tgt att cta gat ggt ggc att aat aaa ata aag cca aca	2115
Pro Arg Ile Cys Ile Leu Asp Gly Gly Ile Asn Lys Ile Lys Pro Thr	
602 607 612 617	
ggc ctc ctc acc atc cca tct cct caa ata tga agaacc aa gagtgtgact	2166
Gly Leu Leu Thr Ile Pro Ser Pro Gln Ile *	
618 623 628	
gccaaaaactt agtgtggcat cagcaccaac agcacagttc ttcatatoca cgccactctc	2226
agacaaaaact agatgtccag attgttgcat ttccgtaaag tttgtcacga gacatttttt	2286
aaaatctcat aaccacatg ttcagttatc catgcaagaa acttgactct acatgtattg	2346
ctgaaagaat tttcttaaca gtgaaatctg atcatatatt tttaccacac tgccacataa	2406
agcccaagaa attcagctga caagacagat ttagcattat caagaaatcc catttgccct	2466
gaaaaagctg tcttcattg tactgaacag acagtcctgt cgattgtgtt atttagaaac	2526
atacactgaa tgtgggctga aatcatcatc tttccataat gaaaactgag aaactattca	2586
caatgcattc cttataaata aatgctacat ttagtaactc atttcaccca aacaagaaaa	2646
aaaaaaaaaa aa	2658

<210> 28
 <211> 4040
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (40)..(1782)

<400> 28

```
gcacgagggga cacgcagcct cgcgtgtcag gggaagctg   atg gag aat cga gct   54
                                     Met Glu Asn Arg Ala
                                     1

ctg gat cca ggg act cgg gac tcc tat ggt gcc acc agc cac ctc ccc   102
Leu Asp Pro Gly Thr Arg Asp Ser Tyr Gly Ala Thr Ser His Leu Pro
 6                               11                               16                               21

aac aag ggg gcc ctg gcg aag gtc aag aac aac ttc aaa gac ttg atg   150
Asn Lys Gly Ala Leu Ala Lys Val Lys Asn Asn Phe Lys Asp Leu Met
22                               27                               32                               37

tcc aaa ctg acg gag ggc cag tat gtg ctg tgc cgg tgg aca gat ggc   198
Ser Lys Leu Thr Glu Gly Gln Tyr Val Leu Cys Arg Trp Thr Asp Gly
38                               43                               48                               53

ctg tac tac ctc ggg aag atc aag agg gtc agc agc tct aag caa agc   246
Leu Tyr Tyr Leu Gly Lys Ile Lys Arg Val Ser Ser Ser Lys Gln Ser
54                               59                               64                               69

tgc ctc gtg act ttc gaa gat aat tcc aaa tac tgg gtc cta tgg aag   294
Cys Leu Val Thr Phe Glu Asp Asn Ser Lys Tyr Trp Val Leu Trp Lys
70                               75                               80                               85

gac ata cag cat gcc ggt gtt cca gga gag gag ccc aag tgc aac atc   342
Asp Ile Gln His Ala Gly Val Pro Gly Glu Glu Pro Lys Cys Asn Ile
86                               91                               96                               101

tgc cta ggg aag aca tca ggg ccg ctg aat gag atc ctc atc tgc ggg   390
Cys Leu Gly Lys Thr Ser Gly Pro Leu Asn Glu Ile Leu Ile Cys Gly
102                               107                               112                               117

aag tgt ggc ctg ggt tac cac cag cag tgc cac atc ccc ata gcg ggc   438
Lys Cys Gly Leu Gly Tyr His Gln Gln Cys His Ile Pro Ile Ala Gly
118                               123                               128                               133

agt gct gac cag ccc ctg ctc aca cct tgg ttc tgc cga cgc tgc atc   486
Ser Ala Asp Gln Pro Leu Leu Thr Pro Trp Phe Cys Arg Arg Cys Ile
134                               139                               144                               149

ttc gca ctg gct gtg cgg aaa ggc ggc gcg ctg aag aag ggc gcc atc   534
Phe Ala Leu Ala Val Arg Lys Gly Gly Ala Leu Lys Lys Gly Ala Ile
150                               155                               160                               165

gcc agg acg ctg cag gcc gtg aag atg gtg ctg tcc tac cag ccc gag   582
Ala Arg Thr Leu Gln Ala Val Lys Met Val Leu Ser Tyr Gln Pro Glu
166                               171                               176                               181

gag ctc gag tgg gac tcg ccc cat cgc acc aac cag cag caa tgc tac   630
Glu Leu Glu Trp Asp Ser Pro His Arg Thr Asn Gln Gln Gln Cys Tyr
```

182	187	192	197	
tgc tac tgc ggc ggg ccc gga gaa tgg tac ctg cgg atg ctg caa tgt				678
Cys Tyr Cys Gly Gly Pro Gly Glu Trp Tyr Leu Arg Met Leu Gln Cys				
198	203	208	213	
tac cgg tgc agg cag tgg ttc cac gag gcc tgc acc cag tgc ctc aat				726
Tyr Arg Cys Arg Gln Trp Phe His Glu Ala Cys Thr Gln Cys Leu Asn				
214	219	224	229	
gag ccc atg atg ttt gga gac cgg ttt tac ctg ttc ttc tgc tcc gtg				774
Glu Pro Met Met Phe Gly Asp Arg Phe Tyr Leu Phe Phe Cys Ser Val				
230	235	240	245	
tgt aac cag ggc cca gag tac atc gag agg ctg ccc ctg cga tgg gtg				822
Cys Asn Gln Gly Pro Glu Tyr Ile Glu Arg Leu Pro Leu Arg Trp Val				
246	251	256	261	
gat gtg gtt cac ctg gcc ctc tat aat ctg ggg gta cag agc aag aag				870
Asp Val Val His Leu Ala Leu Tyr Asn Leu Gly Val Gln Ser Lys Lys				
262	267	272	277	
aag tac ttt gac ttt gag gag att ctg gcc ttt gtc aac cac cac tgg				918
Lys Tyr Phe Asp Phe Glu Glu Ile Leu Ala Phe Val Asn His His Trp				
278	283	288	293	
gag ctc ctg cag ctt ggc aag ctc acc agc acc cca gtg aca gat cga				966
Glu Leu Leu Gln Leu Gly Lys Leu Thr Ser Thr Pro Val Thr Asp Arg				
294	299	304	309	
gga cca cat ctc ctc aac gct ctg aac agt tat aaa agc cgg ttc ctc				1014
Gly Pro His Leu Leu Asn Ala Leu Asn Ser Tyr Lys Ser Arg Phe Leu				
310	315	320	325	
tgc ggc aag gag atc aag aag aag aag tgc atc ttc cgc ctg cgc atc				1062
Cys Gly Lys Glu Ile Lys Lys Lys Lys Cys Ile Phe Arg Leu Arg Ile				
326	331	336	341	
cgc gtc cca ccc aac ccg cca ggg aag ctg ctg cct gac aaa gga ctg				1110
Arg Val Pro Pro Asn Pro Pro Gly Lys Leu Leu Pro Asp Lys Gly Leu				
342	347	352	357	
ctg cca aat gag aac agc gcc tcc tct gag ctg cgt aag aga gga aag				1158
Leu Pro Asn Glu Asn Ser Ala Ser Ser Glu Leu Arg Lys Arg Gly Lys				
358	363	368	373	
agc aag cct ggt ttg ttg cct cac gaa ttc cag cag cag aaa agg cga				1206
Ser Lys Pro Gly Leu Leu Pro His Glu Phe Gln Gln Gln Lys Arg Arg				
374	379	384	389	
gtt tat aga aga aaa aga tca aag ttt ttg ctg gaa gat gct att ccc				1254
Val Tyr Arg Arg Lys Arg Ser Lys Phe Leu Leu Glu Asp Ala Ile Pro				
390	395	400	405	
agt agt gac ttc acc tca gcc tgg agc acc aac cac cac ctg gct agc				1302
Ser Ser Asp Phe Thr Ser Ala Trp Ser Thr Asn His His Leu Ala Ser				
406	411	416	421	

ata ttt gac ttc acg ctg gat gaa att caa agt tta aaa agt gcc agc	1350
Ile Phe Asp Phe Thr Leu Asp Glu Ile Gln Ser Leu Lys Ser Ala Ser	
422 427 432 437	
tca ggc cag acc ttc ttc tca gat gtc gac tcc acc gac gct gcc agc	1398
Ser Gly Gln Thr Phe Phe Ser Asp Val Asp Ser Thr Asp Ala Ala Ser	
438 443 448 453	
acc tct ggc tct gcc tcc acc agc ctc tcc tat gac tcc aga tgg aca	1446
Thr Ser Gly Ser Ala Ser Thr Ser Leu Ser Tyr Asp Ser Arg Trp Thr	
454 459 464 469	
gtg ggc agc cga aag agg aag ctg gca gcc aag gca tac atg ccc ctg	1494
Val Gly Ser Arg Lys Arg Lys Leu Ala Ala Lys Ala Tyr Met Pro Leu	
470 475 480 485	
cgg gca aag cgg tgg gca gct gag ctg gat gga cgc tgc ccc tcc gac	1542
Arg Ala Lys Arg Trp Ala Ala Glu Leu Asp Gly Arg Cys Pro Ser Asp	
486 491 496 501	
agc agt gca gag ggg gct tca gtc ccc gag cgg cca gac gaa ggc att	1590
Ser Ser Ala Glu Gly Ala Ser Val Pro Glu Arg Pro Asp Glu Gly Ile	
502 507 512 517	
gac agc cac aca ttt gag agc atc agt gaa gat gac tca tcc ctg tcc	1638
Asp Ser His Thr Phe Glu Ser Ile Ser Glu Asp Asp Ser Ser Leu Ser	
518 523 528 533	
cac ctc aag tca tct atc acc aac tac ttt ggt gca gct ggg cgg ttg	1686
His Leu Lys Ser Ser Ile Thr Asn Tyr Phe Gly Ala Ala Gly Arg Leu	
534 539 544 549	
gcc tgt ggg gag aag tac cag gtg ttg gct cgg agg gtc aca cct gag	1734
Ala Cys Gly Glu Lys Tyr Gln Val Leu Ala Arg Arg Val Thr Pro Glu	
550 555 560 565	
ggc aag gtt cag tac ctg gtg gag tgg gaa ggg acc acc cct tac tga	1782
Gly Lys Val Gln Tyr Leu Val Glu Trp Glu Gly Thr Thr Pro Tyr *	
566 571 576 581	
ctagcccccg ggggtgccag gggtcctgaa aaccaaagga ggagcagcag aagccatagg	1842
ctccccagct ttctccaggc tgggggtggga gaaggaagca ggacagagct gcaagtgcct	1902
ggcagaatgc cctgcctgcc tgcctgcctg ccaggccaag gcctgcgtct ctctgctgta	1962
ccagctctgt tccagggcct cctcaggetc gttacccttg tgcctgtgtc tctacacact	2022
ccacaccccc tcaaactctg tttatctgtt ctctgacctt gtgtcccttg cgctgggacc	2082
cttcctctctg aggcccaggt ctttgtcccc agttgtgtgc cttgacctct ctgcacctt	2142
tctgggtgtg ttgcacatc ctgtgtgtgc acagctgtcc ctccactgga tccccttcac	2202
acgtgacctg tggggcagcc agtcctccca gggactacat aacaggcacc tttgagagag	2262

catgggagaa ggtggataag aggatgctgc tcagtgtttt tctcttccac tttcctgcc	2322
ctccccacta ccctcggaga gaggtggtgg gatgggagag agccctgtg aaagcctgtg	2382
aggatctgaa gagtaaaggg ctgggtctgc ctcagaaggc accagcacca gggcccaggt	2442
attaaggctg agagtgaagg ctgccaatgt cagctttgga ggtcccagaa gtcttctgtt	2502
ctctggcctc accccctcag tcgcataga gctgggcctg gccttgctgg aatggaggca	2562
tccttccaaa cctgggggac gggggtgggg ggtggtagtg gtgggaggga aaccatgtct	2622
tgctaaacct gtttctggtg cctcccatcc ccagaccac cagacaccac acagcagaca	2682
atacacacc actcgcacaa gcttccatcc acatgtgttg tactttcagc tctaggcatg	2742
cagacaacc cacacggcca caccaccaca tgcccaagtg tacacacaca gagccacacc	2802
gtccctctgg gcctgctggc tctccttg gctttccctt gggccacttc cagggccag	2862
gtgctgcaac taaatgtgaa agctcagtgg ccgctccttc tttcagccca tcaaccagca	2922
ttgggtccat agggaagcac aggggactca ccctctttca tatcccttg cctgccctga	2982
aatggacaat cacttttttg gataggttga aatttttaaa gagcctgcat cattcggttc	3042
cctcaaaggg aagcccttg tagtgggggt ttgaaagaga atttttggaa ccaacattca	3102
aattctgcct catctggagg gaaacaaaa ttgggagggg gaagaggacc cctgatgttt	3162
tgctgcttcc agagatatta gaaactgact cacttgattg gaaaatggac aaaagtgcct	3222
tgacgtggag ggtgggcacc agatggggac cagccttgcc aactgctgct gtggcctcca	3282
gcttggtctg ttttgcaggc cgccagcagg aaggcgaagg tggtagtaca gcaagaggca	3342
ctggcggggc agcaggcctg caggagctgt ttttccattg ctaggcctga cccctctcta	3402
cctgtgagcg ttcaggggggt ccctgagata gtttagatgc ccccccatc ttagacctca	3462
gtccacacag tgctttttaa gggggacctc acctcctgtg cacagccac ccactttcct	3522
ctgcttccct ggcacagccc aggcatagac gagctggcgt tggaccagt tcttccccct	3582
tttcagcccc acagctgctg ccacaggggc caactagggc cagggtggaag gggagctgag	3642
aagccaacc ctagcccagg ggtgctgtgg gaactgggat ccaatttgta gcttcccgcc	3702
tggcttcaga gagccagca accttctagg cctgctttcc agacttctga gatagcctgg	3762
gatgagcaat cctgttacag tacatctgga ccttccctac ctgggctctg gggaggctgt	3822
gggcctggag agggaaaagg agggaggggg tgtctgcacc acctgggaag atagcacaag	3882
gcctaagtag gtcaccctga ctccccacc cagcatttca ttcataccag ataatagctg	3942
cattactgcc aactgaacct ataaccctct gcaccttcaa aaagattcat ggtttttaat	4002

tgctgctttt aataacattt gtaaagttaa aaaaaaaa

4040

<210> 29
<211> 1813
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (221)..(1189)

<400> 29
agcgattact cactataggg ctcgagcggc cgcccgggca ggtgttcccc cgaagtttag 60
agtgaagatt tttccacctg gacacctgac catgtgcctg ccctgagcag cgaggcccac 120
caggcatctc tgttgtgggc agcagggcca ggtcctggtc tgtggaccct cggcagttgg 180
caggctccct ctgcagtga gtctgggcct cggcctcacc atg tcg agc ctc ggc 235
Met Ser Ser Leu Gly
1
ggg ggc tcc cag gat gcc ggc ggc agt agc agc agc agc acc aat ggc 283
Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser Ser Ser Thr Asn Gly
6 11 16 21
agc ggt ggc agt ggc agc agt ggc cca aag gca gga gca gca gac aag 331
Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala Gly Ala Ala Asp Lys
22 27 32 37
agt gca gtg gtg gct gcc gcc gca cca gcc tca gtg gca gat gac aca 379
Ser Ala Val Val Ala Ala Ala Pro Ala Ser Val Ala Asp Asp Thr
38 43 48 53
cca ccc ccc gag cgt cgg aac aag agc ggt atc atc agt gag ccc ctc 427
Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile Ile Ser Glu Pro Leu
54 59 64 69
aac aag agc ctg cgc cgc tcc cgc ccg ctc tcc cac tac tct tct ttt 475
Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser His Tyr Ser Ser Phe
70 75 80 85
ggc agc agt ggt ggt agt ggc ggt ggc agc atg atg ggc gga gag tct 523
Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met Met Gly Gly Glu Ser
86 91 96 101
gct gac aag gcc act gcg gct gca gcc gct gcc tcc ctg ttg gcc aat 571
Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ser Leu Leu Ala Asn
102 107 112 117
ggg cat gac ctg gcg gcg gcc atg gcg gtg gac aaa agc aac cct acc 619
Gly His Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser Asn Pro Thr
118 123 128 133

tca aag cac aaa agt ggt gct gtg gcc agc ctg ctg agc aag gca gag	667
Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser Lys Ala Glu	
134 139 144 149	
cgg gcc acg gag ctg gca gcc gag gga cag ctg acg ctg cag cag ttt	715
Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu Gln Gln Phe	
150 155 160 165	
gcg cag tcc aca gag atg ctg aag cgc gtg gtg cag gag cat ctc ccg	763
Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu His Leu Pro	
166 171 176 181	
ctg atg agc gag gcg ggt gct ggc ctg cct gac atg gag gct gtg gca	811
Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu Ala Val Ala	
182 187 192 197	
ggt gcc gaa gcc ctc aat ggc cag tcc gac ttc ccc tac ctg ggc gct	859
Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr Leu Gly Ala	
198 203 208 213	
ttc ccc atc aac cca ggc ctc ttc att atg acc ccg gca ggt gtg ttc	907
Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala Gly Val Phe	
214 219 224 229	
ctg gcc gag agc gcg ctg cac atg gcg ggc ctg gct gag tac ccc atg	955
Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu Tyr Pro Met	
230 235 240 245	
cag gga gag ctg gcc tct gcc atc agc tcc ggc aag aag aag cgg aaa	1003
Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys Lys Arg Lys	
246 251 256 261	
cgc tgc ggc atg tgc gcg ccc tgc cgg cgg cgc atc aac tgc gag cag	1051
Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn Cys Glu Gln	
262 267 272 277	
tgc agc agt tgt agg aat cga aag act ggc cat cag att tgc aaa ttc	1099
Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile Cys Lys Phe	
278 283 288 293	
aga aaa tgt gag gaa ctc aaa aag aag cct tcc gct gct ctg gag aag	1147
Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala Leu Glu Lys	
294 299 304 309	
gtg atg ctt ccg acg gga gcc gcc ttc cgg tgg ttt cag tga cggcggc	1196
Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln *	
310 315 320	
ggaacccaaa gctgcctct ccgtgcaatg tcaactgctcg tgtggtctcc agcaaggat	1256
tcgggcgaag acaaacggat gcacccgtct ttagaaccaa aaatattctc tcacagattt	1316
cattcctgtt tttatatata ttttttttgt tgtcgtttta acatctccac gtccctagca	1376
taaatattct ctacagatt tcattcctgt ttttatatat atattttttg ttgtcgtttt	1436

aacatctcca cgtccctagc ataaaaagaa aaagaaaaaa atttaaactg ctttttcgga 1496
 agaacaacaa caaaaaagag gtaaagccga atttataaag tcccagagact tcctgggcaa 1556
 agaatggcca atcagtttcc ttctggggtc gatgtcgatg ttgtctgggc aggaaaacca 1616
 gtttttgtgt aaagaaggta aattttctga caccttttga aatttagtta ctaataagcc 1676
 ctactgtaat ttagcccagt ttaactcccc cctcatttaa acttcctttg attttttccg 1736
 cccatgaaaa agggcatagt ttgcctggag aatcccctcc cgttcataaa aagaatgttg 1796
 atggcaaaaa aaaaaaa 1813

<210> 30
 <211> 3650
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (319)..(1452)

<400> 30
 gcatgatgta tataactatc tattcgatga tgaagatacc ccaccaaacc caaaaaaaga 60
 gatctctcga ggatccgaat tcgcgggccgc gtcgacctac gatccaccgc attcctcccc 120
 tcattgatat tcaggaagca gctctccttc cctgccttc agctcaagtt tgctgagctt 180
 ttgtttcatt tgtgaatact tcttgctgga agtccctcac ccagagacca gtgctcccaa 240
 cggcagagca gcggggggaga taaagaactg gtgacacgtg gctgtacatt cagcacagct 300
 gtggtgtccc caagtgcc atg acc cag gag cca ttc aga gag gag ctg gcc 351
 Met Thr Gln Glu Pro Phe Arg Glu Glu Leu Ala
 1 5
 tat gac cgg atg ccc acg ctg gag cgg ggc cgg caa gac ccc gcc agc 399
 Tyr Asp Arg Met Pro Thr Leu Glu Arg Gly Arg Gln Asp Pro Ala Ser
 12 17 22 27
 tat gcc cca gac gcg aag ccg agc gac ctg cag ctg tcg aag aga ctg 447
 Tyr Ala Pro Asp Ala Lys Pro Ser Asp Leu Gln Leu Ser Lys Arg Leu
 28 33 38 43
 ccc ccc tgc ttc agc cac aag acg tgg gtc ttc tct gtg ctg atg ggg 495
 Pro Pro Cys Phe Ser His Lys Thr Trp Val Phe Ser Val Leu Met Gly
 44 49 54 59
 agc tgc ctc ctg gtg acc tcg ggg ttt tcg ctg tac ctg ggg aac gtg 543
 Ser Cys Leu Leu Val Thr Ser Gly Phe Ser Leu Tyr Leu Gly Asn Val
 60 65 70 75

ttc ccg gct gag atg gat tac ttg cgc tgt gct gca ggc tct tgc atc	591
Phe Pro Ala Glu Met Asp Tyr Leu Arg Cys Ala Ala Gly Ser Cys Ile	
76 81 86 91	
ccc tcg gca att gtg agc ttc acc gtc tcc agg agg aac gcc aat gtg	639
Pro Ser Ala Ile Val Ser Phe Thr Val Ser Arg Arg Asn Ala Asn Val	
92 97 102 107	
att ccc aac ttt cag ata ttg ttt gtt tcc acg ttt gct gtg acc act	687
Ile Pro Asn Phe Gln Ile Leu Phe Val Ser Thr Phe Ala Val Thr Thr	
108 113 118 123	
acg tgt tta att tgg ttt gga tgc aaa cta gtc ctg aac cca tca gca	735
Thr Cys Leu Ile Trp Phe Gly Cys Lys Leu Val Leu Asn Pro Ser Ala	
124 129 134 139	
ata aac atc aac ttc aac ctc atc ctg ctg ctc ctg ctg gag ctg ctc	783
Ile Asn Ile Asn Phe Asn Leu Ile Leu Leu Leu Leu Leu Glu Leu Leu	
140 145 150 155	
atg gcg gcc acg gtg atc atc gct gca cgg tcc agc gag gag gac tgc	831
Met Ala Ala Thr Val Ile Ile Ala Ala Arg Ser Ser Glu Glu Asp Cys	
156 161 166 171	
aag aaa aag aag ggc tcc atg tct gac agc gcc aac att ctg gac gaa	879
Lys Lys Lys Lys Gly Ser Met Ser Asp Ser Ala Asn Ile Leu Asp Glu	
172 177 182 187	
gtg cca ttt cct gct cgg gtc ctg aaa tct tac tca gtc gtc gag gta	927
Val Pro Phe Pro Ala Arg Val Leu Lys Ser Tyr Ser Val Val Glu Val	
188 193 198 203	
atc gca ggc atc tct gcc gtc ctc ggg ggg atc att gcc ctg aac gtg	975
Ile Ala Gly Ile Ser Ala Val Leu Gly Gly Ile Ile Ala Leu Asn Val	
204 209 214 219	
gat gac tca gtt tca ggc cca cac ctc tca gtg acg ttc ttt tgg atc	1023
Asp Asp Ser Val Ser Gly Pro His Leu Ser Val Thr Phe Phe Trp Ile	
220 225 230 235	
cta gtg gcc tgc ttt cca agt gcc att gcc agt cat gtg gca gca gag	1071
Leu Val Ala Cys Phe Pro Ser Ala Ile Ala Ser His Val Ala Ala Glu	
236 241 246 251	
tgt ccc agc aag tgt ctg gtg gag gtc ctg att gcc ata agc agc ctc	1119
Cys Pro Ser Lys Cys Leu Val Glu Val Leu Ile Ala Ile Ser Ser Leu	
252 257 262 267	
acg tct ccg ctg ctg ttc aca gcc tct gga tat ctg tca ttc agc atc	1167
Thr Ser Pro Leu Leu Phe Thr Ala Ser Gly Tyr Leu Ser Phe Ser Ile	
268 273 278 283	
atg aga atc gtg gag atg ttt aag gat tac ccg cca gcc ata aaa cca	1215
Met Arg Ile Val Glu Met Phe Lys Asp Tyr Pro Pro Ala Ile Lys Pro	
284 289 294 299	
tcc tac gat gtg ctg ctg ctg ctg ctg ctg cta gtg ctc ctg ctg cag	1263

Ser Tyr Asp Val Leu Leu Leu Leu Leu Leu Leu Val Leu Leu Leu Gln	
300 305 310 315	
gcc ggc ctc aac acg ggc acc gcc atc cag tgc gtg cgc ttc aag gtc	1311
Ala Gly Leu Asn Thr Gly Thr Ala Ile Gln Cys Val Arg Phe Lys Val	
316 321 326 331	
agt gca agg ctg cag ggt gca tcc tgg gac acc cag aac ggc ccg cag	1359
Ser Ala Arg Leu Gln Gly Ala Ser Trp Asp Thr Gln Asn Gly Pro Gln	
332 337 342 347	
gag cgc ctg gct ggg gag gtg gcc agg agc ccc ctg aag gag ttc gac	1407
Glu Arg Leu Ala Gly Glu Val Ala Arg Ser Pro Leu Lys Glu Phe Asp	
348 353 358 363	
aag gag aaa gcc tgg aga gcc gtc gtg gtg caa atg gcc cag tga ccc	1455
Lys Glu Lys Ala Trp Arg Ala Val Val Val Gln Met Ala Gln *	
364 369 374	
ccagacgcgg aaaccgggtg gcagcgccca gcctggcccc aagcatggaa acgcacaacc	1515
cctaatacgcc ctgagctact gcttctaaca cctcttttcc cttgtgtgag ggcaaaccag	1575
gctgcagggtg gggttttcac ttcctagggt agtttaattt taaaataggc caatgttggc	1635
tagtctgtgc ctcaagtgaga tcagtcagct ccgagtggct cccgtgtcgt aacagcagga	1695
gcatggccgc aacttcccag gccgaggaag ggcccccgcc tcggcctctt gagagcccca	1755
cccctgaact ggccccagct cctcttcctg cctctctcat ggcttgggct ggagtgggct	1815
ctctggacct gaaccagactg tgggtccctg cgtctcctgc ccactctgac cgggcttctt	1875
ccctccacgc ttaggggtctg tcccgggtac tcagtcagcc cagtgggatc ttaccactt	1935
ccctgcaagg tgcacctgcc ccaggctcag gctgcccagc ggctcttctt ggacagtgag	1995
agcagggctg ggcgcctctg tcctggcccc ggagccgcag gggccctcc tccagagcct	2055
gggcgcaagc gacacaggct gccgtgctc tcccaggtga aatccacacc agtccacgcc	2115
gggtcgctg cctgtctcc ctacttagac ccagtcattc tagagggatc caccgccaca	2175
ctggccggcc cagctcctgg gtgctgtcat gccagcttg gagtgccacg tggccgctgc	2235
ccacgtcccg ggcactgtca tgcccagctt ggagtgccac atggccgctg ccacgtccc	2295
gggcactgtc atgccagct tggagtgcc cgtggccgct gctgtgacag gcagtgttct	2355
tgggggtggg gctgcatcca aggctttgta aaccggctgg accacgtctc cctggcccca	2415
gtgaccgggg gaagctgagc cctccctcc tgtgtttgct ccattactc aaaatgcagg	2475
acagatcagg tcagagccca ggaattctca caggttcacc cagcgccctc tacctctag	2535
caagtacttt gtcttgatcc tcaactgagaa ggccccaggg cagtggctct ctccatctcc	2595

gctgttttgg	ggtcttaggg	tacagcccag	gcggtcactg	cccacctgcc	aggctgcagg	2655
gacagttggg	tgtgagaata	aaactggctt	tggttagtgc	catggccagg	agtgggtttc	2715
cctgcgtctc	ctcgtcccga	gggcgcctgg	gtcctcccag	ctgacggcag	taaattccaca	2775
gtgagttggg	gcgactgtga	aactggaatg	ctgttacttt	gataattact	ttccagcagg	2835
tgttttcctt	cacaatgggt	ttgtttcttt	ccttctgata	tgagaagaca	tgaacgtttt	2895
ctcttcaccg	ccgtgggggtg	tattgactgg	tccccatgg	gctgctggaa	aggcccggag	2955
atgcatctgt	ggcctggggc	catcaagatc	aaagaaccag	gaggcctggg	agatgcagct	3015
ggatggggcg	gcctgcagac	cctgccaggg	ggtttgagga	ccctcccagg	tttcccactt	3075
cggaacagga	gtgactctgg	ctgccaagat	accttcatgg	tgttcatgac	aagtggaatc	3135
attattttca	accattgaag	ggggatgcag	gcaagacacc	ttcccagctg	ctcctagagg	3195
ggacaagcca	ggccctctct	gcagtcctcg	gcagctccgg	aaggacacag	tcagggggcg	3255
ggcaaact	ttggccacag	ccccaaacaa	gcgccaccgt	gggagaggag	aggctgctgt	3315
cactggtacc	ggatgcagac	cccaccctgt	ctgcaggcca	ccccacctc	cctgcagctt	3375
tgaggctggc	ggggtctgct	cctgggaatg	gggtgggagc	cacagggacg	accggggcg	3435
ggctgatgtc	ttcttggggg	cagaccagag	agctcaagtt	tcagagtcag	aattaggcac	3495
ttggagcggt	tttgcaggct	tgactttct	tattttctta	ttttagagcg	cttaaaaaat	3555
ccggaaaaat	ggggtttaaa	agaactgtct	ctttcagttc	acatttttgt	ttaatacgct	3615
tgagcaataa	acgctgactt	gcaaaaaaaaa	aaaaa			3650

<210> 31
 <211> 2299
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (335)..(1417)

<400> 31	
gcacgagggt	gtccttgga
gggtttcctc	ggcgcttctc
catggaggag	gcggtgcgaa
60	
cggttcagc	cccgaatgct
cgcatctccc	actggacggc
gacgaaggcg	gtggccgtgc
120	
gagcgcagga	ctgggcggcc
tgtgtggggg	tgtgagccgc
ggtgcccaag	gctgcgccgg
180	
cgaggggaag	ccgcgcggcc
ggccggccga	ctagggtgag
gtcgccactc	cttcctttca
240	

ggtttgaaga ctgcttcatt ctgcctctag taccagcggg ttctctgttc tgtgatcaat 300

gtgattcaca ggaactcctt aagtaacaaa cgaa atg agc cag ggg cgt gga 352
Met Ser Gln Gly Arg Gly
1

aaa tat gac ttc tat att ggt ctg gga ttg gct atg agc tcc agc att 400
Lys Tyr Asp Phe Tyr Ile Gly Leu Gly Leu Ala Met Ser Ser Ser Ile
7 12 17 22

ttc att gga gga agt ttc att ttg aaa aaa aag ggc ctc ctt cga ctt 448
Phe Ile Gly Gly Ser Phe Ile Leu Lys Lys Lys Gly Leu Leu Arg Leu
23 28 33 38

gcc agg aaa ggc tct atg aga gca ggt caa ggt ggc cat gca tat ctt 496
Ala Arg Lys Gly Ser Met Arg Ala Gly Gln Gly Gly His Ala Tyr Leu
39 44 49 54

aag gaa tgg ttg tgg tgg gct gga ctg ctg tca atg gga gct ggt gag 544
Lys Glu Trp Leu Trp Trp Ala Gly Leu Leu Ser Met Gly Ala Gly Glu
55 60 65 70

gtg gcc aac ttc gct gcg tat gcg ttt gca cca gcc act cta gtg act 592
Val Ala Asn Phe Ala Ala Tyr Ala Phe Ala Pro Ala Thr Leu Val Thr
71 76 81 86

cca cta gga gct ctc agc gtg cta gta agt gcc att ctt tct tca tac 640
Pro Leu Gly Ala Leu Ser Val Leu Val Ser Ala Ile Leu Ser Ser Tyr
87 92 97 102

ttt ctc aat gaa aga ctt aat ctt cat ggg aaa att ggg tgt ttg cta 688
Phe Leu Asn Glu Arg Leu Asn Leu His Gly Lys Ile Gly Cys Leu Leu
103 108 113 118

agt att cta gga tct aca gtt atg gtc att cat gct cca aag gaa gag 736
Ser Ile Leu Gly Ser Thr Val Met Val Ile His Ala Pro Lys Glu Glu
119 124 129 134

gag att gag act tta aat gaa atg tct cac aag cta ggt gat cca ggt 784
Glu Ile Glu Thr Leu Asn Glu Met Ser His Lys Leu Gly Asp Pro Gly
135 140 145 150

ttt gtg gtc ttt gca acc ctt gtg gtc att gtg gcc ttg ata tta atc 832
Phe Val Val Phe Ala Thr Leu Val Val Ile Val Ala Leu Ile Leu Ile
151 156 161 166

ttc gtg gtg ggt cct cgc cat gga cag aca aac att ctt gtg tac ata 880
Phe Val Val Gly Pro Arg His Gly Gln Thr Asn Ile Leu Val Tyr Ile
167 172 177 182

aca atc tgc tct gta atc ggc gcg ttt tca gtc tcc tgt gtg aag ggc 928
Thr Ile Cys Ser Val Ile Gly Ala Phe Ser Val Ser Cys Val Lys Gly
183 188 193 198

ctg ggc att gct atc aag gag ctg ttt gca ggg aag cct gtg ctg cgg 976
Leu Gly Ile Ala Ile Lys Glu Leu Phe Ala Gly Lys Pro Val Leu Arg
199 204 209 214

cat ccc ctg gct tgg att ctg ctg ctg agc ctc atc gtc tgt gtg agc	1024
His Pro Leu Ala Trp Ile Leu Leu Leu Ser Leu Ile Val Cys Val Ser	
215 220 225 230	
aca cag att aat tac cta aat agg gcc ctg gat ata ttc aac act tcc	1072
Thr Gln Ile Asn Tyr Leu Asn Arg Ala Leu Asp Ile Phe Asn Thr Ser	
231 236 241 246	
att gtg act cca ata tat tat gta ttc ttt aca aca tca gtt tta act	1120
Ile Val Thr Pro Ile Tyr Tyr Val Phe Phe Thr Thr Ser Val Leu Thr	
247 252 257 262	
tgt tca gct att ctt ttt aag gag tgg caa gat atg cct gtt gac gat	1168
Cys Ser Ala Ile Leu Phe Lys Glu Trp Gln Asp Met Pro Val Asp Asp	
263 268 273 278	
gtc att ggt act ttg agt ggc ttc ttt aca atc att gtg ggg ata ttc	1216
Val Ile Gly Thr Leu Ser Gly Phe Phe Thr Ile Ile Val Gly Ile Phe	
279 284 289 294	
ttg ttg cat gcc ttt aaa gac gtc agc ttt agt cta gca agt ctg cct	1264
Leu Leu His Ala Phe Lys Asp Val Ser Phe Ser Leu Ala Ser Leu Pro	
295 300 305 310	
gtg tct ttt cga aaa gac gag aaa gca atg aat ggc aat ctc tct aat	1312
Val Ser Phe Arg Lys Asp Glu Lys Ala Met Asn Gly Asn Leu Ser Asn	
311 316 321 326	
atg tat gaa gtt ctt aat aat aat gaa gaa agc tta acc tgt gga atc	1360
Met Tyr Glu Val Leu Asn Asn Asn Glu Glu Ser Leu Thr Cys Gly Ile	
327 332 337 342	
gaa caa cac act ggt gaa aat gtc tcc cga aga aat gga aat ctg aca	1408
Glu Gln His Thr Gly Glu Asn Val Ser Arg Arg Asn Gly Asn Leu Thr	
343 348 353 358	
gct ttt taa gaaagggt gtaattaaag gttaatctgt gattgttatg aagtgaattt	1464
Ala Phe *	
359	
gaatatcatc agaatgtgtc tgaaaaaaca ttgtcctcaa ataatgttct ttaaaggcaa	1524
tctttttaaa gatttcaacta atttggacca agaaattact tttcttgtat ttaaacaac	1584
aatggtagct cactaaaatg acctcagcac atgacgattt ctattaacat tttattgttg	1644
tagaagtatt ttacattttc atcccttctc caaaagccga atgcactaat gacagtttta	1704
agtctatgaa aatgctttat tttttcattg gtgatgaaag tctgaaatgt gcatttgtca	1764
tccccactcc atcaatccct gaccatgtaa ggctttttta ttttaaaaaa acagagttat	1824
cccaatacat tatcctgtga tttaccttac ctacaaaagt ggctcctgtt tgtttgatga	1884
tgattggttt tatttttgaa atatttatta agggaaaact aagtactga atgaaggaac	1944

ctctttctta caaaacaaaa aaaagggcag aaatcacccc aaggaacgat ttctcaggtt 2004
gagatgatca ccgtgaatcc ggcttcctct gagcattcga tggccttagc acctcatcaa 2064
gccagcacat cctgcctgct gttgcagcct ggctgggttt attcttcagt taccctaate 2124
ccatgatgcc tggaaccttg attaccgttt tacatcagct cttgtacttt tcagtatat 2184
ttcataatga gttatatattgt catttagact ttgaacagct ctgggaaata gaagactagg 2244
gttgtttctt aaatttagct catgttataa taaaaagttg aaatgaaaaa aaaaa 2299

<210> 32
<211> 1558
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (50)..(1174)

<400> 32
taagcttgcg gccgcaggcc ggaggcgcgt cgggctggag ccggtcacg atg ccc 55
Met Pro
1
cga agg aag caa agc cac ccg cag ccc gtg aaa tgc gag ggg gtc aaa 103
Arg Arg Lys Gln Ser His Pro Gln Pro Val Lys Cys Glu Gly Val Lys
3 8 13 18
gtg gat act gaa gac tcc ctc gac gaa gga ccc ggg gcc ctg gta ttg 151
Val Asp Thr Glu Asp Ser Leu Asp Glu Gly Pro Gly Ala Leu Val Leu
19 24 29 34
gag agt gat ttg cta cta ggc cag gat ctg gag ttt gag gag gaa gag 199
Glu Ser Asp Leu Leu Leu Gly Gln Asp Leu Glu Phe Glu Glu Glu Glu
35 40 45 50
gaa gag gag gaa ggc gac ggc aac agt gac cag ctc atg ggc ttc gag 247
Glu Glu Glu Glu Gly Asp Gly Asn Ser Asp Gln Leu Met Gly Phe Glu
51 56 61 66
aga gac tcg gaa gga gac tct ctg ggg gcc agg cct ggg ctt ccc tat 295
Arg Asp Ser Glu Gly Asp Ser Leu Gly Ala Arg Pro Gly Leu Pro Tyr
67 72 77 82
ggg ctg agc gac gat gag tct ggg ggc ggc cgg gca cta agt gcg gag 343
Gly Leu Ser Asp Asp Glu Ser Gly Gly Gly Arg Ala Leu Ser Ala Glu
83 88 93 98
agt gaa gtt gag gag cca gcc agg ggt cca ggg gag gcc agg ggt gag 391
Ser Glu Val Glu Glu Pro Ala Arg Gly Pro Gly Glu Ala Arg Gly Glu
99 104 109 114

agg cca ggc cca gcc tgc cag ctg tgt ggg ggg ccg aca gat ttg agc	439
Arg Pro Gly Pro Ala Cys Gln Leu Cys Gly Gly Pro Thr Asp Leu Ser	
115 120 125 130	
ctc cat gtg cca cca ggt ggt gcc agt ttc ctg cca gac tgt ggg cag	487
Leu His Val Pro Pro Gly Gly Ala Ser Phe Leu Pro Asp Cys Gly Gln	
131 136 141 146	
ctg cgg ggt gaa ggg gag ggc ctc tgc ggg act gga tca gaa cca ctg	535
Leu Arg Gly Glu Gly Glu Gly Leu Cys Gly Thr Gly Ser Glu Pro Leu	
147 152 157 162	
cca gag ctg cta ttc cct tgg acc tgc cgg ggc tgt gga caa gag ctg	583
Pro Glu Leu Leu Phe Pro Trp Thr Cys Arg Gly Cys Gly Gln Glu Leu	
163 168 173 178	
gag gag ggt gag ggt agt cgg ctg gga gct gcc atg tgt ggg cgc tgc	631
Glu Glu Gly Glu Gly Ser Arg Leu Gly Ala Ala Met Cys Gly Arg Cys	
179 184 189 194	
atg cga gga gag gct gga ggg ggt gcc agt ggg ggg ccc cag ggc ccc	679
Met Arg Gly Glu Ala Gly Gly Gly Ala Ser Gly Gly Pro Gln Gly Pro	
195 200 205 210	
agt gac aaa ggc ttt gcc tgt agc ctc tgc ccc ttt gcc act cac tat	727
Ser Asp Lys Gly Phe Ala Cys Ser Leu Cys Pro Phe Ala Thr His Tyr	
211 216 221 226	
ccc aac cac ctg gcc cgg cac atg aag aca cac agt ggt gag aag ccc	775
Pro Asn His Leu Ala Arg His Met Lys Thr His Ser Gly Glu Lys Pro	
227 232 237 242	
ttc cgc tgc gcc cgc tgt cct tat gcc tct gct cat ctg gat aac ctg	823
Phe Arg Cys Ala Arg Cys Pro Tyr Ala Ser Ala His Leu Asp Asn Leu	
243 248 253 258	
aaa cgg cac cag cgc gtc cat aca gga gag aag ccc tac aag tgc ccc	871
Lys Arg His Gln Arg Val His Thr Gly Glu Lys Pro Tyr Lys Cys Pro	
259 264 269 274	
ctc tgc cct tat gcc tgt ggc aat ctg gcc aac ctc aag cgt cat ggt	919
Leu Cys Pro Tyr Ala Cys Gly Asn Leu Ala Asn Leu Lys Arg His Gly	
275 280 285 290	
cgc atc cac tct ggt gac aaa cct ttt cgg tgt agc ctt tgc aac tac	967
Arg Ile His Ser Gly Asp Lys Pro Phe Arg Cys Ser Leu Cys Asn Tyr	
291 296 301 306	
agc tgc aac cag agc atg aac ctc aaa cgt cac atg ctg cgg cac aca	1015
Ser Cys Asn Gln Ser Met Asn Leu Lys Arg His Met Leu Arg His Thr	
307 312 317 322	
ggc gag aag cct tcc gct gtg cca cct gcg cct ata cca cgg gcc act	1063
Gly Glu Lys Pro Ser Ala Val Pro Pro Ala Pro Ile Pro Arg Ala Thr	
323 328 333 338	
ggg aca act aca agc gcc acc aga agg tgc atg gcc acg gtg ggg cag	1111

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

cac cct ctg ttt tga gctctcgggg cccaccagcc ctggggactg ctggcagccg 1214
His Pro Leu Phe *
371

accagaagcc acctttttct ccccgctgg ccaggggctc cacacagact aacgtaggca 1334

ttgactgagg cacttcacga gctcagtga aagggccctg tattcacctc cactgcccc 1454

tttcagtgc t tataataaa ggaacacta acaaaaaaaaa aaaa 1558

```
<220>  
<221> CDS  
<222> (173) .. (874)
```

cgaccacgc gtccgggaga ggcgcacggtg gagccgccag ttgagaagga ctctgatccg 120

gcg gcc acc agt gga act gat gag cgg gtt tcc ggg gag ttg gtg tct 223
Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val Ser
2 7 12 17

gtg gca cat gcg ctt tct ctc cca gca gag tog tat ggc aac gat cct 271
Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Asp Pro
18 23 28 33

gac att gag atg gct tgg gcc atg aga gca atg cag cat gct gaa gtc 319
Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu Val
34 39 44 49

tat tac aag ctg att tca tca gtt qac cca caq ttc ctg aaa ctc acc 367

Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu Thr	
50 55 60 65	
aaa gta gat gac caa att tac tct gag ttc cgg aaa aat ttt gag acc	415
Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu Thr	
66 71 76 81	
ctt agg ata gat gtg ttg gac cca gaa gaa ctc aag tca gaa tca gcc	463
Leu Arg Ile Asp Val Leu Asp Pro Glu Glu Leu Lys Ser Glu Ser Ala	
82 87 92 97	
aaa gag aag tgg agg cca ttc tgc ttg aag ttt aat ggg att gtt gaa	511
Lys Glu Lys Trp Arg Pro Phe Cys Leu Lys Phe Asn Gly Ile Val Glu	
98 103 108 113	
gac ttc aac tat ggt act ttg ctg cga cta gat tgt tct cag ggc tac	559
Asp Phe Asn Tyr Gly Thr Leu Leu Arg Leu Asp Cys Ser Gln Gly Tyr	
114 119 124 129	
act gag gaa aac acc atc ttt gcc ccc agg ata caa ttc ttt gcc att	607
Thr Glu Glu Asn Thr Ile Phe Ala Pro Arg Ile Gln Phe Phe Ala Ile	
130 135 140 145	
gaa att gct cgg aac cgg gaa ggc tat aac aaa gct gtt tat atc agt	655
Glu Ile Ala Arg Asn Arg Glu Gly Tyr Asn Lys Ala Val Tyr Ile Ser	
146 151 156 161	
gtt cag gac aaa gaa gga gag aaa gga gtc aac aat gga gga gaa aaa	703
Val Gln Asp Lys Glu Gly Glu Lys Gly Val Asn Asn Gly Gly Glu Lys	
162 167 172 177	
aga gct gac agt gga gaa gaa gag aac acc aag aat gga gga gag aaa	751
Arg Ala Asp Ser Gly Glu Glu Glu Asn Thr Lys Asn Gly Gly Glu Lys	
178 183 188 193	
gga gct gat agt gga gaa gaa aaa gag gaa gga atc aac aga gaa gac	799
Gly Ala Asp Ser Gly Glu Glu Lys Glu Glu Gly Ile Asn Arg Glu Asp	
194 199 204 209	
aaa act gac aaa gga gga gaa aaa ggg aaa gaa gct gac aaa gaa atc	847
Lys Thr Asp Lys Gly Gly Glu Lys Gly Lys Glu Ala Asp Lys Glu Ile	
210 215 220 225	
aac aaa agt ggt gaa aaa gct atg taa ggtat acaggggaaca gcactctaga	899
Asn Lys Ser Gly Glu Lys Ala Met *	
226 231	
agctatgact caattgagac tacaagtacc acggtgctac ttgcacagac ccctttggtt	959
aaatgtaaatt tcttgtacaa ttgaaggata cgcagaagga catcttttcta gtctaacagt	1019
caggagctgc tctgggtcatt cccttgtatg aactgggtcta aagactgtta gtgggggtgtt	1079
agttgatattt tcctgggtata ctgtttcttg gctgacacta ctgggtcaagt aagaaatttg	1139
taaataaatt tcttttgggtt cttattatct aaaaaaaaaa aa	1181

<210> 34
 <211> 1206
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (135)..(965)

<400> 34
 atgaaccctt gtttgaccgc ctgggggtacc ggtccggaat tcccgggtcg acccacgcgt 60
 ccgatgaggg cacggccttg taaagaaacc caaagcagca cagcctctga gaactgaata 120
 atggcccctt ccag atg cct ctt tgc aat ggt gga aat ttg gca gta aca 170
 Met Pro Leu Cys Asn Gly Gly Asn Leu Ala Val Thr
 1 5 10
 ggt tcc tgg gca gat cga tca cca cta cat gaa gca gca agt caa ggt 218
 Gly Ser Trp Ala Asp Arg Ser Pro Leu His Glu Ala Ala Ser Gln Gly
 13 18 23 28
 cgc ctt ctt gct ctg aga aca tta tta tca cag ggt tat aat gta aat 266
 Arg Leu Leu Ala Leu Arg Thr Leu Leu Ser Gln Gly Tyr Asn Val Asn
 29 34 39 44
 gca gta acc tta gac cat gtc acc cca ttg cac gaa gcc tgc ctt gga 314
 Ala Val Thr Leu Asp His Val Thr Pro Leu His Glu Ala Cys Leu Gly
 45 50 55 60
 gat cac gtg gca tgt gcc aga act ctg ctg gaa gca gga gct aat gta 362
 Asp His Val Ala Cys Ala Arg Thr Leu Leu Glu Ala Gly Ala Asn Val
 61 66 71 76
 aat gca atc acg ata gat ggc gtg act ccg tta ttc aac gca tgc tcc 410
 Asn Ala Ile Thr Ile Asp Gly Val Thr Pro Leu Phe Asn Ala Cys Ser
 77 82 87 92
 caa ggc agt cca agc tgt gca gag ctg ctt ctg gag tat ggt gcc aaa 458
 Gln Gly Ser Pro Ser Cys Ala Glu Leu Leu Leu Glu Tyr Gly Ala Lys
 93 98 103 108
 gcc cag ctg gag tca tgt ctt cca tcc cca acg cat gag gcc gcc agt 506
 Ala Gln Leu Glu Ser Cys Leu Pro Ser Pro Thr His Glu Ala Ala Ser
 109 114 119 124
 aaa ggt cac cat gaa tgt ctt gac atc ctg ata tcc tgg ggc ata gat 554
 Lys Gly His His Glu Cys Leu Asp Ile Leu Ile Ser Trp Gly Ile Asp
 125 130 135 140
 gtt gac caa gaa att cct cat ttg gga act cct ctc tat gta gct tgt 602
 Val Asp Gln Glu Ile Pro His Leu Gly Thr Pro Leu Tyr Val Ala Cys
 141 146 151 156

atg tca cag caa ttc cat tgc atc tgg aag ctt ctt tat gct ggt gct	650
Met Ser Gln Gln Phe His Cys Ile Trp Lys Leu Leu Tyr Ala Gly Ala	
157 162 167 172	
gac gta cag aaa ggc aaa tat tgg gat act cca tta cat gct gct gct	698
Asp Val Gln Lys Gly Lys Tyr Trp Asp Thr Pro Leu His Ala Ala Ala	
173 178 183 188	
caa caa tcc agc aca gaa att gta aac tta ctg cta gaa ttt gga gca	746
Gln Gln Ser Ser Thr Glu Ile Val Asn Leu Leu Leu Glu Phe Gly Ala	
189 194 199 204	
gat atc aat gcc aaa aat aca gag ctt ctg cga cct ata gat gta gct	794
Asp Ile Asn Ala Lys Asn Thr Glu Leu Leu Arg Pro Ile Asp Val Ala	
205 210 215 220	
acg tct agc agt atg gtg gaa aga ata ttg ctt caa cat gaa gct acc	842
Thr Ser Ser Ser Met Val Glu Arg Ile Leu Leu Gln His Glu Ala Thr	
221 226 231 236	
cca agc tct ctt tac caa ctt tgc cga ctc tgt atc cga agc tac ata	890
Pro Ser Ser Leu Tyr Gln Leu Cys Arg Leu Cys Ile Arg Ser Tyr Ile	
237 242 247 252	
gga aaa cca aga ttg cac ctt atc cca caa ctc cag ctg cca acg tta	938
Gly Lys Pro Arg Leu His Leu Ile Pro Gln Leu Gln Leu Pro Thr Leu	
253 258 263 268	
ctg aag aat ttc tta cag tat cga taa aacag taaagtaatt ctaaataacct	990
Leu Lys Asn Phe Leu Gln Tyr Arg *	
269 274	
tgaaaatcaa aatttctatt tcttttgctt aaggaatagt tcatataaaa atatgctaaa	1050
gataggataa aagtgagtgt gagatcaccc aggggaagcag taaaatatca atttttcattt	1110
taagtgtatt agtactattg ttttatcatt tatgctgtct ttggatacga aatcgtcgac	1170
agcgaagtgcg acccggaat tccggaccgg gtacgt	1206

<210> 35
 <211> 2119
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (520) .. (1614)

<400> 35	
gggaggagca tcaactgatgg ccactatcta caccctgag cgtctactcc tggccatcta	60
taccctgac tgtctacacc tccgatcatc tacacccgac ggtctacacc cctgacaggc	120

[illegible]

1

cgg gtg cgc tcc ctt gac ctc gat gac tgg ccg cct gag ctg ctg gct 1062

Arg Val Arg Ser Leu Asp Leu Asp Asp Trp Pro Pro Glu Leu Leu Ala	
166 171 176 181	
gtc atg act gcc atg ggc aat gcc ctc gcc aac agc gtc tgg gag ggg	1110
Val Met Thr Ala Met Gly Asn Ala Leu Ala Asn Ser Val Trp Glu Gly	
182 187 192 197	
gcc ttg ggt ggc tac tcc aag cca ggg cct gat gcc tgc aga gag gag	1158
Ala Leu Gly Gly Tyr Ser Lys Pro Gly Pro Asp Ala Cys Arg Glu Glu	
198 203 208 213	
aag gaa cgc tgg ata cgg gcc aag tat gaa cag aag ctc ttc ctg gcc	1206
Lys Glu Arg Trp Ile Arg Ala Lys Tyr Glu Gln Lys Leu Phe Leu Ala	
214 219 224 229	
cca ctg cca agc tca gat gtg cca ctg ggg cag cag ctg ctc cgg gcc	1254
Pro Leu Pro Ser Ser Asp Val Pro Leu Gly Gln Gln Leu Leu Arg Ala	
230 235 240 245	
gtg gtg gaa gat gac ctg cgg ctg ttg gtg atg ctc ctg gca cat ggc	1302
Val Val Glu Asp Asp Leu Arg Leu Leu Val Met Leu Leu Ala His Gly	
246 251 256 261	
tcc aaa gag gag gtg aat gag acc tat ggg gac ggg gac ggg cgg acg	1350
Ser Lys Glu Glu Val Asn Glu Thr Tyr Gly Asp Gly Asp Gly Arg Thr	
262 267 272 277	
gct cta cat ctc tcc agt gcc atg gcc aac gtt gtc ttc acg cag ctg	1398
Ala Leu His Leu Ser Ser Ala Met Ala Asn Val Val Phe Thr Gln Leu	
278 283 288 293	
ctc atc tgg tac ggg gtg gac gtg agg agc cgg gac gcc cgg ggc ctg	1446
Leu Ile Trp Tyr Gly Val Asp Val Arg Ser Arg Asp Ala Arg Gly Leu	
294 299 304 309	
act cca ctg gca tat gct cgc cgg gcc ggc agc cag gag tgt gca gac	1494
Thr Pro Leu Ala Tyr Ala Arg Arg Ala Gly Ser Gln Glu Cys Ala Asp	
310 315 320 325	
atc ttg atc cag cat ggc tgc cct ggg gag ggc tgt ggc tta gcg cct	1542
Ile Leu Ile Gln His Gly Cys Pro Gly Glu Gly Cys Gly Leu Ala Pro	
326 331 336 341	
acc ccc aac aga gag cct gcc aat ggc acc aac ccc tct gct gag ctg	1590
Thr Pro Asn Arg Glu Pro Ala Asn Gly Thr Asn Pro Ser Ala Glu Leu	
342 347 352 357	
cac cgt agt cct agc ctc cta taa ggcccaggaa gagggcagag gggccagaag	1644
His Arg Ser Pro Ser Leu Leu *	
358 363	
gactccatgg cccaaagacc ctccctccctg caggcactgt gggaacagac acagagatgg	1704
agaagcaggg acatgctgag aggacgaagc caaggaaatt agggaggaga gtcaaagggg	1764
tcaaggagag ttggggattt gagctgcagc agagagggat gagggattta gccctctgcc	1824

ctaaggtgcc attgaaaagg gacaggaccc ttcggagggtg cctgtgagga gaggggagca 1884
ggacctctcc ctccctccaga tccctgcctc ctagtgccag cccctcacac gccttcatcc 1944
tgaaacagga agaggacggc accaagttgg ggggtgctgga tgaaagagac gaggggtgat 2004
ctgtgagtcc catgtaaact ttgtacattg gaatatttat gtttgtgtac atatttgatg 2064
tgtgtgtgta tgatgagcca ataaaccaga ctgtgtgcgt gaaaaaaaaa aaaaa 2119

<210> 36
<211> 1364
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (48)..(1364)

<400> 36

gctggagaat cctcatccag gagcgggagc tgcgggagca ggagctg atg aga gca 56
Met Arg Ala
1

gct gtg aca cgg gag cag cgg agg cac ctc ctg gag acc ttt ttc agg 104
Ala Val Thr Arg Glu Gln Arg Arg His Leu Leu Glu Thr Phe Phe Arg
4 9 14 19

cac ctt ttc tcc cag gtg ctg gac atc aac cag gcc gac gca ggg acc 152
His Leu Phe Ser Gln Val Leu Asp Ile Asn Gln Ala Asp Ala Gly Thr
20 25 30 35

ctg ccc ctg gac tcc tcc cag aag gtg cgg gag gcc ctg acc tgt gag 200
Leu Pro Leu Asp Ser Ser Gln Lys Val Arg Glu Ala Leu Thr Cys Glu
36 41 46 51

ctg agc agg gcc gag ttt gcc gag tcc ctg ggc ctc aag ccc cag gac 248
Leu Ser Arg Ala Glu Phe Ala Glu Ser Leu Gly Leu Lys Pro Gln Asp
52 57 62 67

atg ttt gtg gag tcc atg ttc tct ctg gct gac aag gat ggc aat ggc 296
Met Phe Val Glu Ser Met Phe Ser Leu Ala Asp Lys Asp Gly Asn Gly
68 73 78 83

tac ctg tcc ttc cga gag ttc ctg gac atc ctg gtg gtc ttc atg aaa 344
Tyr Leu Ser Phe Arg Glu Phe Leu Asp Ile Leu Val Val Phe Met Lys
84 89 94 99

ggc tct cct gag gaa aag tct cgc ctt atg ttc cgc atg tac gac ttt 392
Gly Ser Pro Glu Glu Lys Ser Arg Leu Met Phe Arg Met Tyr Asp Phe
100 105 110 115

gat ggg aat ggc ctc att tcc aag gat gag ttc atc agg atg ctg aga 440
Asp Gly Asn Gly Leu Ile Ser Lys Asp Glu Phe Ile Arg Met Leu Arg

116	121	126	131	
tcc ttc atc gag atc	tcc aac aac tgc ctg	tcc aag gcc cag ctg	gct	488
Ser Phe Ile Glu Ile	Ser Asn Asn Cys Leu	Ser Lys Ala Gln Leu	Ala	
132	137	142	147	
gag gtg gtg gag tcc atg	ttc cgg gag tgc	gga ttc cag gac aag	gag	536
Glu Val Val Glu Ser	Met Phe Arg Glu Ser	Gly Phe Gln Asp Lys	Glu	
148	153	158	163	
gaa ctg aca tgg gaa gat	ttt cac ttc atg	ctg cgg gac cac aat	agc	584
Glu Leu Thr Trp Glu	Asp Phe His Phe Met	Leu Arg Asp His Asn	Ser	
164	169	174	179	
gag ctc cgc ttc acg cag	ctc tgt gtc aaa	ggg gtg gag gtg cct	gaa	632
Glu Leu Arg Phe Thr	Gln Leu Cys Val Lys	Gly Val Glu Val Pro	Glu	
180	185	190	195	
gtc atc aag gac ctc tgc	cgg cga gcc tcc	tac atc agc cag gat	atg	680
Val Ile Lys Asp Leu	Cys Arg Arg Ala Ser	Tyr Ile Ser Gln Asp	Met	
196	201	206	211	
atc tgt ccc tct ccc aga	gtg agt gcc cgc	tgt tcc cgc agc gac	att	728
Ile Cys Pro Ser Pro	Arg Val Ser Ala Arg	Cys Ser Arg Ser Asp	Ile	
212	217	222	227	
gag act gag ttg aca cct	cag aga ctg cag	tgc ccc atg gac aca	gac	776
Glu Thr Glu Leu Thr	Pro Gln Arg Leu Gln	Cys Pro Met Asp Thr	Asp	
228	233	238	243	
cct ccc cag gag att cgg	cgg agg ttt ggc	aag aag gta acg tca	ttc	824
Pro Pro Gln Glu Ile	Arg Arg Arg Phe Gly	Lys Lys Val Thr Ser	Phe	
244	249	254	259	
cag ccc ttg ctg ttc act	gag gcg cac cga	gag aag ttc caa cgc	agc	872
Gln Pro Leu Leu Phe	Thr Glu Ala His Arg	Glu Lys Phe Gln Arg	Ser	
260	265	270	275	
tgt ctc cac cag acg gtg	caa cag ttc aag	cgc ttc att gag aac	tac	920
Cys Leu His Gln Thr	Val Gln Gln Phe Lys	Arg Phe Ile Glu Asn	Tyr	
276	281	286	291	
cgg cgc cac atc ggc tgc	gtg gcc gtg ttc	tac gcc atc gct ggg	ggg	968
Arg Arg His Ile Gly	Cys Val Ala Val Phe	Tyr Ala Ile Ala Gly	Gly	
292	297	302	307	
ctt ttc ctg gag agg gcc	tac tac tac gcc	ttt gcc gca cat cac	acg	1016
Leu Phe Leu Glu Arg	Ala Tyr Tyr Tyr Ala	Phe Ala Ala His His	Thr	
308	313	318	323	
ggc atc aca gac acc acc	cgc gtg gga atc	atc ctg tgc cgg ggc	aca	1064
Gly Ile Thr Asp Thr	Thr Arg Val Gly Ile	Ile Leu Ser Arg Gly	Thr	
324	329	334	339	
gca gcc agc atc tct ttc	atg ttc tcc tac	atc ttg ctc acc atg	tgc	1112
Ala Ala Ser Ile Ser	Phe Met Phe Ser Tyr	Ile Leu Leu Thr Met	Cys	
340	345	350	355	

cgc aac ctc atc acc ttc ctg cga gaa acc ttc ctc aac cgc tac gtg	1160
Arg Asn Leu Ile Thr Phe Leu Arg Glu Thr Phe Leu Asn Arg Tyr Val	
356 361 366 371	
ccc ttc gac gcc gcc gtg gac ttc cat cgc ctc att gcc tcc acc gcc	1208
Pro Phe Asp Ala Ala Val Asp Phe His Arg Leu Ile Ala Ser Thr Ala	
372 377 382 387	
atc gtc ctc aca ggc agg gcc tgg gtg tcc ctg gga ggc tct cca ggg	1256
Ile Val Leu Thr Gly Arg Ala Trp Val Ser Leu Gly Gly Ser Pro Gly	
388 393 398 403	
cct ccc gcc ccc gct gac ttc ccc tcg tat gag agc ccc cct ctc tgc	1304
Pro Pro Ala Pro Ala Asp Phe Pro Ser Tyr Glu Ser Pro Pro Leu Cys	
404 409 414 419	
tgg cac tta cct tta atg tcc ttc tcc atc agg atg gag ttg gcc tgg	1352
Trp His Leu Pro Leu Met Ser Phe Ser Ile Arg Met Glu Leu Ala Trp	
420 425 430 435	
gcc agg gtg tga	1364
Ala Arg Val *	
436	

<210> 37
 <211> 1030
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (73)..(855)

<400> 37	
tcgccagctc gccccggcac tgcgcacttg ccagccagtc cgcccgtcgc gagccccggct	60
cgctgggggca gc atg gcg ggg tcg ccg ctg ctc tgg ggg ccg cgg gcc	108
Met Ala Gly Ser Pro Leu Leu Trp Gly Pro Arg Ala	
1 5 10	
ggg ggc gtc ggc ctt ttg gtg ctg ctg ctg ctc ggc ctg ttt cgg ccg	156
Gly Gly Val Gly Leu Leu Val Leu Leu Leu Leu Gly Leu Phe Arg Pro	
13 18 23 28	
ccc ccc gcg ctc tgc gcg cgg ccg gta aag gag ccc cgc ggc cta agc	204
Pro Pro Ala Leu Cys Ala Arg Pro Val Lys Glu Pro Arg Gly Leu Ser	
29 34 39 44	
gca gcg tct ccg ccc ttg gct gag act ggc gct cct cgc cgc ttc cgg	252
Ala Ala Ser Pro Pro Leu Ala Glu Thr Gly Ala Pro Arg Arg Phe Arg	
45 50 55 60	

cgg tca gtg ccc cga ggt gag gcg gcg ggg gcg gtg cag gag ctg gcg Arg Ser Val Pro Arg Gly Glu Ala Ala Gly Ala Val Gln Glu Leu Ala 61 66 71 76	300
cgg gcg ctg gcg cat ctg ctg gag gcc gaa cgt cag gag cgg gcg cgg Arg Ala Leu Ala His Leu Leu Glu Ala Glu Arg Gln Glu Arg Ala Arg 77 82 87 92	348
gcc gag gcg cag gag gct gag gat cag cag gcg cgc gtc ctg gcg cag Ala Glu Ala Gln Glu Ala Glu Asp Gln Gln Ala Arg Val Leu Ala Gln 93 98 103 108	396
ctg ctg cgc gtc tgg ggc gcc ccc cgc aac tct gat ccg gct ctg ggc Leu Leu Arg Val Trp Gly Ala Pro Arg Asn Ser Asp Pro Ala Leu Gly 109 114 119 124	444
ctg gac gac gac ccc gac gcg cct gca gcg cag ctc gct cgc gct ctg Leu Asp Asp Asp Pro Asp Ala Pro Ala Ala Gln Leu Ala Arg Ala Leu 125 130 135 140	492
ctc cgc gcc cgc ctt gac cct gcc gcc cta gca gcc cag ctt gtc ccc Leu Arg Ala Arg Leu Asp Pro Ala Ala Leu Ala Ala Gln Leu Val Pro 141 146 151 156	540
gcg ccc gtc ccc gcc gcg gcg ctc cga ccc cgg ccc ccg gtc tac gac Ala Pro Val Pro Ala Ala Ala Leu Arg Pro Arg Pro Pro Val Tyr Asp 157 162 167 172	588
gac ggc ccc gcg ggc ccg gat gct gag gag gca ggc gac gag aca ccc Asp Gly Pro Ala Gly Pro Asp Ala Glu Glu Ala Gly Asp Glu Thr Pro 173 178 183 188	636
gac gtg gac ccc gag ctg ttg agg tac ttg ctg gga cgg att ctt gcg Asp Val Asp Pro Glu Leu Leu Arg Tyr Leu Leu Gly Arg Ile Leu Ala 189 194 199 204	684
gga agc gcg gac tcc gag ggg gtg gca gcc ccg cgc cgc ctc cgc cgt Gly Ser Ala Asp Ser Glu Gly Val Ala Ala Pro Arg Arg Leu Arg Arg 205 210 215 220	732
gcc gcc gac cac gat gtg ggc tct gag ctg ccc cct gag ggc gtg ctg Ala Ala Asp His Asp Val Gly Ser Glu Leu Pro Pro Glu Gly Val Leu 221 226 231 236	780
ggg gcg ctg ctg cgt gtg aaa cgc cta gag acc ccg gcg ccc cag gtg Gly Ala Leu Leu Arg Val Lys Arg Leu Glu Thr Pro Ala Pro Gln Val 237 242 247 252	828
cct gca cgc cgc ctc ttg cca ccc tga gcact gcccgatcc cgtgcaccct Pro Ala Arg Arg Leu Leu Pro Pro * 253 258	880
gggaccacaga agtgcccccg ccatcccgcc accaggactg ctccccgcca gcacgtccag	940
agcaacttac cccggccagc cagccctctc acccgaggat ccctaccccc tggccccaca	1000
ataaacatga tctgaagcaa aaaaaaaaaa	1030

```
<220>
<221> CDS
<222> (73) .. (744)
```

<400> 38
tcgccagctc gccccggcac tgcgcacttg ccagccagtc cgcccgctcg gagcccgget 60

ggg ggc gtc ggc ctt ttg gtg ctg ctg ctg ctc ggc ctg ttt cgg ccg 156
Gly Gly Val Gly Leu Leu Val Leu Leu Leu Leu Gly Leu Phe Arg Pro
13 18 23 28

gca gcg tct ccg ccc ttg gct gag act ggc gct cct cgc cgc ttc cgg 252
Ala Ala Ser Pro Pro Leu Ala Glu Thr Gly Ala Pro Arg Arg Phe Arg
45 50 55 60

cgg gcg ctg gcg cat ctg ctg gag gcc gaa cgt cag gag cgg gcg cgg 348
 Arg Ala Leu Ala His Leu Leu Glu Ala Glu Arg Gln Glu Arg Ala Arg
 77 82 87 92

ctg ctg cgc gtc tgg ggc gcc ccc cgc aac tct gat ccg gct ctg ggc 444
Leu Leu Arg Val Trp Gly Ala Pro Arg Asn Ser Asp Pro Ala Leu Gly
109 114 119 124

ctc cgc gcc cgc ctt gac cct gcc gcc cta gca gcc cag ctt gtc ccc 540
Leu Arg Ala Arg Leu Asp Pro Ala Ala Leu Ala Ala Gln Leu Val Pro
141 146 151 156

106

Ala Pro Val	Pro Ala	Ala Ala	Leu Arg	Pro Arg	Pro Pro	Val Tyr	Asp	
157		162		167			172	
gac ggc ccc gcg gcc ccg gat gct gag gag gca ggc gac gag aca ccc								636
Asp Gly Pro Ala Gly Pro Asp Ala Glu Glu Ala Gly Asp Glu Thr Pro								
173		178		183			188	
gac gtg gac ccc gag ctg ttg agg tac ttg ctg ggg gcg ctg ctg cgt								684
Asp Val Asp Pro Glu Leu Leu Arg Tyr Leu Leu Gly Ala Leu Leu Arg								
189		194		199			204	
gtg aaa cgc cta gag acc ccg gcg ccc cag gtg cct gca cgc cgc ctc								732
Val Lys Arg Leu Glu Thr Pro Ala Pro Gln Val Pro Ala Arg Arg Leu								
205		210		215			220	
ttg cca ccc tga gca ctgcccgcat ccctgtcacc ctgggacctt gaagtgtccc								787
Leu Pro Pro *								
221								
cgccatcccc ccaccaggac tgctccccgc cagcacgtcc agagcaactt accccggcca								847
gccagccctc tcacccgagg atccctaccc cctgggcccc caataaacat gatctgaagc								907
aaaaaaaaaa aa								919

```
<210> 39
<211> 4849
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (355) .. (3744)
```

<400> 39	
tttcgtgtgg aagacaaggc cagcgcctat gaggaccagc tgcagggtca ggcacagcag	60
gtggagaccc tgcagaagga gaagctgagc gccacttttcg agggcagtga gcagggtgcac	120
cagctggagg agcagctgga ggcacgagag gccagcgtgc gcaggctcgc agagcacgtg	180
cagagcctct gtgacgagcg ggacctcctc agacagcggc tccaggagct gacagagcgc	240
gtggccaogt ccgacgagga tgtggctgag ctccgggaaa agctgaggag aagagaggct	300
gacaaccaga gcctggagca ctcctaccag agggctctcca gccagctgca gaggc	357
	Met
	1
cac act ctg ctg aga gag aag gag gaa gag ctg gag cgc att aag gaa	405
His Thr Leu Leu Arg Glu Lys Glu Glu Glu Leu Glu Arg Ile Lys Glu	
2 7 12 17	
gca cat gag aag gtt ctg gag aag aag gag cag gac ctc aat gag gct	453

Ala His Glu Lys Val Leu Glu Lys Lys Glu Gln Asp Leu Asn Glu Ala	
18 23 28 33	
ttg gtt aaa atg gtt gcc ttg ggg agc agc tta gag gaa aca gaa att	501
Leu Val Lys Met Val Ala Leu Gly Ser Ser Leu Glu Glu Thr Glu Ile	
34 39 44 49	
aag ctc cag gca aaa gaa gag att tta agg aaa ttt gca agt gaa tct	549
Lys Leu Gln Ala Lys Glu Glu Ile Leu Arg Lys Phe Ala Ser Glu Ser	
50 55 60 65	
cca aag gac atg gaa gag cca cgg agt acc tct gaa gag aca caa agg	597
Pro Lys Asp Met Glu Glu Pro Arg Ser Thr Ser Glu Glu Thr Gln Arg	
66 71 76 81	
gat ggc tct ttg ctc cca ggt caa cca gtc caa gcc tct agg gca cct	645
Asp Gly Ser Leu Leu Pro Gly Gln Pro Val Gln Ala Ser Arg Ala Pro	
82 87 92 97	
gta ggc ctc cca cac tca agg ctc gag gat gag gac gag gac ctg ggg	693
Val Gly Leu Pro His Ser Arg Leu Glu Asp Glu Asp Glu Asp Leu Gly	
98 103 108 113	
gct cct ccg ggg gaa gag tac ggt gat ggc agc ccc agt agg gaa gac	741
Ala Pro Pro Gly Glu Glu Tyr Gly Asp Gly Ser Pro Ser Arg Glu Asp	
114 119 124 129	
agc atg gtg ccc cca aag tca gtg gaa gtg ctt gac agg gag ggc cat	789
Ser Met Val Pro Pro Lys Ser Val Glu Val Leu Asp Arg Glu Gly His	
130 135 140 145	
cag cag ggc aca gcc aaa ctc gac caa ggg gca cct ggt gtt aaa agg	837
Gln Gln Gly Thr Ala Lys Leu Asp Gln Gly Ala Pro Gly Val Lys Arg	
146 151 156 161	
caa aga atc cgg ttc tcc aca atc cag tgc caa aga tac att cac ccc	885
Gln Arg Ile Arg Phe Ser Thr Ile Gln Cys Gln Arg Tyr Ile His Pro	
162 167 172 177	
gaa ggg tct gag aag acc tgg acc agc agc aca tct tcc gac acc agc	933
Glu Gly Ser Glu Lys Thr Trp Thr Ser Ser Thr Ser Ser Asp Thr Ser	
178 183 188 193	
cag gac cgg tca ccc tcg gaa gaa agc atg tcc tca gag cct gca ccc	981
Gln Asp Arg Ser Pro Ser Glu Glu Ser Met Ser Ser Glu Pro Ala Pro	
194 199 204 209	
agt gta ctg cct gca act ggc gac tct gac acg tac ctc tcc atc atc	1029
Ser Val Leu Pro Ala Thr Gly Asp Ser Asp Thr Tyr Leu Ser Ile Ile	
210 215 220 225	
cac tcc ctg gag acc aag ctc tac gtc aca gag gaa aag ctc aaa gac	1077
His Ser Leu Glu Thr Lys Leu Tyr Val Thr Glu Glu Lys Leu Lys Asp	
226 231 236 241	
gtg acc gtg agg ctg gag agc cag cag ggt cag agc cgt gag gca ctg	1125
Val Thr Val Arg Leu Glu Ser Gln Gln Gly Gln Ser Arg Glu Ala Leu	

242	247	252	257	
ctc gca ctg cac cac cag tgg gcg ggc acc gag gcc cag ctg cgt gag				1173
Leu Ala Leu His His Gln Trp Ala Gly Thr Glu Ala Gln Leu Arg Glu				
258	263	268	273	
cag ctc cgc gcc agc ctg ctc cag gtt ggc gca ctg gcc tcc cag ctg				1221
Gln Leu Arg Ala Ser Leu Leu Gln Val Gly Ala Leu Ala Ser Gln Leu				
274	279	284	289	
gag cag gag agg cag gag agg gcc agg agg gtt gaa ggg cat gtt gga				1269
Glu Gln Glu Arg Gln Glu Arg Ala Arg Arg Val Glu Gly His Val Gly				
290	295	300	305	
gag ctt ggg gac ttc cag gtc aag aat agt cag gcc ctg atg tgc ctg				1317
Glu Leu Gly Asp Phe Gln Val Lys Asn Ser Gln Ala Leu Met Cys Leu				
306	311	316	321	
gaa aat tgc cga gaa caa ctg aga tct ctg cct agg gcc agc cag gag				1365
Glu Asn Cys Arg Glu Gln Leu Arg Ser Leu Pro Arg Ala Ser Gln Glu				
322	327	332	337	
gat gag cag gac gca cgc gca gcc tcc ctg gcc agt gtg gag agt gca				1413
Asp Glu Gln Asp Ala Arg Ala Ala Ser Leu Ala Ser Val Glu Ser Ala				
338	343	348	353	
ctc gtc agc gcc atc caa gcc ctg cag cac tgg ccg gcc cca gcc cat				1461
Leu Val Ser Ala Ile Gln Ala Leu Gln His Trp Pro Ala Pro Ala His				
354	359	364	369	
ggc ggg gcc cgt gca cag ctg gag aca ggt ggc acc gag gag aat ggg				1509
Gly Gly Ala Arg Ala Gln Leu Glu Thr Gly Gly Thr Glu Glu Asn Gly				
370	375	380	385	
aag cct gcc tcc ctg cag cag tgc tcc cag tct gag ttg aca gag cag				1557
Lys Pro Ala Ser Leu Gln Gln Cys Ser Gln Ser Glu Leu Thr Glu Gln				
386	391	396	401	
gag cag gtg agg ctt ctt tct gac cag att gct ctg gag gcc tcg ctg				1605
Glu Gln Val Arg Leu Leu Ser Asp Gln Ile Ala Leu Glu Ala Ser Leu				
402	407	412	417	
atc agc cag ata gca gat tcc ctg aag aac aca aca tca gat gtc tcc				1653
Ile Ser Gln Ile Ala Asp Ser Leu Lys Asn Thr Thr Ser Asp Val Ser				
418	423	428	433	
cga atg ctc cat gag att tct tgg tca gga cag cca ccg atg gaa tct				1701
Arg Met Leu His Glu Ile Ser Trp Ser Gly Gln Pro Pro Met Glu Ser				
434	439	444	449	
gct ggg gcc ccc gta gac acc tgg gcc agg aag gtc cta gtg gat ggt				1749
Ala Gly Ala Pro Val Asp Thr Trp Ala Arg Lys Val Leu Val Asp Gly				
450	455	460	465	
gag ttc tgg agc cag gtt gag tct ctg agg aag cac ttg ggg aca ctg				1797
Glu Phe Trp Ser Gln Val Glu Ser Leu Arg Lys His Leu Gly Thr Leu				
466	471	476	481	

gga gga gag gca gtc ggt gcc tca gga gac ggg cag caa agc atc cca	1845
Gly Gly Glu Ala Val Gly Ala Ser Gly Asp Gly Gln Gln Ser Ile Pro	
482 487 492 497	
cag ggc ctg gcc ccc atc ctg gcc aat gcc aca tgg gtc agg gca gag	1893
Gln Gly Leu Ala Pro Ile Leu Ala Asn Ala Thr Trp Val Arg Ala Glu	
498 503 508 513	
ctc agc ttt gcc aca cag tca gtg agg gag tgc ttc cac cgc agg cta	1941
Leu Ser Phe Ala Thr Gln Ser Val Arg Glu Ser Phe His Arg Arg Leu	
514 519 524 529	
cag agc atc cag gag acc ctg cgg gcc acc cag acg gcc ctg cgg cag	1989
Gln Ser Ile Gln Glu Thr Leu Arg Gly Thr Gln Thr Ala Leu Arg Gln	
530 535 540 545	
cac aaa tgc ctg ctg agg gaa atc ctg gga gcc tac caa acc cca gac	2037
His Lys Cys Leu Leu Arg Glu Ile Leu Gly Ala Tyr Gln Thr Pro Asp	
546 551 556 561	
ttt gaa aga gtg atg cag cag gtc ttg gaa gcc ctc agg ctt cca gcg	2085
Phe Glu Arg Val Met Gln Gln Val Leu Glu Ala Leu Arg Leu Pro Ala	
562 567 572 577	
ggc cat gaa gat ggt gtt cag ctg tcc tgg gac ctg agc ccc tta gga	2133
Gly His Glu Asp Gly Val Gln Leu Ser Trp Asp Leu Ser Pro Leu Gly	
578 583 588 593	
gaa gtc ctg ggc cga gac tca gac agc tct cag gag ccc ttc gat gtg	2181
Glu Val Leu Gly Arg Asp Ser Asp Ser Ser Gln Glu Pro Phe Asp Val	
594 599 604 609	
tct gac cag agc cct ggg gcc ttt gtt gct att cag gag gag ctt gcc	2229
Ser Asp Gln Ser Pro Gly Ala Phe Val Ala Ile Gln Glu Glu Leu Ala	
610 615 620 625	
cag cag ctg aag gag aag gcc agc ctc tta gag gag ata gcg gct gcc	2277
Gln Gln Leu Lys Glu Lys Ala Ser Leu Leu Glu Glu Ile Ala Ala Ala	
626 631 636 641	
tta cca tct ctg cca cct gtg gaa tgc ctg aga gat tgc cag aag ctt	2325
Leu Pro Ser Leu Pro Pro Val Glu Ser Leu Arg Asp Cys Gln Lys Leu	
642 647 652 657	
ctc cag gtg tcc cag agt ctc tgc tat aac act tgt ttg gga gcc ctc	2373
Leu Gln Val Ser Gln Ser Leu Ser Tyr Asn Thr Cys Leu Gly Gly Leu	
658 663 668 673	
ggt cag tat tct tca ttg ttg gtt cag gat gcc att att cag gcc cag	2421
Gly Gln Tyr Ser Ser Leu Leu Val Gln Asp Ala Ile Ile Gln Ala Gln	
674 679 684 689	
gtt tgc tat gcg tcc tgc aga atc cgg cta gaa tat gag aag gag ctc	2469
Val Cys Tyr Ala Ser Cys Arg Ile Arg Leu Glu Tyr Glu Lys Glu Leu	
690 695 700 705	

cag ctc tgc aag gag tcc tgg caa acc cgg gag ccc tcc tgc tca gag Gln Leu Cys Lys Glu Ser Trp Gln Thr Arg Glu Pro Ser Cys Ser Glu 706 711 716 721	2517
cag gca cag gca gcc cgg gcc ctg agg gag gag tat gag gag ctt ctc Gln Ala Gln Ala Ala Arg Ala Leu Arg Glu Glu Tyr Glu Glu Leu Leu 722 727 732 737	2565
cgc aag cag aag agc gag tac ctg gat gtg atc gcc att gtt gaa agg Arg Lys Gln Lys Ser Glu Tyr Leu Asp Val Ile Ala Ile Val Glu Arg 738 743 748 753	2613
gag aat gca gag ctc aag gcc aag gcc gcc cag cta gag cat cag cag Glu Asn Ala Glu Leu Lys Ala Lys Ala Ala Gln Leu Asp His Gln Gln 754 759 764 769	2661
cag tgt ctg gag gat gca gag agc aag cac agc atg agc atg ttc acc Gln Cys Leu Glu Asp Ala Glu Ser Lys His Ser Met Ser Met Phe Thr 770 775 780 785	2709
ctg cgg ggc agg tat gaa aag gag att cgg tgt gtg gtg gag cag ctg Leu Arg Gly Arg Tyr Glu Lys Glu Ile Arg Cys Val Val Glu Gln Leu 786 791 796 801	2757
acc agg acc gag agc aca ctg cag gct gag cgc agc cgg gtc ctg agc Thr Arg Thr Glu Ser Thr Leu Gln Ala Glu Arg Ser Arg Val Leu Ser 802 807 812 817	2805
cag ctg gat gcc tcg gtc aga gac agg cag gac atg gag agg cat cat Gln Leu Asp Ala Ser Val Arg Asp Arg Gln Asp Met Glu Arg His His 818 823 828 833	2853
ggg gag cag ata cag acc ctg gag gac agg ttc cag ctc aag gtc cgg Gly Glu Gln Ile Gln Thr Leu Glu Asp Arg Phe Gln Leu Lys Val Arg 834 839 844 849	2901
gag ctg cag acg atc cac gag gag gag ctg agg acc ctg cag gag cac Glu Leu Gln Thr Ile His Glu Glu Glu Leu Arg Thr Leu Gln Glu His 850 855 860 865	2949
tac tcg cag agc ctg agg tgc ctt cag gac acc ctc tgc ctc cac cag Tyr Ser Gln Ser Leu Arg Cys Leu Gln Asp Thr Leu Cys Leu His Gln 866 871 876 881	2997
ggg cca cac ccc aag gcc ctg cca gcc cct gcc ccc aac tgg cag gcc Gly Pro His Pro Lys Ala Leu Pro Ala Pro Ala Pro Asn Trp Gln Ala 882 887 892 897	3045
acc cag gga gag gct gac tcc atg acg ggg ctg agg gag cgc atc cag Thr Gln Gly Glu Ala Asp Ser Met Thr Gly Leu Arg Glu Arg Ile Gln 898 903 908 913	3093
gag ctg gag gcc cag atg gat gtc atg cgg gag gag ctg gga cac aag Glu Leu Glu Ala Gln Met Asp Val Met Arg Glu Glu Leu Gly His Lys 914 919 924 929	3141
gac ctg gag ggc gac gcg gcc aca ctg cgt gag aag tac cag agg gac	3189

Asp Leu Glu Gly Asp Ala Ala Thr Leu Arg Glu Lys Tyr Gln Arg Asp	
930 935 940 945	
ttg gag agc ctt aag gcc acg tgc gag cga ggg ttt gca gca atg gaa	3237
Leu Glu Ser Leu Lys Ala Thr Cys Glu Arg Gly Phe Ala Ala Met Glu	
946 951 956 961	
gaa acg cac cag aag aag att gaa gat ctc cag agg cag cac cag cgg	3285
Glu Thr His Gln Lys Lys Ile Glu Asp Leu Gln Arg Gln His Gln Arg	
962 967 972 977	
gag cta gag aaa ctt cga gaa gag aaa gac cgc ctc cta gcc gag gag	3333
Glu Leu Glu Lys Leu Arg Glu Glu Lys Asp Arg Leu Leu Ala Glu Glu	
978 983 988 993	
aca gcg gcc acc atc tca gcc atc gaa gcc atg aag aac gcc cac cgg	3381
Thr Ala Ala Thr Ile Ser Ala Ile Glu Ala Met Lys Asn Ala His Arg	
994 999 1004 1009	
gag gaa atg gag cgg gag ctg gag aag agc cag cgg tcc cag atc agc	3429
Glu Glu Met Glu Arg Glu Leu Glu Lys Ser Gln Arg Ser Gln Ile Ser	
1010 1015 1020 1025	
agc gtc aac tcg gat gtt gag gcc ctg cgg cgc cag tac ctg gag gag	3477
Ser Val Asn Ser Asp Val Glu Ala Leu Arg Arg Gln Tyr Leu Glu Glu	
1026 1031 1036 1041	
ctg cag tcg gtg cag cgg gaa ctg gag gtc ctc tcg gag cag tac tcg	3525
Leu Gln Ser Val Gln Arg Glu Leu Glu Val Leu Ser Glu Gln Tyr Ser	
1042 1047 1052 1057	
cag aag tgc ctg gag aat gcc cat ctg gcc cag gcg ctg gag gcc gag	3573
Gln Lys Cys Leu Glu Asn Ala His Leu Ala Gln Ala Leu Glu Ala Glu	
1058 1063 1068 1073	
cgg cag gcc ctg cgg cag tgc cag cgt gag aac cag gag ctc aat gcc	3621
Arg Gln Ala Leu Arg Gln Cys Gln Arg Glu Asn Gln Glu Leu Asn Ala	
1074 1079 1084 1089	
cac aac cag gag ctg aac aac cgc ctg gct gca gag atc aca cgg ttg	3669
His Asn Gln Glu Leu Asn Asn Arg Leu Ala Ala Glu Ile Thr Arg Leu	
1090 1095 1100 1105	
cgg acg ctg ctg act ggg gac ggc ggt ggg gag gcc act ggg tca ccc	3717
Arg Thr Leu Leu Thr Gly Asp Gly Gly Gly Glu Ala Thr Gly Ser Pro	
1106 1111 1116 1121	
ctt gca cag ggc aag gat gcc cat taa cttaa aggggtaatg gcgggtaaag	3769
Leu Ala Gln Gly Lys Asp Ala His *	
1122 1127	
gaatcggaaa tacagtacct gaaacaggag attagctccc tcaaggatga gctgcagacg	3829
gcactgcggg acaagaagta cgcaagtgc aagtacaaag acatctacac agagctcagc	3889
atcgogaagg ctaaggctga ctgtgacatc agcaggttga aggagcagct caaggctgca	3949

acggaagcac tgggggagaa gtccctgac agtgccacgg tgtccggata tgatataatg 4009
 aaatctaaaa gcaaccctga cttcttgaag aaagacagat cctgtgtcac ccggcaactc 4069
 agaaacatca ggtccaagag tctgaaggaa ggcctgacgg tgcaagaacg gttgaagctc 4129
 tttgaatcca gggacttgaa gaaagactag gtgtgtccca tccaagttga gcacgcgcct 4189
 tccccagctt gcagcagcac accccaagcg ctgcttttca cctgtacott tgttttatta 4249
 ttattattat tattgctggt gttgtcatcg ttaactgtgg gcatggaatg cgtgaggctg 4309
 gcttctgggt tgtccacacc actctctgct gtgttgactt cctgttgtct tcaacaaagc 4369
 ttttttccgt ggtattctaa aattaggcca gcagtggggg ctgggagggc atctgtgtta 4429
 gtcctttcct ggctgtgacc cgccacactc actgtcagta ttaaggccca gcagcctgtt 4489
 gataagctac cctgtctcac catgtgctgg tgtggaaaacg gggcccagcc agcacgcctc 4549
 aaggtagatg gaatccccac tggtcagaga aaaagctatg cggacactcc agcttggcct 4609
 gggtcacagc actgactcct caccgctag tctggctggt aagaggagaa agtgcactgc 4669
 cttccagccc aggaggagga cagcattttg tatttgttcc actgatgcag cttagacca 4729
 caccctgag agtcgtggca aacctttcac aacctggaaa atgttgaaag caaccattcc 4789
 tatttttgtt tgttttttat taaatcttgc acaaaatccc cggccctct ccttccttcc 4849

<210> 40
 <211> 5199
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (241)..(3156)

<400> 40
 ggaaaccagg ccgaacccca acccccacca aaaccaccta ctcttgttct gtgggaggcc 60
 agtccacata cgctttgacc cgagagagat attcagatgg atccaatgtg actgatgaag 120
 ggaaggaaat catgtctagc gaagccttga aaaagctgcc ctgagacgga gtgccgccga 180
 aagaatggtg gctoaattaa gaaacatcag ggagataaat gccaccaggt gaggctaaaa 240
 atg act aca aac cga agt ttg ttt gtg cgg ttg gta cca tgt cgc tgt 288
 Met Thr Thr Asn Arg Ser Leu Phe Val Arg Leu Val Pro Cys Arg Cys
 1 5 10 15
 cta cga ggg gaa gag gag act gtc act act ctt gat tat tct cat tgc 336
 Leu Arg Gly Glu Glu Glu Thr Val Thr Thr Leu Asp Tyr Ser His Cys

17	22	27	32	
agc tta gaa caa gtt	ccg aaa gag att ttt	act ttt gaa aaa acc ttg		384
Ser Leu Glu Gln Val	Pro Lys Glu Ile Phe	Thr Phe Glu Lys Thr Leu		
33	38	43	48	
gag gaa ctc tat tta	gat gct aat cag att	gaa gag ctt cca aag caa		432
Glu Glu Leu Tyr Leu	Asp Ala Asn Gln Ile	Glu Glu Leu Pro Lys Gln		
49	54	59	64	
ctt ttt aac tgt cag	tct tta cac aaa ctg	agt ttg cca gac aat gat		480
Leu Phe Asn Cys Gln	Ser Leu His Lys Leu	Ser Leu Pro Asp Asn Asp		
65	70	75	80	
tta aca acg tta cca	gca tcc att gca aac	ctt att aat ctc agg gaa		528
Leu Thr Thr Leu Pro	Ala Ser Ile Ala Asn	Leu Ile Asn Leu Arg Glu		
81	86	91	96	
ctg gat gtc agc aag	aat gga ata cag gag	ttt cca gaa aat ata aaa		576
Leu Asp Val Ser Lys	Asn Gly Ile Gln Glu	Phe Pro Glu Asn Ile Lys		
97	102	107	112	
aat tgt aaa gtt ttg	aca att gtg gag gcc	agt gta aac cct att tcc		624
Asn Cys Lys Val Leu	Thr Ile Val Glu Ala	Ser Val Asn Pro Ile Ser		
113	118	123	128	
aag ctc cct gat gga	ttt tct cag ctg tta	aac cta acc cag ttg tat		672
Lys Leu Pro Asp Gly	Phe Ser Gln Leu Leu	Asn Leu Thr Gln Leu Tyr		
129	134	139	144	
ctg aat gat gct ttt	ctt gag ttc ttg cca	gca aat ttt ggc aga tta		720
Leu Asn Asp Ala Phe	Leu Glu Phe Leu Pro	Ala Asn Phe Gly Arg Leu		
145	150	155	160	
act aaa ctc caa ata	tta gag ctt aga gaa	aac cag tta aaa atg ttg		768
Thr Lys Leu Gln Ile	Leu Glu Leu Arg Glu	Asn Gln Leu Lys Met Leu		
161	166	171	176	
cct aaa act atg aat	aga ctg acc cag ctg	gaa aga ttg gat ttg gga		816
Pro Lys Thr Met Asn	Arg Leu Thr Gln Leu	Glu Arg Leu Asp Leu Gly		
177	182	187	192	
agt aac gaa ttc acg	gaa gtg cct gaa gta	ctt gag caa cta agt gga		864
Ser Asn Glu Phe Thr	Glu Val Pro Glu Val	Leu Glu Gln Leu Ser Gly		
193	198	203	208	
ttg aaa gag ttt tgg	atg gat gct aat aga	ctg act ttt att cca ggg		912
Leu Lys Glu Phe Trp	Met Asp Ala Asn Arg	Leu Thr Phe Ile Pro Gly		
209	214	219	224	
ttt att ggt agt ttg	aaa cag ctc aca tat	ttg gat gtt tct aaa aat		960
Phe Ile Gly Ser Leu	Lys Gln Leu Thr Tyr	Leu Asp Val Ser Lys Asn		
225	230	235	240	
aat att gaa atg gtt	gaa gaa gga att tca	aca tgt gaa aac ctt caa		1008
Asn Ile Glu Met Val	Glu Glu Gly Ile Ser	Thr Cys Glu Asn Leu Gln		
241	246	251	256	

gac ctc cta tta tca agc aat tca ctt cag cag ctt cct gag act att	1056
Asp Leu Leu Leu Ser Ser Asn Ser Leu Gln Gln Leu Pro Glu Thr Ile	
257 262 267 272	
ggt tgc ttg aag aat ata aca acg ctt aaa ata gat gaa aac cag tta	1104
Gly Ser Leu Lys Asn Ile Thr Thr Leu Lys Ile Asp Glu Asn Gln Leu	
273 278 283 288	
atg tat ctg cca gac tct ata gga ggg tta ata tca gta gaa gaa ctg	1152
Met Tyr Leu Pro Asp Ser Ile Gly Gly Leu Ile Ser Val Glu Glu Leu	
289 294 299 304	
gat tgt agt ttc aat gaa gtt gaa gct ttg cct tca tct att ggg cag	1200
Asp Cys Ser Phe Asn Glu Val Glu Ala Leu Pro Ser Ser Ile Gly Gln	
305 310 315 320	
ctt act aac tta aga act ttt gct gct gat cat aat tac tta cag cag	1248
Leu Thr Asn Leu Arg Thr Phe Ala Ala Asp His Asn Tyr Leu Gln Gln	
321 326 331 336	
ttg ccc cca gag att gga agc tgg aaa aat ata act gtg ctg ttt ctc	1296
Leu Pro Pro Glu Ile Gly Ser Trp Lys Asn Ile Thr Val Leu Phe Leu	
337 342 347 352	
cat tcc aat aaa ctt gag aca ctt cca gag gaa atg ggt gat atg caa	1344
His Ser Asn Lys Leu Glu Thr Leu Pro Glu Glu Met Gly Asp Met Gln	
353 358 363 368	
aaa tta aaa gtc att aat tta agt gat aat aga tta aag aat tta ccc	1392
Lys Leu Lys Val Ile Asn Leu Ser Asp Asn Arg Leu Lys Asn Leu Pro	
369 374 379 384	
ttt agc ttt aca aag cta cag caa ttg aca gct atg tgg ctc tca gat	1440
Phe Ser Phe Thr Lys Leu Gln Gln Leu Thr Ala Met Trp Leu Ser Asp	
385 390 395 400	
aat cag tcc aaa ccc ctg ata cct ctt caa aaa gaa act gat tca gag	1488
Asn Gln Ser Lys Pro Leu Ile Pro Leu Gln Lys Glu Thr Asp Ser Glu	
401 406 411 416	
acc cag aaa atg gtg ctt acc aac tac atg ttc cct caa cag cca agg	1536
Thr Gln Lys Met Val Leu Thr Asn Tyr Met Phe Pro Gln Gln Pro Arg	
417 422 427 432	
act gag gat gtt atg ttt ata tca gat aat gaa agt ttt aac cct tca	1584
Thr Glu Asp Val Met Phe Ile Ser Asp Asn Glu Ser Phe Asn Pro Ser	
433 438 443 448	
ttg tgg gag gaa cag agg aaa cag cgg gct caa gtt gca ttt gaa tgt	1632
Leu Trp Glu Glu Gln Arg Lys Gln Arg Ala Gln Val Ala Phe Glu Cys	
449 454 459 464	
gat gaa gac aaa gat gaa agg gag gca cct ccc agg gag gga aat tta	1680
Asp Glu Asp Lys Asp Glu Arg Glu Ala Pro Pro Arg Glu Gly Asn Leu	
465 470 475 480	

aaa aga tat cca aca cca tac cca gat gag ctt aag aat atg gtc aaa	1728
Lys Arg Tyr Pro Thr Pro Tyr Pro Asp Glu Leu Lys Asn Met Val Lys	
481 486 491 496	
act gtt caa acc att gta cat aga tta aaa gat gaa gag acc aat gaa	1776
Thr Val Gln Thr Ile Val His Arg Leu Lys Asp Glu Glu Thr Asn Glu	
497 502 507 512	
gac tca gga aga gat ttg aaa cca cat gaa gat caa caa gat ata aat	1824
Asp Ser Gly Arg Asp Leu Lys Pro His Glu Asp Gln Gln Asp Ile Asn	
513 518 523 528	
aaa gat gtg ggt gtg aag acc tca gaa agt act act aca gta aaa agc	1872
Lys Asp Val Gly Val Lys Thr Ser Glu Ser Thr Thr Thr Val Lys Ser	
529 534 539 544	
aaa gtt gat gaa aga gaa aaa tat atg ata gga aac tct gta cag aag	1920
Lys Val Asp Glu Arg Glu Lys Tyr Met Ile Gly Asn Ser Val Gln Lys	
545 550 555 560	
atc agt gaa cct gaa gct gag att agt cct ggg agt tta cca gtg act	1968
Ile Ser Glu Pro Glu Ala Glu Ile Ser Pro Gly Ser Leu Pro Val Thr	
561 566 571 576	
gca aat atg aaa gcc tct gag aac ttg aag cat att gtt aac cat gat	2016
Ala Asn Met Lys Ala Ser Glu Asn Leu Lys His Ile Val Asn His Asp	
577 582 587 592	
gat gtt ttt gag gaa tct gaa gaa ctt tct tct gat gaa gag atg aaa	2064
Asp Val Phe Glu Glu Ser Glu Glu Leu Ser Ser Asp Glu Glu Met Lys	
593 598 603 608	
atg gcg gag atg cga cca cca tta att gaa acc tct att aac cag cca	2112
Met Ala Glu Met Arg Pro Pro Leu Ile Glu Thr Ser Ile Asn Gln Pro	
609 614 619 624	
aaa gtc gta gca ctt agt aat aac aaa aaa gat gat aca aag gaa aca	2160
Lys Val Val Ala Leu Ser Asn Asn Lys Lys Asp Asp Thr Lys Glu Thr	
625 630 635 640	
gat tct tta tca gat gaa gtt aca cac aat agc aat cag aat aac agc	2208
Asp Ser Leu Ser Asp Glu Val Thr His Asn Ser Asn Gln Asn Asn Ser	
641 646 651 656	
aat tgt tct tct cca tct cgg atg tct gat tca gtt tct ctt aat act	2256
Asn Cys Ser Ser Pro Ser Arg Met Ser Asp Ser Val Ser Leu Asn Thr	
657 662 667 672	
gat agt agt caa gac acc tca ctc tgc tct cca gtg aaa caa act cat	2304
Asp Ser Ser Gln Asp Thr Ser Leu Cys Ser Pro Val Lys Gln Thr His	
673 678 683 688	
att gat att aat tcc aaa atc agg caa gaa gat gaa aat ttt aac agc	2352
Ile Asp Ile Asn Ser Lys Ile Arg Gln Glu Asp Glu Asn Phe Asn Ser	
689 694 699 704	
ctt tta caa aat gga gat att tta aac agt tca aca gag gaa aag ttc	2400

Leu Leu Gln Asn Gly Asp Ile Leu Asn Ser Ser Thr Glu Glu Lys Phe	
705 710 715 720	
aaa gct cat gat aaa aaa gat ttt aac tta cct gaa tat gat ttg aat	2448
Lys Ala His Asp Lys Lys Asp Phe Asn Leu Pro Glu Tyr Asp Leu Asn	
721 726 731 736	
ggt gaa gag cga tta gtt cta att gag aaa agt gtt gac tca aca gcc	2496
Val Glu Glu Arg Leu Val Leu Ile Glu Lys Ser Val Asp Ser Thr Ala	
737 742 747 752	
aca gct gat gac act cac aaa tta gat cat atc aat atg aat ctt aat	2544
Thr Ala Asp Asp Thr His Lys Leu Asp His Ile Asn Met Asn Leu Asn	
753 758 763 768	
aaa ctt ata act aat gat aca ttt caa cca gag atc atg gaa aga tca	2592
Lys Leu Ile Thr Asn Asp Thr Phe Gln Pro Glu Ile Met Glu Arg Ser	
769 774 779 784	
aaa aca cag gat att gtg ctt gga aca agc ttt tta agc att aat tct	2640
Lys Thr Gln Asp Ile Val Leu Gly Thr Ser Phe Leu Ser Ile Asn Ser	
785 790 795 800	
aaa gag gaa act gag cac ttg gaa aat gga aac aag tat cct aat ttg	2688
Lys Glu Glu Thr Glu His Leu Glu Asn Gly Asn Lys Tyr Pro Asn Leu	
801 806 811 816	
gaa tcc gta aat aag gta aat gga cat tct gag gaa act tcc cag tct	2736
Glu Ser Val Asn Lys Val Asn Gly His Ser Glu Glu Thr Ser Gln Ser	
817 822 827 832	
cct aat agg act gaa cca cat gac agt gat tgt tct gtt gac tta ggt	2784
Pro Asn Arg Thr Glu Pro His Asp Ser Asp Cys Ser Val Asp Leu Gly	
833 838 843 848	
att tcc aaa agc act gaa gat ctc tcc cct cag aaa agt ggt cca gtt	2832
Ile Ser Lys Ser Thr Glu Asp Leu Ser Pro Gln Lys Ser Gly Pro Val	
849 854 859 864	
gga tct gtt gtg aaa tct cat agc ata act aat atg gag att gga ggg	2880
Gly Ser Val Val Lys Ser His Ser Ile Thr Asn Met Glu Ile Gly Gly	
865 870 875 880	
cta aaa atc tat gat att ctt agt gat aat gga cct cag cag cca agt	2928
Leu Lys Ile Tyr Asp Ile Leu Ser Asp Asn Gly Pro Gln Gln Pro Ser	
881 886 891 896	
aca acc gtt aaa atc aca tct gct gtt gat gga aaa aat ata gtc agg	2976
Thr Thr Val Lys Ile Thr Ser Ala Val Asp Gly Lys Asn Ile Val Arg	
897 902 907 912	
agc aag tct gcc aca ctg ttg tat gat caa cca ttg cag gta ttt act	3024
Ser Lys Ser Ala Thr Leu Leu Tyr Asp Gln Pro Leu Gln Val Phe Thr	
913 918 923 928	
ggt tct tcc tca tct tct gat tta ata tca gga aca aag gca att ttc	3072
Gly Ser Ser Ser Ser Ser Asp Leu Ile Ser Gly Thr Lys Ala Ile Phe	

929	934	939	944	
aag ttt gat tca aat cat aat ccc gaa gag cca aat ata ata aga ggc				3120
Lys Phe Asp Ser Asn His Asn Pro Glu Glu Pro Asn Ile Ile Arg Gly				
945	950	955	960	
ccc aca agt ggc cca caa tct gca oct caa ata tag tggt cctccacagt				3170
Pro Thr Ser Gly Pro Gln Ser Ala Pro Gln Ile *				
961	966	971		
ataatatcca atacagtagc agtgctgcag tcaaagacac tttgtggcac tccaaacaaa				3230
atccccaaat agaccatgcc agttttctct ctcagctcct tcttagatca gagagcacag				3290
aaaatcaaag ttatgctaaa cattctgccg atatgaattt ctctaatacat aacaatgttc				3350
gagctaatac tgcataccat ttacatcaga gacttggccc agcaagacat ggggaaatgt				3410
gggccatctc accaaacgac cgacttattc ctgcagtaac tcgaagtaca atccagcgac				3470
aaagtagtgt gtctccaca gcctctgtaa atcttggtga tccaggctct acaaggcggg				3530
ctcagattcc tgaaggagat tatttatcat acagagagtt ccaactcagcg ggaagaactc				3590
ctccaatgat gccaggatca cagagacccc tttctgcacg aacatacagc atagatggtc				3650
caaatgcac aagacctcag agtgctcgac cctctattaa tgaaatacca gagagaacta				3710
tgctcagttag tgatttcaat tattcacgga ctagtccttc aaaaagacca aatgcaaggg				3770
ttggttctga gcattcttta ttagatctct caggaaaaag taaagttcct cgtgactgga				3830
gagaacaagt acttcgacat attgaagcca aaaagttaga aaagatgcct ttgagtaatg				3890
gacagatggg ccagcctctc aggcctcagg caaattatag tcaaatacat cccccctc				3950
aggcatctgt ggcaaggcat cctctagag aacaactaat tgattacttg atgctgaaag				4010
tggcccacca gcctccatat acacagcccc attgttctcc tagacaaggc catgaactgg				4070
caaaacaaga gattcgagtg aggggtgaaa aggatccaga acttggattt agcatatcag				4130
gtggtgtcgg gggtagagga aaccattca gacctgatga tgatggtata tttgtaacaa				4190
gggtacaacc tgaaggacca gcatcaaaat tactgcagcc aggtgataaa attattcagg				4250
ctaattggcta cagttttata aatattgaac atggacaagc agtgccttg ctaaaaactt				4310
tccagaatac agttgaactc atcattgtac gagaagtttc ctcataagca ctgtggacaa				4370
aaaaagcggg gaagacagca agatttattg gaagatactt acaggggaaa ttaatatttt				4430
gactattttt atatataaag aagaactcaa aaaattatgt tcaaatttgt acattaatga				4490
aataatggaa cttgtgggta gagggaaaga accactgtac agaataataa ggagactggt				4550
gaattcatat catataaaac ttgttaggtt tttaaacata gcaatcaagg ctacaaaaac				4610

aaacotgtgt tgtttttgta tagattgtag gtttattttt ggatttcata tacatgactg 4670
 aactgtgtgc aaggcaatag ttagccttga ttttagccca gagacagatg gcagagctat 4730
 ctctctcata gcttttatgc ccttattttt attcaactgg tattaatgtt tttctcctga 4790
 aactactttt tttgatgtgg gcaagagatt tgaagtgttg gcttttgcta tgtgcatatt 4850
 gaattgaaga gtgagtacgt gaagggtggg ctgggtgggtt cactttccaa ggccagacta 4910
 aaacagttat tttctataaa aatctggaag caaagaatgg ggatggggag agctacctgg 4970
 tagtatgttt ttattaggag aataatgcaa taaaatatgt aatggccttt ttataaagca 5030
 aaaaagacaa taattgcatt tatgagctcg gcaggatctg ttcttgtcat agccattgac 5090
 tatacatttg ctactggtga ttcagttttt aatttttttag tcacaggaaa tttttaactc 5150
 tactgtagat gcatgtccat gcattttctg agttatggaa atccactga 5199

<210> 41
 <211> 5640
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (549)..(5354)

<400> 41
 ccactttgta caagaaagct ggggtacgct aagcttgggc ccctcgaggg atactctaga 60
 gcggcgcac ccagtgcctc tgcaaacctg gttatgcagg tgccctcctgc gagcgggtgtg 120
 cgcccggatt ctttggaac ccactggtgc tgggcagctc ctgccagcca tgcgactgca 180
 gcggcaacgg tgaccccaac ttgctcttca gcgactgca cccctgacg ggcgctgcc 240
 gtggctgcct gcgccacacc actgggcccc gctgcgagat ctgtgcccc ggctttctacg 300
 gcaacgcct gctgccggc aactgcaccc ggtgcgactg taccatgt gggacagagg 360
 cctgcgaccc ccacagcggg cactgcctgt gcaaggcggg cgtgactggg cggcgctgtg 420
 accgctgcca ggagggacat tttggtttca atggctgcgg gggctgccgc ccgtgtgctt 480
 gtggaccggc cgccgagggc tccgagtgcc acccccagag cggacagtgc cactgccgac 540
 cagggacc atg gga ccc cag tgc cgc gag tgt gcc cct ggc tac tgg ggg 590
 Met Gly Pro Gln Cys Arg Glu Cys Ala Pro Gly Tyr Trp Gly
 1 5 10
 ctc cct gag cag ggc tgc agg cgc tgc cag tgc cct ggg ggc cgc tgt 638

Leu	Pro	Glu	Gln	Gly	Cys	Arg	Arg	Cys	Gln	Cys	Pro	Gly	Gly	Arg	Cys		
15					20					25					30		
gac	cct	cac	acg	ggc	cgc	tgc	aac	tgc	ccc	ccg	ggg	ctc	agc	ggg	gag	686	
Asp	Pro	His	Thr	Gly	Arg	Cys	Asn	Cys	Pro	Pro	Gly	Leu	Ser	Gly	Glu		
31					36					41					46		
cgc	tgc	gac	acc	tgc	agc	cag	cag	cat	cag	gtg	cct	gtt	cca	ggc	ggg	734	
Arg	Cys	Asp	Thr	Cys	Ser	Gln	Gln	His	Gln	Val	Pro	Val	Pro	Gly	Gly		
47					52					57					62		
cct	gtg	ggc	cac	agc	atc	cac	tgt	gaa	gtg	tgt	gac	cac	tgt	gtg	gtc	782	
Pro	Val	Gly	His	Ser	Ile	His	Cys	Glu	Val	Cys	Asp	His	Cys	Val	Val		
63					68					73					78		
ctg	ctc	ctg	gat	gac	ctg	gaa	cgg	gcc	ggc	gcc	ctc	ctc	ccc	gcc	att	830	
Leu	Leu	Leu	Asp	Asp	Leu	Glu	Arg	Ala	Gly	Ala	Leu	Leu	Pro	Ala	Ile		
79					84					89					94		
cac	gag	caa	ctg	cgt	ggc	atc	aat	gcc	agc	tcc	atg	gcc	tgg	gcc	cgt	878	
His	Glu	Gln	Leu	Arg	Gly	Ile	Asn	Ala	Ser	Ser	Met	Ala	Trp	Ala	Arg		
95					100					105					110		
ctg	cac	agg	ctg	aac	gcc	tcc	atc	gct	gac	ctg	cag	agc	cag	ctc	cgg	926	
Leu	His	Arg	Leu	Asn	Ala	Ser	Ile	Ala	Asp	Leu	Gln	Ser	Gln	Leu	Arg		
111					116					121					126		
agc	ccc	ctg	ggc	ccc	cgc	cat	gag	acg	gca	cag	cag	ctg	gag	gtg	ctg	974	
Ser	Pro	Leu	Gly	Pro	Arg	His	Glu	Thr	Ala	Gln	Gln	Leu	Glu	Val	Leu		
127					132					137					142		
gag	cag	cag	agc	aca	agc	ctc	ggg	cag	gac	gca	cgg	cgg	cta	ggc	ggc	1022	
Glu	Gln	Gln	Ser	Thr	Ser	Leu	Gly	Gln	Asp	Ala	Arg	Arg	Leu	Gly	Gly		
143					148					153					158		
cag	gcc	gtg	ggg	acc	cga	gac	cag	gcg	agc	caa	ttg	ctg	gcc	ggc	acc	1070	
Gln	Ala	Val	Gly	Thr	Arg	Asp	Gln	Ala	Ser	Gln	Leu	Leu	Ala	Gly	Thr		
159					164					169					174		
gag	gcc	aca	ctg	ggc	cat	gcg	aag	acg	ctg	ttg	gcg	gcc	atc	cgg	gct	1118	
Glu	Ala	Thr	Leu	Gly	His	Ala	Lys	Thr	Leu	Leu	Ala	Ala	Ile	Arg	Ala		
175					180					185					190		
gtg	gac	cgc	acc	ctg	agc	gag	ctc	atg	tcc	cag	acg	ggc	cac	ctg	ggg	1166	
Val	Asp	Arg	Thr	Leu	Ser	Glu	Leu	Met	Ser	Gln	Thr	Gly	His	Leu	Gly		
191					196					201					206		
ctg	gcc	aat	gcc	tgc	gct	cca	tca	ggt	gag	cag	ctg	ctc	cgg	aca	ctg	1214	
Leu	Ala	Asn	Ala	Ser	Ala	Pro	Ser	Gly	Glu	Gln	Leu	Leu	Arg	Thr	Leu		
207					212					217					222		
gcc	gag	gtg	gag	cgg	ctg	ctc	tgg	gag	atg	cgg	gcc	cgg	gac	ctg	ggg	1262	
Ala	Glu	Val	Glu	Arg	Leu	Leu	Trp	Glu	Met	Arg	Ala	Arg	Asp	Leu	Gly		
223					228					233					238		
gcc	ccg	cag	gca	gca	gct	gag	gct	gag	ttg	gct	gca	gca	cag	aga	ttg	1310	
Ala	Pro	Gln	Ala	Ala	Ala	Glu	Ala	Glu	Leu	Ala	Ala	Ala	Gln	Arg	Leu		

239	244	249	254	
ctg gcc cgg gtg cag gag cag ctg agc agc ctc tgg gag gag aac cag				1358
Leu Ala Arg Val Gln Glu Gln Leu Ser Ser Leu Trp Glu Glu Asn Gln				
255	260	265	270	
gca ctg gcc aca caa acc cgc gac cgg ctg gcc cag cac gag gcc ggc				1406
Ala Leu Ala Thr Gln Thr Arg Asp Arg Leu Ala Gln His Glu Ala Gly				
271	276	281	286	
ctc atg gac ctg cga gag gct ttg aac cgg gca gtg gac gcc aca cgg				1454
Leu Met Asp Leu Arg Glu Ala Leu Asn Arg Ala Val Asp Ala Thr Arg				
287	292	297	302	
gag gcc cag gag ctc aac agc cgc aac cag gag cgc ctg gag gaa gcc				1502
Glu Ala Gln Glu Leu Asn Ser Arg Asn Gln Glu Arg Leu Glu Glu Ala				
303	308	313	318	
ctg caa agg aag cag gag ctg tcc cgg gac aat gcc acc ctg cag gcc				1550
Leu Gln Arg Lys Gln Glu Leu Ser Arg Asp Asn Ala Thr Leu Gln Ala				
319	324	329	334	
act ctg cat gcg gct agg gac acc ctg gcc agc gtc ttc aga ttg ctg				1598
Thr Leu His Ala Ala Arg Asp Thr Leu Ala Ser Val Phe Arg Leu Leu				
335	340	345	350	
cac agc ctg gac cag gct aag gag gag ctg gag cgc ctc gcc gcc agc				1646
His Ser Leu Asp Gln Ala Lys Glu Glu Leu Glu Arg Leu Ala Ala Ser				
351	356	361	366	
ctg gac ggg gct cgg acc cca ctg ctg cag agg atg cag acc ttc tcc				1694
Leu Asp Gly Ala Arg Thr Pro Leu Leu Gln Arg Met Gln Thr Phe Ser				
367	372	377	382	
ccg gcg ggc agc aag ctg cgt cta gtg gag gcc gcc gag gcc cac gca				1742
Pro Ala Gly Ser Lys Leu Arg Leu Val Glu Ala Ala Glu Ala His Ala				
383	388	393	398	
cag cag ctg ggc cag ctg gca ctc aat ctg tcc agc atc atc ctg gac				1790
Gln Gln Leu Gly Gln Leu Ala Leu Asn Leu Ser Ser Ile Ile Leu Asp				
399	404	409	414	
gtc aac cag gac cgc ctc acc cag agg gcc atc gag gcc tcc aac gcc				1838
Val Asn Gln Asp Arg Leu Thr Gln Arg Ala Ile Glu Ala Ser Asn Ala				
415	420	425	430	
tac agc cgc atc ctg cag gcc gtg cag gct gcc gag gat gct gct ggc				1886
Tyr Ser Arg Ile Leu Gln Ala Val Gln Ala Ala Glu Asp Ala Ala Gly				
431	436	441	446	
cag gcc ctg cag cag gcg gac cac acg tgg gcg acg gtg gtg cgg cag				1934
Gln Ala Leu Gln Gln Ala Asp His Thr Trp Ala Thr Val Val Arg Gln				
447	452	457	462	
ggc ctg gtg gac cga gcc cag cag ctc ctg gcc aac agc act gca cta				1982
Gly Leu Val Asp Arg Ala Gln Gln Leu Leu Ala Asn Ser Thr Ala Leu				
463	468	473	478	

gaa gag gcc atg ctc cag gaa cag cag agg ctg ggc ctt gtg tgg gct	2030
Glu Glu Ala Met Leu Gln Glu Gln Arg Leu Gly Leu Val Trp Ala	
479 484 489 494	
gac cag ctg gag ggc cag acc cag ctc cga gat gtc cgg gcc aag aag	2078
Ala Leu Gln Gly Ala Arg Thr Gln Leu Arg Asp Val Arg Ala Lys Lys	
495 500 505 510	
gac cag ctg gag ggc cag atc cag ggc ggc cag gcc atg ctt gcc atg	2126
Asp Gln Leu Glu Ala His Ile Gln Ala Ala Gln Ala Met Leu Ala Met	
511 516 521 526	
gac aca gac gag aca agc aag aag atc gca cat gcc aag gct gtg gct	2174
Asp Thr Asp Glu Thr Ser Lys Lys Ile Ala His Ala Lys Ala Val Ala	
527 532 537 542	
gct gaa gcc cag gac acc gcc acc cgt gtg cag tcc cag ctg cag gcc	2222
Ala Glu Ala Gln Asp Thr Ala Thr Arg Val Gln Ser Gln Leu Gln Ala	
543 548 553 558	
atg cag gag aat gtg gag cgg tgg cag ggc cag tac gag ggc ctg cgg	2270
Met Gln Glu Asn Val Glu Arg Trp Gln Gly Gln Tyr Glu Gly Leu Arg	
559 564 569 574	
ggc cag gac ctg ggc cag gca gtg ctt gac gca ggc cac tca gtg tcc	2318
Gly Gln Asp Leu Gly Gln Ala Val Leu Asp Ala Gly His Ser Val Ser	
575 580 585 590	
acc ctg gag aag acg ctg ccc cag ctg ctg gcc aag ctg agc atc ctg	2366
Thr Leu Glu Lys Thr Leu Pro Gln Leu Leu Ala Lys Leu Ser Ile Leu	
591 596 601 606	
gag aac cgt ggg gtg cac aac gcc agc ctg gcc ctg tcc gcc agc att	2414
Glu Asn Arg Gly Val His Asn Ala Ser Leu Ala Leu Ser Ala Ser Ile	
607 612 617 622	
ggc cgc gtg cga gag ctc att gcc cag gcc cgg ggg gct gcc agt aag	2462
Gly Arg Val Arg Glu Leu Ile Ala Gln Ala Arg Gly Ala Ala Ser Lys	
623 628 633 638	
gtc aag gtg ccc atg aag ttc aac ggg cgc tca ggg gtg cag ctg cgc	2510
Val Lys Val Pro Met Lys Phe Asn Gly Arg Ser Gly Val Gln Leu Arg	
639 644 649 654	
acc cca cgg gat ctt gcc gac ctt gct gcc tac act gcc ctc aag ttc	2558
Thr Pro Arg Asp Leu Ala Asp Leu Ala Ala Tyr Thr Ala Leu Lys Phe	
655 660 665 670	
tac ctg cag ggc cca gag cct gag cct ggg cag ggt acc gag gat cgc	2606
Tyr Leu Gln Gly Pro Glu Pro Glu Pro Gly Gln Gly Thr Glu Asp Arg	
671 676 681 686	
ttt gtg atg tac atg ggc agc cgc cag gcc act ggg gac tac atg ggt	2654
Phe Val Met Tyr Met Gly Ser Arg Gln Ala Thr Gly Asp Tyr Met Gly	
687 692 697 702	

gtg tct ctg cgt gac aag aag gtg cac tgg gtg tat cag ctg ggt gag	2702
Val Ser Leu Arg Asp Lys Lys Val His Trp Val Tyr Gln Leu Gly Glu	
703 708 713 718	
gcg ggc cct gca gtc cta agc atc gat gag gac att ggg gag cag ttc	2750
Ala Gly Pro Ala Val Leu Ser Ile Asp Glu Asp Ile Gly Glu Gln Phe	
719 724 729 734	
gca gct gtc agc ctg gac agg act ctc cag ttt ggc cac atg tcc gtc	2798
Ala Ala Val Ser Leu Asp Arg Thr Leu Gln Phe Gly His Met Ser Val	
735 740 745 750	
aca gtg gag aga cag atg atc cag gaa acc aag ggt gac acg gtg gcc	2846
Thr Val Glu Arg Gln Met Ile Gln Glu Thr Lys Gly Asp Thr Val Ala	
751 756 761 766	
cct ggg gca gag ggg ctg ctc aac ctg cgg cca gac gac ttc gtc ttc	2894
Pro Gly Ala Glu Gly Leu Leu Asn Leu Arg Pro Asp Asp Phe Val Phe	
767 772 777 782	
tac gtc ggg ggg tac ccc agt acc ttc acg ccc cct ccc ctg ctt cgc	2942
Tyr Val Gly Gly Tyr Pro Ser Thr Phe Thr Pro Pro Pro Leu Leu Arg	
783 788 793 798	
ttc ccc ggc tac cgg ggc tgc atc gag atg gac acg ctg aat gag gag	2990
Phe Pro Gly Tyr Arg Gly Cys Ile Glu Met Asp Thr Leu Asn Glu Glu	
799 804 809 814	
gtg gtc agc ctc tac aac ttc gag agg acc ttc cag ctg gac acg gct	3038
Val Val Ser Leu Tyr Asn Phe Glu Arg Thr Phe Gln Leu Asp Thr Ala	
815 820 825 830	
gtg gac agg cct tgt gcc cgc tcc aag tgc acc ggg gac ccg tgg ctc	3086
Val Asp Arg Pro Cys Ala Arg Ser Lys Ser Thr Gly Asp Pro Trp Leu	
831 836 841 846	
acg gac ggc tcc tac ctg gac ggc acc ggc ttc gcc cgc atc agc ttc	3134
Thr Asp Gly Ser Tyr Leu Asp Gly Thr Gly Phe Ala Arg Ile Ser Phe	
847 852 857 862	
gac agt cag atc agc acc acc aag cgc ttc gag cag gag ctg cgg ctc	3182
Asp Ser Gln Ile Ser Thr Thr Lys Arg Phe Glu Gln Glu Leu Arg Leu	
863 868 873 878	
gtg tcc tac agc ggg gtg ctc ttc ttc ctg aag cag cag agc cag ttc	3230
Val Ser Tyr Ser Gly Val Leu Phe Phe Leu Lys Gln Gln Ser Gln Phe	
879 884 889 894	
ctg tgc ttg gcc gtg caa gaa ggc agc ctc gtg ctg ttg tat gac ttt	3278
Leu Cys Leu Ala Val Gln Glu Gly Ser Leu Val Leu Leu Tyr Asp Phe	
895 900 905 910	
ggg gct ggc ctg aaa aag gcc gtc cca ctg cag ccc cca ccg ccc ctg	3326
Gly Ala Gly Leu Lys Lys Ala Val Pro Leu Gln Pro Pro Pro Pro Leu	
911 916 921 926	
acc tgc gcc agc aag gcg atc cag gtg ttc ctg ctg ggg ggc agc cgc	3374

Thr	Ser	Ala	Ser	Lys	Ala	Ile	Gln	Val	Phe	Leu	Leu	Gly	Gly	Ser	Arg		
927					932					937					942		
aag	cgt	gtg	ctg	gtg	cgt	gtg	gag	cgg	gcc	acg	gtg	tac	agc	gtg	gag	3422	
Lys	Arg	Val	Leu	Val	Arg	Val	Glu	Arg	Ala	Thr	Val	Tyr	Ser	Val	Glu		
943					948					953					958		
cag	gac	aat	gat	ctg	gag	ctg	gcc	gac	gcc	tac	tac	ctg	ggg	ggc	gtg	3470	
Gln	Asp	Asn	Asp	Leu	Glu	Leu	Ala	Asp	Ala	Tyr	Tyr	Leu	Gly	Gly	Val		
959					964					969					974		
ccg	ccc	gac	cag	ctg	ccc	ccg	agc	ctg	cga	tgg	ctc	ttc	ccc	acc	gga	3518	
Pro	Pro	Asp	Gln	Leu	Pro	Pro	Ser	Leu	Arg	Trp	Leu	Phe	Pro	Thr	Gly		
975					980					985					990		
ggc	tca	gtc	cgt	ggc	tgc	gtc	aaa	ggc	atc	aag	gcc	ctg	ggc	aag	tat	3566	
Gly	Ser	Val	Arg	Gly	Cys	Val	Lys	Gly	Ile	Lys	Ala	Leu	Gly	Lys	Tyr		
991					996					1001					1006		
gtg	gac	ctc	aag	cgg	ctg	aac	acg	aca	ggc	gtg	agc	gcc	ggc	tgc	acc	3614	
Val	Asp	Leu	Lys	Arg	Leu	Asn	Thr	Thr	Gly	Val	Ser	Ala	Gly	Cys	Thr		
1007					1012					1017					1022		
gcc	gac	ctg	ctg	gtg	ggg	cgc	gcc	atg	act	ttc	cat	ggc	cac	ggc	ttc	3662	
Ala	Asp	Leu	Leu	Val	Gly	Arg	Ala	Met	Thr	Phe	His	Gly	His	Gly	Phe		
1023					1028					1033					1038		
ctt	cgc	ctg	gcg	ctc	tgc	aac	gtg	gca	ccg	ctc	act	ggc	aac	gtc	tac	3710	
Leu	Arg	Leu	Ala	Leu	Ser	Asn	Val	Ala	Pro	Leu	Thr	Gly	Asn	Val	Tyr		
1039					1044					1049					1054		
tcc	ggc	ttc	ggc	ttc	cac	agc	gcc	cag	gac	agt	gcc	ctg	ctc	tac	tac	3758	
Ser	Gly	Phe	Gly	Phe	His	Ser	Ala	Gln	Asp	Ser	Ala	Leu	Leu	Tyr	Tyr		
1055					1060					1065					1070		
cgg	gcg	tcc	ccg	gat	ggg	cta	tgc	cag	gtg	tcc	ctg	cag	cag	ggc	cgt	3806	
Arg	Ala	Ser	Pro	Asp	Gly	Leu	Cys	Gln	Val	Ser	Leu	Gln	Gln	Gly	Arg		
1071					1076					1081					1086		
gtg	agc	cta	cag	ctc	ctg	agg	act	gaa	gtg	aaa	act	caa	gcg	ggc	ttc	3854	
Val	Ser	Leu	Gln	Leu	Leu	Arg	Thr	Glu	Val	Lys	Thr	Gln	Ala	Gly	Phe		
1087					1092					1097					1102		
gcc	gat	ggt	gcc	ccc	cat	tac	gtc	gcc	ttc	tac	agc	aat	gcc	acg	gga	3902	
Ala	Asp	Gly	Ala	Pro	His	Tyr	Val	Ala	Phe	Tyr	Ser	Asn	Ala	Thr	Gly		
1103					1108					1113					1118		
gtc	tgg	ctg	tat	gtc	gat	gac	cag	ctc	cag	cag	atg	aag	ccc	cac	cgg	3950	
Val	Trp	Leu	Tyr	Val	Asp	Asp	Gln	Leu	Gln	Gln	Met	Lys	Pro	His	Arg		
1119					1124					1129					1134		
gga	cca	ccc	ccc	gag	ctc	cag	ccg	cag	cct	gag	ggg	ccc	ccg	agg	ctc	3998	
Gly	Pro	Pro	Pro	Glu	Leu	Gln	Pro	Gln	Pro	Glu	Gly	Pro	Pro	Arg	Leu		
1135					1140					1145					1150		
ctc	ctg	gga	ggc	ctg	cct	gag	tct	ggc	acc	att	tac	aac	ttc	agt	ggc	4046	
Leu	Leu	Gly	Gly	Leu	Pro	Glu	Ser	Gly	Thr	Ile	Tyr	Asn	Phe	Ser	Gly		

1151	1156	1161	1166	
tgc atc agc aac gtc ttc gtg cag cgg ctc ctg ggc cca cag cgc gta				4094
Cys Ile Ser Asn Val Phe Val Gln Arg Leu Leu Gly Pro Gln Arg Val				
1167	1172	1177	1182	
ttt gat ctg cag cag aac ctg ggc agc gtc aat gtg agc acg ggc tgt				4142
Phe Asp Leu Gln Gln Asn Leu Gly Ser Val Asn Val Ser Thr Gly Cys				
1183	1188	1193	1198	
gca ccc gcc ctg caa gcc cag acc ccg ggc ctg ggg cct aga gga ctg				4190
Ala Pro Ala Leu Gln Ala Gln Thr Pro Gly Leu Gly Pro Arg Gly Leu				
1199	1204	1209	1214	
cag gcc acc gcc cgg aag gcc tcc cgc cgc agc cgt cag ccc gcc cgg				4238
Gln Ala Thr Ala Arg Lys Ala Ser Arg Arg Ser Arg Gln Pro Ala Arg				
1215	1220	1225	1230	
cat cct gcc tgc atg ctg ccc cca cac ctc agg acc acc cga gac tcc				4286
His Pro Ala Cys Met Leu Pro Pro His Leu Arg Thr Thr Arg Asp Ser				
1231	1236	1241	1246	
tac cag ttt ggg ggt tcc ctg tcc agt cac ctg gag ttt gtg ggc atc				4334
Tyr Gln Phe Gly Gly Ser Leu Ser Ser His Leu Glu Phe Val Gly Ile				
1247	1252	1257	1262	
ctg gcc cga cat agg aac tgg ccc agt ctc tcc atg cac gtc ctc ccg				4382
Leu Ala Arg His Arg Asn Trp Pro Ser Leu Ser Met His Val Leu Pro				
1263	1268	1273	1278	
cga agc tcc cga ggc ctc ctc ctc ttc act gcc cgt ctg agg ccc gcc				4430
Arg Ser Ser Arg Gly Leu Leu Leu Phe Thr Ala Arg Leu Arg Pro Gly				
1279	1284	1289	1294	
agc ccc tcc ctg gcg ctc ttc ctg agc aat ggc cac ttc gtt gca cag				4478
Ser Pro Ser Leu Ala Leu Phe Leu Ser Asn Gly His Phe Val Ala Gln				
1295	1300	1305	1310	
atg gaa ggc ctc ggg act cgg ctc cgc gcc cag agc cgc cag cgc tcc				4526
Met Glu Gly Leu Gly Thr Arg Leu Arg Ala Gln Ser Arg Gln Arg Ser				
1311	1316	1321	1326	
cgg cct ggc cgc tgg cac aag gtc tcc gtg cgc tgg gag aag aac cgg				4574
Arg Pro Gly Arg Trp His Lys Val Ser Val Arg Trp Glu Lys Asn Arg				
1327	1332	1337	1342	
atc ctg ctg gtg acg gac ggg gcc cgg gcc tgg agc cag gag ggg ccg				4622
Ile Leu Leu Val Thr Asp Gly Ala Arg Ala Trp Ser Gln Glu Gly Pro				
1343	1348	1353	1358	
cac cgg cag cac cag ggg gca gag cac ccc cag ccc cac acc ctc ttt				4670
His Arg Gln His Gln Gly Ala Glu His Pro Gln Pro His Thr Leu Phe				
1359	1364	1369	1374	
gtg ggc ggc ctc ccg gcc agc agc cac agc tcc aaa ctt ccg gtg acc				4718
Val Gly Gly Leu Pro Ala Ser Ser His Ser Ser Lys Leu Pro Val Thr				
1375	1380	1385	1390	

gtc ggg ttc agc ggc tgt gtg aag aga ctg agg ctg cac ggg agg ccc	4766
Val Gly Phe Ser Gly Cys Val Lys Arg Leu Arg Leu His Gly Arg Pro	
1391 1396 1401 1406	
ctg ggg gcc ccc aca cgg atg gca ggg gtc aca ccc tgc atc ttg ggc	4814
Leu Gly Ala Pro Thr Arg Met Ala Gly Val Thr Pro Cys Ile Leu Gly	
1407 1412 1417 1422	
ccc ctg gag gcg ggc ctg ttc ttc cca ggc agc ggg gga gtt atc act	4862
Pro Leu Glu Ala Gly Leu Phe Phe Pro Gly Ser Gly Gly Val Ile Thr	
1423 1428 1433 1438	
tta gac ctc cca gga gct aca ctg cct gat gtg ggc ctg gaa ctg gag	4910
Leu Asp Leu Pro Gly Ala Thr Leu Pro Asp Val Gly Leu Glu Leu Glu	
1439 1444 1449 1454	
gtg cgg ccc ctg gca gtc acc gga ctg atc ttc cac ttg ggc cag gcc	4958
Val Arg Pro Leu Ala Val Thr Gly Leu Ile Phe His Leu Gly Gln Ala	
1455 1460 1465 1470	
cgg acg ccc ccc tac ttg cag ttg cag gtg acc gag aag caa gtc ctg	5006
Arg Thr Pro Pro Tyr Leu Gln Leu Gln Val Thr Glu Lys Gln Val Leu	
1471 1476 1481 1486	
ctg cgg gcg gat gac gga gca ggg gag ttc tcc acg tca gtg acc cgc	5054
Leu Arg Ala Asp Asp Gly Ala Gly Glu Phe Ser Thr Ser Val Thr Arg	
1487 1492 1497 1502	
ccc tca gtg ctg tgt gat ggc cag tgg cac cgg cta gcg gtg atg aaa	5102
Pro Ser Val Leu Cys Asp Gly Gln Trp His Arg Leu Ala Val Met Lys	
1503 1508 1513 1518	
agc ggg aat gtg ctc cgg ctg gag gtg gac gcg cag agc aac cac acc	5150
Ser Gly Asn Val Leu Arg Leu Glu Val Asp Ala Gln Ser Asn His Thr	
1519 1524 1529 1534	
gtg ggc ccc ttg ctg gcg gct gca gct ggt gcc cca gcc cct ctg tac	5198
Val Gly Pro Leu Leu Ala Ala Ala Ala Gly Ala Pro Ala Pro Leu Tyr	
1535 1540 1545 1550	
ctc ggg ggc ctg cct gag ccc atg gcc gtg cag ccc tgg ccc ccc gcc	5246
Leu Gly Gly Leu Pro Glu Pro Met Ala Val Gln Pro Trp Pro Pro Ala	
1551 1556 1561 1566	
tac tgc ggc tgc atg agg agg ctg gcg gtg aac cgg tcc ccc gtc gcc	5294
Tyr Cys Gly Cys Met Arg Arg Leu Ala Val Asn Arg Ser Pro Val Ala	
1567 1572 1577 1582	
atg act cgc tct gtg gag gtc cac ggg gca gtg ggg gcc agt ggc tgc	5342
Met Thr Arg Ser Val Glu Val His Gly Ala Val Gly Ala Ser Gly Cys	
1583 1588 1593 1598	
cca gcc gcc tag gac acagccaacc ccggcccctg gtcaggcccc tgcagctgcc	5397
Pro Ala Ala *	
1599	

tcacaccgcc ccttgtgctc gcctcatagg tgtctatttg gactctaagc tctacgggtg 5457
acagatcttg tttctgaaga tggtttaagt tatagcttct taaacgaaag aataaaatac 5517
tgcaaaatgt ttttatattt ggcccttcca cccattttta attgtgagag atttgtcacc 5577
aatcatcact ggttcctcct taaaaattaa aaagtaactt ctgtgtaacc gaaaaaaaaa 5637
aaa 5640

<210> 42
<211> 1887
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (55)..(1563)

<400> 42
cgcggtaccg gtccggaatt cccgggtcga gtgaaatctg ccgtggccaa tttc atg 57
Met
1

ggc ggc atc atg gct ggc agc tca ggc tcc gag cac ggc ggc ggc agc 105
Gly Gly Ile Met Ala Gly Ser Ser Gly Ser Glu His Gly Gly Gly Ser
2 7 12 17

tgc gga ggc tcg gac ctg ccc ctg cgt ttc ccc tac ggg cgg cca gag 153
Cys Gly Gly Ser Asp Leu Pro Leu Arg Phe Pro Tyr Gly Arg Pro Glu
18 23 28 33

ttc ctg ggg ctg tct cag gac gag gtg gag tgc agc gcc gac cac atc 201
Phe Leu Gly Leu Ser Gln Asp Glu Val Glu Cys Ser Ala Asp His Ile
34 39 44 49

gcc cgc ccc atc ctc atc ctc aag gag act cgg cgg ctg ccc tgg gcc 249
Ala Arg Pro Ile Leu Ile Leu Lys Glu Thr Arg Arg Leu Pro Trp Ala
50 55 60 65

act ggc tac gca gag gtt atc aat gcc ggg aag agc aca cac aat gaa 297
Thr Gly Tyr Ala Glu Val Ile Asn Ala Gly Lys Ser Thr His Asn Glu
66 71 76 81

gac caa gcc agc tgt gag gtg ctc act gtg aag aag aag gca ggg gcc 345
Asp Gln Ala Ser Cys Glu Val Leu Thr Val Lys Lys Lys Ala Gly Ala
82 87 92 97

gtg acc tca acc cca aac agg aac tca tcc aag aga cgg tcc tcc ctt 393
Val Thr Ser Thr Pro Asn Arg Asn Ser Ser Lys Arg Arg Ser Ser Leu
98 103 108 113

ccc aat ggg gaa ggg ctg cag ctg aag gag aac tcg gaa tcc gag ggt 441
Pro Asn Gly Glu Gly Leu Gln Leu Lys Glu Asn Ser Glu Ser Glu Gly

114	119	124	129	
gtt tcc tgc cac tat tgg tgc ctg ttt gac ggg cac gcg ggg tcc ggg				489
Val Ser Cys His Tyr Trp Ser Leu Phe Asp Gly His Ala Gly Ser Gly				
130	135	140	145	
gcc gcg gtg gtg gcg tca cgc ctg ctg cag cac cac atc acg gag cag				537
Ala Ala Val Val Ala Ser Arg Leu Leu Gln His His Ile Thr Glu Gln				
146	151	156	161	
ctg cag gac atc gtg gac atc ctg aag aac tcc gcc gtc ctg ccc cct				585
Leu Gln Asp Ile Val Asp Ile Leu Lys Asn Ser Ala Val Leu Pro Pro				
162	167	172	177	
acc tgc ctg ggg gag gag cct gag aac acg ccc gcc aac agc cgg act				633
Thr Cys Leu Gly Glu Glu Pro Glu Asn Thr Pro Ala Asn Ser Arg Thr				
178	183	188	193	
ctg acc cgg gca gcc tcc ctg cgc gga ggg gtg ggg gcc ccg ggc tcc				681
Leu Thr Arg Ala Ala Ser Leu Arg Gly Gly Val Gly Ala Pro Gly Ser				
194	199	204	209	
ccc agc acg ccc ccc aca cgc ttc ttt acc gag aag aag att ccc cat				729
Pro Ser Thr Pro Pro Thr Arg Phe Phe Thr Glu Lys Lys Ile Pro His				
210	215	220	225	
gag tgc ctg gtc atc gga gcg ctt gaa agt gca ttc aag gaa atg gac				777
Glu Cys Leu Val Ile Gly Ala Leu Glu Ser Ala Phe Lys Glu Met Asp				
226	231	236	241	
cta cag ata gaa cga gag agg agt tca tat aat ata tct ggt ggc tgc				825
Leu Gln Ile Glu Arg Glu Arg Ser Ser Tyr Asn Ile Ser Gly Gly Cys				
242	247	252	257	
acg gcc ctc att gtg att tgc ctt ttg ggg aag ctg tat gtt gca aat				873
Thr Ala Leu Ile Val Ile Cys Leu Leu Gly Lys Leu Tyr Val Ala Asn				
258	263	268	273	
gct ggg gat agc agg gcc ata atc atc aga aat gga gaa att atc ccc				921
Ala Gly Asp Ser Arg Ala Ile Ile Ile Arg Asn Gly Glu Ile Ile Pro				
274	279	284	289	
atg tct tca gaa ttt acc ccc gag acg gag cgc cag cga ctt cag tac				969
Met Ser Ser Glu Phe Thr Pro Glu Thr Glu Arg Gln Arg Leu Gln Tyr				
290	295	300	305	
ctg gca ttc atg cag cct cac ttg ctg gga aat gag ttc aca cat ttg				1017
Leu Ala Phe Met Gln Pro His Leu Leu Gly Asn Glu Phe Thr His Leu				
306	311	316	321	
gag ttt cca agg aga gta cag aga aag gag ctt gga aag aag atg ctc				1065
Glu Phe Pro Arg Arg Val Gln Arg Lys Glu Leu Gly Lys Lys Met Leu				
322	327	332	337	
tac agg gac ttt aat atg aca ggc tgg gca tac aaa acc att gag gat				1113
Tyr Arg Asp Phe Asn Met Thr Gly Trp Ala Tyr Lys Thr Ile Glu Asp				
338	343	348	353	

gag gac ttg aag ttc ccc ctt ata tat gga gaa ggc aag aag gcc cgg	1161
Glu Asp Leu Lys Phe Pro Leu Ile Tyr Gly Glu Gly Lys Lys Ala Arg	
354 359 364 369	
gta atg gca act att gga gtg acc agg gga ctt ggg gac cat gac ctg	1209
Val Met Ala Thr Ile Gly Val Thr Arg Gly Leu Gly Asp His Asp Leu	
370 375 380 385	
aag gtg cat gac tcc aac atc tac att aaa cca ttc ctg tct tca gct	1257
Lys Val His Asp Ser Asn Ile Tyr Ile Lys Pro Phe Leu Ser Ser Ala	
386 391 396 401	
cca gag gta aga atc tac gat ctt tca aaa tat gat cat gga tca gat	1305
Pro Glu Val Arg Ile Tyr Asp Leu Ser Lys Tyr Asp His Gly Ser Asp	
402 407 412 417	
gat gtg ctg atc ttg gcc act gat gga ctc tgg gac gtt tta tca aat	1353
Asp Val Leu Ile Leu Ala Thr Asp Gly Leu Trp Asp Val Leu Ser Asn	
418 423 428 433	
gaa gaa gta gca gaa gca atc act cag ttt ctt cct aac tgt gat cca	1401
Glu Glu Val Ala Glu Ala Ile Thr Gln Phe Leu Pro Asn Cys Asp Pro	
434 439 444 449	
gat gat cct cac agg tac aca ctg gca gct cag gac ctg gtg atg cgt	1449
Asp Asp Pro His Arg Tyr Thr Leu Ala Ala Gln Asp Leu Val Met Arg	
450 455 460 465	
gcc cgg ggt gtg ctg aag gac aga gga tgg cgg ata tct aat gac cga	1497
Ala Arg Gly Val Leu Lys Asp Arg Gly Trp Arg Ile Ser Asn Asp Arg	
466 471 476 481	
ctg ggc tca gga gac gac att tct gta tat gtc att cct tta ata cat	1545
Leu Gly Ser Gly Asp Asp Ile Ser Val Tyr Val Ile Pro Leu Ile His	
482 487 492 497	
gga aac aag ctg tca tga aaatgg cccaggggat tgggaggaca gaggggaaga	1599
Gly Asn Lys Leu Ser *	
498 503	
aagctgggat gcctcttggc aggacggaac tgggaagtgc cccagctgag ttccaagtga	1659
tgcagtctct tcccagccca agcggggagt tcatggccaa aagactatgc ttcaagatga	1719
ccctttgggt tccatttctt ctttagtaac aggccaactc aacaagagca aaacacaaag	1779
gctgctacca agtggtgttg tatttcagtt cctttcatag gcctccgagg tggccattga	1839
ctatttgggg tatatatggc atatttat tttatctagagt agctgggg	1887

<210> 43
 <211> 1416
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (240)..(1097)

<400> 43

ctatacgact cactataggg aatttggcct cgagcagtaa ttccggcacga gggtcgtatt	60
tccaaggact ccaaagcgag gccggggact gaaggtgtgg gtgtcgagcc ctctggcaga	120
gggttaacct ggggtcaaag caccgattct caccctcgta agttacgctc tcccgcggca	180
cgccccgag gacttgaagt cctgagcgcct caagtttgtc cgtagggtcga gagaaggcc	239
atg gag gtg ccg cca ccg gca ccg cgg agc ttt ctc tgt aga gca ttg	287
Met Glu Val Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu	
1 5 10 15	
tgc cta ttt ccc cga gtc ttt gct gcc gaa gct gtg act gcc gat tcg	335
Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser	
17 22 27 32	
gaa gtc ctt gag gag cgt cag aag cgg ctt ccc tac gtc cca gag ccc	383
Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val Pro Glu Pro	
33 38 43 48	
tat tac ccg gaa tct gga tgg gac cgc ctc cgg gag ctg ttt ggc aaa	431
Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu Leu Phe Gly Lys	
49 54 59 64	
gat gaa cag cag aga att tca aag gac ctt gct gat atc tgt aag acg	479
Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala Asp Ile Cys Lys Thr	
65 70 75 80	
gca gct aca gca ggc atc att ggc tgg gtg tat ggg gga ata cca gct	527
Ala Ala Thr Ala Gly Ile Ile Gly Trp Val Tyr Gly Gly Ile Pro Ala	
81 86 91 96	
ttt att cat gct aaa caa caa tac att gag cag agc cag gca gaa att	575
Phe Ile His Ala Lys Gln Gln Tyr Ile Glu Gln Ser Gln Ala Glu Ile	
97 102 107 112	
tat cat aac cgg ttt gat gct gtg caa tct gca cat cgt gct gcc aca	623
Tyr His Asn Arg Phe Asp Ala Val Gln Ser Ala His Arg Ala Ala Thr	
113 118 123 128	
cga ggc ttc att cgt tat ggc tgg cgc tgg ggt tgg aga act gca gtg	671
Arg Gly Phe Ile Arg Tyr Gly Trp Arg Trp Gly Trp Arg Thr Ala Val	
129 134 139 144	
ttt gtg act ata ttc aac aca gtg aac act agt ctg aat gta tac cga	719
Phe Val Thr Ile Phe Asn Thr Val Asn Thr Ser Leu Asn Val Tyr Arg	
145 150 155 160	
aat aaa gat gcc tta agc cat ttt gta att gca gga gct gtc acg gga	767
Asn Lys Asp Ala Leu Ser His Phe Val Ile Ala Gly Ala Val Thr Gly	
161 166 171 176	

agt ctt ttt agg ata aac gta ggc ctg cgt ggc ctg gtg get ggt ggc	815
Ser Leu Phe Arg Ile Asn Val Gly Leu Arg Gly Leu Val Ala Gly Gly	
177 182 187 192	
ata att gga gcc ttg ctg ggc act cct gta gga ggc ctg ctg atg gca	863
Ile Ile Gly Ala Leu Leu Gly Thr Pro Val Gly Gly Leu Leu Met Ala	
193 198 203 208	
ttt cag aag tac tct ggt gag act gtt cag gaa aaa aaa cag aag gat	911
Phe Gln Lys Tyr Ser Gly Glu Thr Val Gln Glu Lys Lys Gln Lys Asp	
209 214 219 224	
cga aag gca ctc cat gag cta aaa ctg gaa gag tgg aaa ggc aga cta	959
Arg Lys Ala Leu His Glu Leu Lys Leu Glu Glu Trp Lys Gly Arg Leu	
225 230 235 240	
caa gtt act gag cac ctc cct gag aaa att gaa agt agt tta cag gaa	1007
Gln Val Thr Glu His Leu Pro Glu Lys Ile Glu Ser Ser Leu Gln Glu	
241 246 251 256	
gat gaa cct gag aat gat gct aag aaa att gaa gca ctg cta aac ctt	1055
Asp Glu Pro Glu Asn Asp Ala Lys Lys Ile Glu Ala Leu Leu Asn Leu	
257 262 267 272	
cct aga aac cct tca gta ata gat aaa caa gac aag gac tga aagtgt	1104
Pro Arg Asn Pro Ser Val Ile Asp Lys Gln Asp Lys Asp *	
273 278 283	
ctgaacttga aactcactgg agagctgaag ggagctgcc a tgtccgatga atgccaacag	1164
acaggccact ctttggtcag cctgctgaca aatttaagtg ctggtacctg tgggtggcagt	1224
ggcttgctct tgtctttttt ttttcttttt aactaagaat ggggctgttg tactctcact	1284
ttacttatcc ttcaatttaa atacatactt atgtttgtat taatctatca atatatgcat	1344
acatgaatat atccaccac ctagatttta agcagtaaataaaaacatttc gcaaaagatt	1404
aaaaaaaaaa aa	1416

<210> 44
 <211> 2401
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (73)..(1752)

cctgccaagc caatcggcta ggagcagcga gcggcgcggc tgaggcgcgg cgccccgtg	60
gagcagcgca gt atg gcg ggc ggg gcc egg gag gtg ctc aca ctg cag	108

Met Ala Gly Gly Ala Arg Glu Val Leu Thr Leu Gln
1 5 10

ttg gga cat ttt gcc ggt ttc gtg ggc ggc cac tgg tgg aac cag cag	156
Leu Gly His Phe Ala Gly Phe Val Gly Ala His Trp Trp Asn Gln Gln	
13 18 23 28	
gat gct gcg ctg ggc cga gcg acc gat tcc aag gag ccc ccg gga gag	204
Asp Ala Ala Leu Gly Arg Ala Thr Asp Ser Lys Glu Pro Pro Gly Glu	
29 34 39 44	
ctg tgc ccc gac gtc ctg tat cgt acg ggc cgg acg ctg cac ggc cag	252
Leu Cys Pro Asp Val Leu Tyr Arg Thr Gly Arg Thr Leu His Gly Gln	
45 50 55 60	
gag acc tac acg ccg cga ctc atc ctc atg gat ctg aag ggt agt ttg	300
Glu Thr Tyr Thr Pro Arg Leu Ile Leu Met Asp Leu Lys Gly Ser Leu	
61 66 71 76	
agc tcc cta aaa gag gaa ggt gga ctc tac agg gac aaa cag ttg gat	348
Ser Ser Leu Lys Glu Glu Gly Gly Leu Tyr Arg Asp Lys Gln Leu Asp	
77 82 87 92	
gat gca ata gca tgg cag ggg aag ctc acc aca cac aaa gag gaa ctc	396
Asp Ala Ile Ala Trp Gln Gly Lys Leu Thr Thr His Lys Glu Glu Leu	
93 98 103 108	
tat ccc aag aac cct tat ctc caa gac ttt ctg agt gca gag gga gtg	444
Tyr Pro Lys Asn Pro Tyr Leu Gln Asp Phe Leu Ser Ala Glu Gly Val	
109 114 119 124	
ctg agt agt gat ggt gtc tgg agg gtc aaa tcc att ccc aat ggc aaa	492
Leu Ser Ser Asp Gly Val Trp Arg Val Lys Ser Ile Pro Asn Gly Lys	
125 130 135 140	
ggg tcc tca cca ctc ccc acc gct aca act cca aaa cca ctt atc cct	540
Gly Ser Ser Pro Leu Pro Thr Ala Thr Thr Pro Lys Pro Leu Ile Pro	
141 146 151 156	
aca gag gcc agc atc agg gtc tgg tca gac ttc ctc aga gtc cat ctc	588
Thr Glu Ala Ser Ile Arg Val Trp Ser Asp Phe Leu Arg Val His Leu	
157 162 167 172	
cat ccc cgg agc atc tgt atg att cag aag tac aac cac gat ggg gaa	636
His Pro Arg Ser Ile Cys Met Ile Gln Lys Tyr Asn His Asp Gly Glu	
173 178 183 188	
gca ggt cgg ctg gag gct ttt ggc caa ggg gaa agt gtc cta aag gaa	684
Ala Gly Arg Leu Glu Ala Phe Gly Gln Gly Glu Ser Val Leu Lys Glu	
189 194 199 204	
ccc aag tac cag gaa gag ctg gag gac agg ctg cat ttc tac gtg gag	732
Pro Lys Tyr Gln Glu Glu Leu Glu Asp Arg Leu His Phe Tyr Val Glu	
205 210 215 220	
gaa tgt gac tac ttg cag ggc ttc cag atc ctg tgt gac ctg cac gat	780
Glu Cys Asp Tyr Leu Gln Gly Phe Gln Ile Leu Cys Asp Leu His Asp	

221	226	231	236	
ggc ttc tct ggg gta	ggc gcg aag gcg gca	gag ctg cta caa gat gaa	828	
Gly Phe Ser Gly Val	Gly Ala Lys Ala Ala	Glu Leu Leu Gln Asp Glu		
237	242	247	252	
tat tca ggg cgg gga	ata ata acc tgg ggc	ctg cta cct ggt ccc tac	876	
Tyr Ser Gly Arg Gly	Ile Ile Thr Trp Gly	Leu Leu Pro Gly Pro Tyr		
253	258	263	268	
cat cgt ggg gag gcc	cag aga aac atc tat	cgt cta tta aac aca gct	924	
His Arg Gly Glu Ala	Gln Arg Asn Ile Tyr	Arg Leu Leu Asn Thr Ala		
269	274	279	284	
ttt ggt ctc gtg cac	ctg act gct cac agc	tct ctt gtc tgc ccc ttg	972	
Phe Gly Leu Val His	Leu Thr Ala His Ser	Ser Leu Val Cys Pro Leu		
285	290	295	300	
tcc ttg ggt ggg agc	ctg ggc ctg cga ccc	gag cca cct gtc agc ttc	1020	
Ser Leu Gly Gly Ser	Leu Gly Leu Arg Pro	Glu Pro Pro Val Ser Phe		
301	306	311	316	
cct tac ctg cat tat	gat gcc act ctg ccc	ttc cac tgc agt gcc atc	1068	
Pro Tyr Leu His Tyr	Asp Ala Thr Leu Pro	Phe His Cys Ser Ala Ile		
317	322	327	332	
ctg gct aca gcc ctg	gac aca gtc act gtt	cct tat cgc ctg tgt tcc	1116	
Leu Ala Thr Ala Leu	Asp Thr Val Thr Val	Pro Tyr Arg Leu Cys Ser		
333	338	343	348	
tct cca gtt tcc atg	gtt cat ctg gct gac	atg ctg agc ttc tgt ggg	1164	
Ser Pro Val Ser Met	Val His Leu Ala Asp	Met Leu Ser Phe Cys Gly		
349	354	359	364	
aaa aag gtg gtg aca	gca gga gca atc atc	cct ttc ccc ttg gct cca	1212	
Lys Lys Val Val Thr	Ala Gly Ala Ile Ile	Pro Phe Pro Leu Ala Pro		
365	370	375	380	
ggc cag tcc ctt cct	gat tcc ctg atg cag	ttt gga gga gcc acc cca	1260	
Gly Gln Ser Leu Pro	Asp Ser Leu Met Gln	Phe Gly Gly Ala Thr Pro		
381	386	391	396	
tgg acc cca ctg tct	gca tgt ggg gag cct	tct gga aca cgt tgt ttt	1308	
Trp Thr Pro Leu Ser	Ala Cys Gly Glu Pro	Ser Gly Thr Arg Cys Phe		
397	402	407	412	
gcc cag tca gtg gtg	ctg agg ggt ata gac	aga gca tgc cac aca agc	1356	
Ala Gln Ser Val Val	Leu Arg Gly Ile Asp	Arg Ala Cys His Thr Ser		
413	418	423	428	
cag ctc acc cca ggg	aca cct cca ccc tct	gcc ctt cat gca tgt acc	1404	
Gln Leu Thr Pro Gly	Thr Pro Pro Pro Ser	Ala Leu His Ala Cys Thr		
429	434	439	444	
act ggg gaa gaa atc	ttg gct cag tat tta	caa cag cag cag cct gga	1452	
Thr Gly Glu Glu Ile	Leu Ala Gln Tyr Leu	Gln Gln Gln Gln Pro Gly		
445	450	455	460	

gtc atg agt tct tcc cat ctg ctg ctg act ccc tgc agg gtg gct cct	1500
Val Met Ser Ser Ser His Leu Leu Leu Thr Pro Cys Arg Val Ala Pro	
461 466 471 476	
cct tac ccc cac ctg ttc tca agc tgc agt cca ccg gca gtg gag agc	1548
Pro Tyr Pro His Leu Phe Ser Ser Cys Ser Pro Pro Ala Val Glu Ser	
477 482 487 492	
atc cca gtg ttt ggg gca ctg tgt tcc tct tgc tcc ctg cac cag acc	1596
Ile Pro Val Phe Gly Ala Leu Cys Ser Ser Ser Ser Leu His Gln Thr	
493 498 503 508	
ctg gaa gcc ttg gcc aga gac ctg acc aaa ctg gac ttg cgg cgc tgg	1644
Leu Glu Ala Leu Ala Arg Asp Leu Thr Lys Leu Asp Leu Arg Arg Trp	
509 514 519 524	
gcc agc ttc atg gat gct gga gtg gag cac gat gac gta gca gag ctg	1692
Ala Ser Phe Met Asp Ala Gly Val Glu His Asp Asp Val Ala Glu Leu	
525 530 535 540	
ctg cag gag cta caa agc ctg gcc cag tgc tac cag ggt ggt gac agc	1740
Leu Gln Glu Leu Gln Ser Leu Ala Gln Cys Tyr Gln Gly Gly Asp Ser	
541 546 551 556	
ctc gtg gac taa agt tcccagtgtg ggagaaagga gctagtgtgc aataaaaaca	1795
Leu Val Asp *	
557	
gctggatgca ggagcccagt gtcttcatgc agaggagctc aatgtcgcgg gactagctac	1855
accaacatat gcacttttta catttagaaa cactgtgatt agaccacaga acaataaata	1915
tgtgccatca gaccaaaaaa aagtagagaa aggagctgaa ctccactctc gatgctactt	1975
acagaggaca tctgtaaagt cttcataaaa gaccttgaat gatgcctagg atggcagagc	2035
ccctgggtcc tactccatcc tccagccttt gtccttgtcc tggcctcctg ctctccagat	2095
ctgtaaaactg ggctcaagga ctgtacaagc agagtacaac taccgcctc cccggtgcca	2155
gggcgcctgt tgggttttggc cctgtgtaga tgattcccag agtctcattc atccagctcc	2215
tcttcagaca gaagggtccc atgggtcagac agctggctctg cattgctggc actggttgca	2275
tcattcctcat cctcagagct ggcttcacag gcagtgtgga agagctgcat gagttctcga	2335
aaatggtggg aaacctaaga aaggaggagg gctgtattca ctgacctta gtaacatgtt	2395
aacatt	2401

<210> 45
 <211> 2905
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (173)..(2452)

<400> 45

ccttgataat cgtcacgact gccggaccgg tccggaattc ccgggtcgac gatttcgtag 60

cagcttggtc gcgacaggtg cgctaggtag agcgccggga cctgtgacag ggctggtagc 120

agcgagagg aaaggcggt tttagccagg tatttcagtg tctgtagaca ag atg 175
Met
1

gaa tca tct cca ttt aat aga cgg caa tgg acc tca cta tca ttg agg 223
Glu Ser Ser Pro Phe Asn Arg Arg Gln Trp Thr Ser Leu Ser Leu Arg
2 7 12 17

gta aca gcc aaa gaa ctt tct ctt gtc aac aag aac aag tca tcg gct 271
Val Thr Ala Lys Glu Leu Ser Leu Val Asn Lys Asn Lys Ser Ser Ala
18 23 28 33

att gtg gaa ata ttc tcc aag tac cag aaa gca gct gaa gaa aca aac 319
Ile Val Glu Ile Phe Ser Lys Tyr Gln Lys Ala Ala Glu Glu Thr Asn
34 39 44 49

atg gag aag aag aga agt aac acc gaa aat ctc tcc cag cac ttt aga 367
Met Glu Lys Lys Arg Ser Asn Thr Glu Asn Leu Ser Gln His Phe Arg
50 55 60 65

aag ggg acc ctg act gtg tta aag aag aag tgg gag aac cca ggg ctg 415
Lys Gly Thr Leu Thr Val Leu Lys Lys Lys Trp Glu Asn Pro Gly Leu
66 71 76 81

gga gca gag tct cac aca gac tct cta cgg aac agc agc act gag att 463
Gly Ala Glu Ser His Thr Asp Ser Leu Arg Asn Ser Ser Thr Glu Ile
82 87 92 97

agg cac aga gca gac cat cct cct gct gaa gtg aca agc cac gct gct 511
Arg His Arg Ala Asp His Pro Pro Ala Glu Val Thr Ser His Ala Ala
98 103 108 113

tct gga gcc aaa gct gac caa gaa gaa caa atc cac ccc aga tct aga 559
Ser Gly Ala Lys Ala Asp Gln Glu Glu Gln Ile His Pro Arg Ser Arg
114 119 124 129

ctc agg tca cct cct gaa gcc ctc gtt cag ggt cga tat ccc cac atc 607
Leu Arg Ser Pro Pro Glu Ala Leu Val Gln Gly Arg Tyr Pro His Ile
130 135 140 145

aag gac ggt gag gat ctt aaa gac cac tca aca gaa agt aaa aaa atg 655
Lys Asp Gly Glu Asp Leu Lys Asp His Ser Thr Glu Ser Lys Lys Met
146 151 156 161

gaa aat tgt cta gga gaa tcc agg cat gaa gta gaa aaa tca gaa atc 703
Glu Asn Cys Leu Gly Glu Ser Arg His Glu Val Glu Lys Ser Glu Ile

162	167	172	177	
agt gaa aac aca gat gct tgc ggc aaa ata gag aaa tat aat gtt ccg				751
Ser Glu Asn Thr Asp Ala Ser Gly Lys Ile Glu Lys Tyr Asn Val Pro				
178	183	188	193	
ctg aac agg ctt aag atg atg ttt gag aaa ggt gaa cca act caa act				799
Leu Asn Arg Leu Lys Met Met Phe Glu Lys Gly Glu Pro Thr Gln Thr				
194	199	204	209	
aag att ctc cgg gcc caa agc cga agt gca agt gga agg aag atc tct				847
Lys Ile Leu Arg Ala Gln Ser Arg Ser Ala Ser Gly Arg Lys Ile Ser				
210	215	220	225	
gaa aac agc tat tct cta gat gac ctg gaa ata ggc cca ggt cag ttg				895
Glu Asn Ser Tyr Ser Leu Asp Asp Leu Glu Ile Gly Pro Gly Gln Leu				
226	231	236	241	
tca tct tct aca ttt gac tgc gag aaa aat gag agt aga cga aat ctg				943
Ser Ser Ser Thr Phe Asp Ser Glu Lys Asn Glu Ser Arg Arg Asn Leu				
242	247	252	257	
gaa ctt cca cgc ctc tca gaa acc tct ata aag gat cga atg gcc aag				991
Glu Leu Pro Arg Leu Ser Glu Thr Ser Ile Lys Asp Arg Met Ala Lys				
258	263	268	273	
tac cag gca gct gtg tcc aaa caa agc agc tca acc aac tat aca aat				1039
Tyr Gln Ala Ala Val Ser Lys Gln Ser Ser Ser Thr Asn Tyr Thr Asn				
274	279	284	289	
gag ctg aaa gcc agt ggt ggc gaa atc aaa att cat aaa atg gag caa				1087
Glu Leu Lys Ala Ser Gly Gly Glu Ile Lys Ile His Lys Met Glu Gln				
290	295	300	305	
aag gag aat gtg ccc cca ggt cct gag gtc tgc atc acc cat cag gaa				1135
Lys Glu Asn Val Pro Pro Gly Pro Glu Val Cys Ile Thr His Gln Glu				
306	311	316	321	
ggg gaa aag att tct gca aat gag aat agc ctg gca gtc cgt tcc acc				1183
Gly Glu Lys Ile Ser Ala Asn Glu Asn Ser Leu Ala Val Arg Ser Thr				
322	327	332	337	
cct gcc gaa gat gac tcc cgt gac tcc cag gtt aag agt gag gtt caa				1231
Pro Ala Glu Asp Asp Ser Arg Asp Ser Gln Val Lys Ser Glu Val Gln				
338	343	348	353	
cag cct gtc cat ccc aag cca cta agt cca gat tcc aga gcc tcc agt				1279
Gln Pro Val His Pro Lys Pro Leu Ser Pro Asp Ser Arg Ala Ser Ser				
354	359	364	369	
ctt tct gaa agt tct cct ccc aaa gca atg aag aag ttt cag gca cct				1327
Leu Ser Glu Ser Ser Pro Pro Lys Ala Met Lys Lys Phe Gln Ala Pro				
370	375	380	385	
gca aga gag acc tgc gtg gaa tgt cag aag aca gtc tat cca atg gag				1375
Ala Arg Glu Thr Cys Val Glu Cys Gln Lys Thr Val Tyr Pro Met Glu				
386	391	396	401	

cgt ctc ttg gcc aac cag cag gtg ttt cac atc agc tgc ttc cgt tgc	1423
Arg Leu Leu Ala Asn Gln Gln Val Phe His Ile Ser Cys Phe Arg Cys	
402 407 412 417	
tcc tat tgc aac aac aaa ctc agt cta gga aca tat gca tct tta cat	1471
Ser Tyr Cys Asn Asn Lys Leu Ser Leu Gly Thr Tyr Ala Ser Leu His	
418 423 428 433	
gga aga atc tat tgt aag cct cac ttc aat caa ctc ttt aaa tct aag	1519
Gly Arg Ile Tyr Cys Lys Pro His Phe Asn Gln Leu Phe Lys Ser Lys	
434 439 444 449	
ggc aac tat gat gaa ggc ttt ggg cac aga cca cac aag gat cta tgg	1567
Gly Asn Tyr Asp Glu Gly Phe Gly His Arg Pro His Lys Asp Leu Trp	
450 455 460 465	
gca agc aaa aat gaa aac gaa gag att ttg gag aga cca gcc cag ctt	1615
Ala Ser Lys Asn Glu Asn Glu Glu Ile Leu Glu Arg Pro Ala Gln Leu	
466 471 476 481	
gca aat gca agg gag acc cct cac agc cca ggg gta gaa gat gcc cct	1663
Ala Asn Ala Arg Glu Thr Pro His Ser Pro Gly Val Glu Asp Ala Pro	
482 487 492 497	
att gct aag gtg ggt gtc ctg gct gca agt atg gaa gcc aag gcc tcc	1711
Ile Ala Lys Val Gly Val Leu Ala Ala Ser Met Glu Ala Lys Ala Ser	
498 503 508 513	
tct cag cag gag aag gaa gac aag cca gct gaa acc aag aag ctg agg	1759
Ser Gln Gln Glu Lys Glu Asp Lys Pro Ala Glu Thr Lys Lys Leu Arg	
514 519 524 529	
atc gcc tgg cca ccc ccc act gaa ctt gga agt tca gga agt gcc ttg	1807
Ile Ala Trp Pro Pro Thr Glu Leu Gly Ser Ser Gly Ser Ala Leu	
530 535 540 545	
gag gaa ggg atc aaa atg tca aag ccc aaa tgg cct cct gaa gac gaa	1855
Glu Glu Gly Ile Lys Met Ser Lys Pro Lys Trp Pro Pro Glu Asp Glu	
546 551 556 561	
atc agc aag ccc gaa gtt cct gag gat gtc gat cta gat ctg aag aag	1903
Ile Ser Lys Pro Glu Val Pro Glu Asp Val Asp Leu Asp Leu Lys Lys	
562 567 572 577	
cta aga cga tct tct tca ctg aag gaa aga agc cgc cca ttc act gta	1951
Leu Arg Arg Ser Ser Ser Leu Lys Glu Arg Ser Arg Pro Phe Thr Val	
578 583 588 593	
gca gct tca ttt caa agc acc tct gtc aag agc cca aaa act gtg tcc	1999
Ala Ala Ser Phe Gln Ser Thr Ser Val Lys Ser Pro Lys Thr Val Ser	
594 599 604 609	
cca cct atc agg aaa ggc tgg agc atg tca gag cag agt gaa gag tct	2047
Pro Pro Ile Arg Lys Gly Trp Ser Met Ser Glu Gln Ser Glu Glu Ser	
610 615 620 625	

gtg ggt gga aga gtt gca gaa agg aaa caa gtg gaa aat gcc aag gct	2095
Val Gly Gly Arg Val Ala Glu Arg Lys Gln Val Glu Asn Ala Lys Ala	
626 631 636 641	
tct aag aag aat ggg aat gtg gga aaa aca acc tgg caa aac aaa gaa	2143
Ser Lys Lys Asn Gly Asn Val Gly Lys Thr Thr Trp Gln Asn Lys Glu	
642 647 652 657	
tct aaa gga gag aca ggg aag aga agt aag gaa ggt cat agt ttg gag	2191
Ser Lys Gly Glu Thr Gly Lys Arg Ser Lys Glu Gly His Ser Leu Glu	
658 663 668 673	
atg gag aat gag aat ctt gta gaa aat ggt gca gac tcc gat gaa gat	2239
Met Glu Asn Glu Asn Leu Val Glu Asn Gly Ala Asp Ser Asp Glu Asp	
674 679 684 689	
gat aac agc ttc ctc aaa caa caa tct cca caa gaa ccc aag tct ctg	2287
Asp Asn Ser Phe Leu Lys Gln Gln Ser Pro Gln Glu Pro Lys Ser Leu	
690 695 700 705	
aat tgg tcg agt ttt gta gac aac acc ttt gct gaa gaa ttc act act	2335
Asn Trp Ser Ser Phe Val Asp Asn Thr Phe Ala Glu Glu Phe Thr Thr	
706 711 716 721	
cag aat cag aaa tcc cag gat gtg gaa ctc tgg gag gga gaa gtg gtc	2383
Gln Asn Gln Lys Ser Gln Asp Val Glu Leu Trp Glu Gly Glu Val Val	
722 727 732 737	
aaa gag ctc tct gtg gaa gaa cag ata aag aga aat cgg tat tat gat	2431
Lys Glu Leu Ser Val Glu Glu Gln Ile Lys Arg Asn Arg Tyr Tyr Asp	
738 743 748 753	
gag gat gag gat gaa gag tga ca aattgcaatg atgctgggccc ttaaattcat	2484
Glu Asp Glu Asp Glu Glu *	
754 759	
gtagtggtta gcgagccact gccctttgtc aaaatgtgat gcacataagc aggtatccca	2544
gcatgaaatg taattttactt ggaagtaact ttggaaaaga attccttctt aaaatcaaaa	2604
acaaaacaaa aaaacacatt ctaaatacta gagataactt tacttaaatt cttcatttta	2664
gcagtgatga tatgcataag tgctgtaagg cttgtaactg gggaaatatt ccacctgata	2724
atagcctttt ttttctttat ttccatatgg caatattaag gtagacagat gattagtagt	2784
atattgttac acactatttt tgaattagag atcatacaga aggatttttag gggcttaaac	2844
attacgactg aatgcacttt agtataaagg gcacagtttg tatattttta aatgaatacc	2904
a	2905

<210> 46
<211> 585

[illegible][illegible][illegible][illegible][illegible][illegible]

<221> misc_feature
 <222> (1)...(2497)
 <223> n = a,t,c or g

<400> 47

gagggnnnnn attgatcgct tgaggtaccg gtccggaatt cccgggtcga cccacgcgtc	60
cgcttccatc tgcccagaga ggagcatctg gatcaagggtg ctggcc atg tcc cag	115
	Met Ser Gln
	1
ctg gtg gaa tgc gtc ccc aac ttt tgc gag ggg aag aac cag gag gtg	163
Leu Val Glu Cys Val Pro Asn Phe Ser Glu Gly Lys Asn Gln Glu Val	
4 9 14 19	
atc gac gcc atc tct gga gcc atc aca cag acc ccg ggc tgc gtg ctg	211
Ile Asp Ala Ile Ser Gly Ala Ile Thr Gln Thr Pro Gly Cys Val Leu	
20 25 30 35	
ctg gat gtg gac gca ggc cct tcc acc aac cgc acc gtg tac acc ttc	259
Leu Asp Val Asp Ala Gly Pro Ser Thr Asn Arg Thr Val Tyr Thr Phe	
36 41 46 51	
gtg ggg ccg ccg gag tgc gtg gtg gag ggg gcc ctc aac gct gcc cgg	307
Val Gly Pro Pro Glu Cys Val Val Glu Gly Ala Leu Asn Ala Ala Arg	
52 57 62 67	
gta gct tcc cga ctt atc gac atg agc agg cac caa gga gag cac ccc	355
Val Ala Ser Arg Leu Ile Asp Met Ser Arg His Gln Gly Glu His Pro	
68 73 78 83	
cgc atg ggg gcc cta gac gtc tgc ccc ttc atc ccc gtg agg ggc gtc	403
Arg Met Gly Ala Leu Asp Val Cys Pro Phe Ile Pro Val Arg Gly Val	
84 89 94 99	
agc gtg gat gag tgt gtg ctc tgc gcc cag gcc ttt ggc cag agg ctg	451
Ser Val Asp Glu Cys Val Leu Cys Ala Gln Ala Phe Gly Gln Arg Leu	
100 105 110 115	
gca gag gag ctg gac gtg cca ggc ctg acc gcc ggg ctc tcc tgc agt	499
Ala Glu Glu Leu Asp Val Pro Gly Leu Thr Ala Gly Leu Ser Cys Ser	
116 121 126 131	
tac ctg tac ggc gag gca gcc agg atg gac agt cgc cgg acc ctg ccg	547
Tyr Leu Tyr Gly Glu Ala Ala Arg Met Asp Ser Arg Arg Thr Leu Pro	
132 137 142 147	
gcc atc cgg gcc ggg gag tac gag gcc ctc cct aag aag ctc cag cag	595
Ala Ile Arg Ala Gly Glu Tyr Glu Ala Leu Pro Lys Lys Leu Gln Gln	
148 153 158 163	
gcc gac tgg gcg ccc gac ttt ggt ccc agc tcc ttt gtc ccc agt tgg	643
Ala Asp Trp Ala Pro Asp Phe Gly Pro Ser Ser Phe Val Pro Ser Trp	
164 169 174 179	
ggg gcc acg gcc acg ggg gcg agg aag ttc ctc att gct ttt aac atc	691
Gly Ala Thr Ala Thr Gly Ala Arg Lys Phe Leu Ile Ala Phe Asn Ile	

180	185	190	195	
aac ctg ctc ggc aca aag gag caa gcc cac	cgc atc gcg ctc aac ctg	739		
Asn Leu Leu Gly Thr Lys Glu Gln Ala His	Arg Ile Ala Leu Asn Leu			
196	201	206	211	
cgg gag cag ggc cgc ggg aag gac cag cca	gga cgt ctg aag aaa gtt	787		
Arg Glu Gln Gly Arg Gly Lys Asp Gln Pro	Gly Arg Leu Lys Lys Val			
212	217	222	227	
cag ggc ttt ggc tgg tac ctg gat gag aag	aac ctg gct cag gtg tcc	835		
Gln Gly Phe Gly Trp Tyr Leu Asp Glu Lys	Asn Leu Ala Gln Val Ser			
228	233	238	243	
acc aat ctt ctg gac ttt gag gtc acg gca	ctg cac acg gtc tac gag	883		
Thr Asn Leu Leu Asp Phe Glu Val Thr Ala	Leu His Thr Val Tyr Glu			
244	249	254	259	
gag acc tgc cga gaa gca cag gag ctg agc	ctc cca gtg gtg ggc tca	931		
Glu Thr Cys Arg Glu Ala Gln Glu Leu Ser	Leu Pro Val Val Gly Ser			
260	265	270	275	
cag ctg gtg ggc ctg gtg ccc ctg aag gct	ctg ctg gat gcg gcc gcc	979		
Gln Leu Val Gly Leu Val Pro Leu Lys Ala	Leu Leu Asp Ala Ala Ala			
276	281	286	291	
ttc tac tgc gag aag gag aac ctc ttc atc	ctg gag gag gag cag cgg	1027		
Phe Tyr Cys Glu Lys Glu Asn Leu Phe Ile	Leu Glu Glu Glu Gln Arg			
292	297	302	307	
atc agg ctg gtg gtg agc cgg ctg ggc ctg	gac tcc ctg tgc ccc ttc	1075		
Ile Arg Leu Val Val Ser Arg Leu Gly Leu	Asp Ser Leu Cys Pro Phe			
308	313	318	323	
agc cct aag gag cgg atc atc gag tac ctg	gtc cct gag cgc ggg cct	1123		
Ser Pro Lys Glu Arg Ile Ile Glu Tyr Leu	Val Pro Glu Arg Gly Pro			
324	329	334	339	
gag cga ggc ctg ggc agc aag tcc ctg cgc	gcc ttc gtg ggg gag gtg	1171		
Glu Arg Gly Leu Gly Ser Lys Ser Leu Arg	Ala Phe Val Gly Glu Val			
340	345	350	355	
ggg gcc cgc tct gcg gcc ccc ggg ggc ggc	tcg gtg gcg gcg gcc gct	1219		
Gly Ala Arg Ser Ala Ala Pro Gly Gly Gly	Ser Val Ala Ala Ala Ala			
356	361	366	371	
gcg gcc atg ggt gcg gcg ctg ggc tcc atg	gtg ggc ctc atg acc tac	1267		
Ala Ala Met Gly Ala Ala Leu Gly Ser Met	Val Gly Leu Met Thr Tyr			
372	377	382	387	
ggg cgg cgc caa ttc cag tcc ctg gac acg	acg atg cgg cgc ctg atc	1315		
Gly Arg Arg Gln Phe Gln Ser Leu Asp Thr	Thr Met Arg Arg Leu Ile			
388	393	398	403	
ccg ccc ttc cgc gag gct tcg gcc aag cta	acc acg ctg gtg gat gcc	1363		
Pro Pro Phe Arg Glu Ala Ser Ala Lys Leu	Thr Thr Leu Val Asp Ala			
404	409	414	419	

gac gcc gag gcc ttc acc gcc tac ctg gaa gca atg agg ctc ccc aag	1411
Asp Ala Glu Ala Phe Thr Ala Tyr Leu Glu Ala Met Arg Leu Pro Lys	
420 425 430 435	
aac aca cct gag gaa aag gac agg cgc acg gcg gcc cta cag gag ggt	1459
Asn Thr Pro Glu Glu Lys Asp Arg Arg Thr Ala Ala Leu Gln Glu Gly	
436 441 446 451	
ctg agg cgg gca gtc tct gtg ccg ctg acg ctg gcg gag acg gtg gcc	1507
Leu Arg Arg Ala Val Ser Val Pro Leu Thr Leu Ala Glu Thr Val Ala	
452 457 462 467	
tcg ctg tgg ccg gcg ctg cag gaa ctg gcc cgg tgt ggg aac ctg gcc	1555
Ser Leu Trp Pro Ala Leu Gln Glu Leu Ala Arg Cys Gly Asn Leu Ala	
468 473 478 483	
tgc cgg tca gac ctc cag gtg gcg gcc aaa gcc ctg gag atg ggc gtg	1603
Cys Arg Ser Asp Leu Gln Val Ala Ala Lys Ala Leu Glu Met Gly Val	
484 489 494 499	
ttt ggc gca tat ttc aac gtg ctc atc aac ctg agg gac atc aca gac	1651
Phe Gly Ala Tyr Phe Asn Val Leu Ile Asn Leu Arg Asp Ile Thr Asp	
500 505 510 515	
gag gca ttt aag gac cag atc cac cat cgt gtt tcc agc ctc ctg cag	1699
Glu Ala Phe Lys Asp Gln Ile His His Arg Val Ser Ser Leu Leu Gln	
516 521 526 531	
gaa gcc aag acc cag gct gca ctg gtg ctg gac tgc ttg gag acc cgg	1747
Glu Ala Lys Thr Gln Ala Ala Leu Val Leu Asp Cys Leu Glu Thr Arg	
532 537 542 547	
cag gag tga cgggtgcg ggaggcctct ccgggctctg tggccctcc ctcgcccatc	1803
Gln Glu *	
548	
cccagagggc agagctgtga cctcgggtggg gacacagctt gttcgtgtgg ggcccggagg	1863
ataggtgggc aggcagcggg gcatcgccctg ggaatggagg cgctggcagg gacagaaggc	1923
ccctagtccc atgtgacctc cagtaaagtt ttggcaccaa acctgtgttg tgtgttggcg	1983
gttttggggg cagggctgag agctgagctg cgggtcttgg ggcaggagca ggacatatgg	2043
tcagtggccc atgggagcca gggttggagg gaatgggggt gcagcgtgag gagacagacc	2103
tcagcgccag ggtccccaga caccagtgcc agcccacagt gggcagggtc acaggtattc	2163
agaggacctg gggttcagtg caggtccctg ggctgtgagg ccccttgtct gagggaaagg	2223
ggccctgggt ctgtgcatgg gacagaaacc ccagggacag caggaccttc gacgctggaa	2283
ggatagcctc gcttcccagg tgcagctccc ggcaggctctg gacagttcca cagagcacgg	2343
tactggccct gtcctcagtt ccggtccacc cttcaaccag tggtcctctgg gagacttttc	2403

ctccctgcct cagctccctg ccagccagc ctctgtctc cagagaagtt ctccattaaa 2463
aaataattta gcaaataaaa aaaaaaaaaa aaaa 2497

<210> 48
<211> 2597
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (592)..(1272)

<400> 48

tacgcgcct gataagcaga atggcatcgt tccggtggtg ggcgttgatg gctgggtcccg 60
catcatcaat gaaaaccagc agtttgatgg catggacttt gagcaggaca atgaatcctg 120
tacatgccgg atttaccgca aggaccgtaa tcatccgata tgcgttaccg aatggatgga 180
tgaatgccgc cgcgaaccat tcaaaactcg cgaaggcaga gaaatcacgg ggccgtggca 240
gtcgcacccc aaacggatgt tacgtcataa agccatgatt cagtgtgccc gtctggcctt 300
cggatttgct ggtatctatg acaaggatga agccgagcgc attgtcgaaa atactgcata 360
cactgcagaa cgtcagccgg aacgcgacat cactccgggt aacgatgaaa ccatgcagga 420
gattaacact ctgctgatcg ccttgataa aacatgggat gacgacttat tgccgctctg 480
ttccagata ttccgccgcg acattcgtgc atcgtcagaa ctgacacagg ccgaagcagt 540
aaaagctott ggattcctga aacagaaagc cgcagagcag aagggtggcag c atg aca 597
Met Thr
1

ccg gac att atc ctg cag cgt acc ggg atc gat gtg aga gct gtc gaa 645
Pro Asp Ile Ile Leu Gln Arg Thr Gly Ile Asp Val Arg Ala Val Glu
3 8 13 18

cag ggg gaa gat gcg tgg cac aaa tta cgg ctc ggc gtc atc acc gct 693
Gln Gly Glu Asp Ala Trp His Lys Leu Arg Leu Gly Val Ile Thr Ala
19 24 29 34

tca gaa gtt cac aac gtg ata gca aaa ccc cgc tcc gga aag aag tgg 741
Ser Glu Val His Asn Val Ile Ala Lys Pro Arg Ser Gly Lys Lys Trp
35 40 45 50

cct gac atg aaa atg tcc tac ttc cac acc ctg ctt gct gag gtt tgc 789
Pro Asp Met Lys Met Ser Tyr Phe His Thr Leu Leu Ala Glu Val Cys
51 56 61 66

acc ggt gtg gct ccg gaa gtt aac gct aaa gca ctg gcc tgg gga aaa 837
Thr Gly Val Ala Pro Glu Val Asn Ala Lys Ala Leu Ala Trp Gly Lys

67	72	77	82	
cag tac gag aac gac gcc aga acc ctg ttt gaa ttt act tcc ggc gtg				885
Gln Tyr Glu Asn Asp Ala Arg Thr Leu Phe Glu Phe Thr Ser Gly Val				
83	88	93	98	
aat gtt act gaa tcc ccg atc atc tat cgc gac gaa agt atg cgt acc				933
Asn Val Thr Glu Ser Pro Ile Ile Tyr Arg Asp Glu Ser Met Arg Thr				
99	104	109	114	
gcc tgc tct ccc gat ggt tta tgc agt gac ggc aac ggc ctt gaa ctg				981
Ala Cys Ser Pro Asp Gly Leu Cys Ser Asp Gly Asn Gly Leu Glu Leu				
115	120	125	130	
aaa tgc ccg ttt acc tcc cgg gat ttc atg aag ttc cgg ctc ggt ggt				1029
Lys Cys Pro Phe Thr Ser Arg Asp Phe Met Lys Phe Arg Leu Gly Gly				
131	136	141	146	
ttc gag gcc ata aag tca gct tac atg gcc cag gtg cag tac agc atg				1077
Phe Glu Ala Ile Lys Ser Ala Tyr Met Ala Gln Val Gln Tyr Ser Met				
147	152	157	162	
tgg gtg acg cga aaa aat gcc tgg tac ttt gcc aac tat gac ccg cgt				1125
Trp Val Thr Arg Lys Asn Ala Trp Tyr Phe Ala Asn Tyr Asp Pro Arg				
163	168	173	178	
atg aag cgt gaa ggc ctg cat tat gtc gtg att gag cgg gat gaa aag				1173
Met Lys Arg Glu Gly Leu His Tyr Val Val Ile Glu Arg Asp Glu Lys				
179	184	189	194	
tac atg gcg agt ttt gac gag atc gtg ccg gag ttc atc gaa aaa atg				1221
Tyr Met Ala Ser Phe Asp Glu Ile Val Pro Glu Phe Ile Glu Lys Met				
195	200	205	210	
gac gag gca ctg gct gaa att ggt ttt gta ttt ggg gag caa tgg cga				1269
Asp Glu Ala Leu Ala Glu Ile Gly Phe Val Phe Gly Glu Gln Trp Arg				
211	216	221	226	
tga cgca tcctcagat aatatccggg taggcgcaat cactttcgtc tactccgtta				1326
*				
227				
caaagcgagg ctgggtatatt cccggccttt ctgttatccg aaatccactg aaagcacagc				1386
ggctggctga ggagataaat aataaacgag gggctgtatg cacaaagcat cttctgttga				1446
gttaagaacg agtatcgaga tggcacatag ccttgctcaa attggaatca ggtttgtgcc				1506
aataccagta gaaacagacg aagaatttca tacgttagcc gcatcccttt cacaaaagct				1566
ggaaatgatg gtggcgaaag cagaagcaga tgagagagac caggtatgac aaccacggaa				1626
tgcatttttc tggcagcggg cttcatattc tgtgtgctta tgcttgccga catgggactt				1686
gttcaatgac acctcagcag gaaaacgccc ttgcgagcat tgcccgtcag gctaattctg				1746
aatcaaaaaa aagccagaca gcagtttccg gataaaaaacg togatgacat ttgccgtagc				1806

gtactgaaga agcaccgcga aacggtaacg ctgatgggat tcacaccgac tcattttaagc 1866
ctggcaatcg gcatgttaaa cggcgtcttt aaggaacgat gaacatgaaa agcaaaatca 1926
tcagggagct acaggctcct tttttattat tcgcattcac cctcaagcgt attaaccaac 1986
agttcagggg ttaatgaaag atggcagaca tcattgattc agcatcagaa atagaagaat 2046
tacagcgcaa cacagcaata aaaatgcgcc gcctgaacca ccaggctata tctgccactc 2106
attgttgtga gtgtggcgat ccgatagatg aacgaagacg cctggtcggt caggggttgc 2166
ggacttgtgc aagttgccag gaggatctgg aacttatcag taaacagaga ggttcgaagt 2226
gagcgaaatt aactctcagg cactgcgtga agcggcagag caggcaatgc atgacgactg 2286
gggatttgac gcagaccttt tccatgaatt ggtaacacca tcgattgtgc tggaactgct 2346
ggatgaacgg gaaagaaacc agcaatacat caaacgccgc gaccaggaga acgaggatat 2406
tgcgctaaca gtagggaaac tgcgtgttga gcttgaaaca gcaaaatcaa aactcaacga 2466
gcagcgtgag tattacgaag gtgttatctc ggatgggagt aagacgaaat cgtcgacccg 2526
ggaaaatccc gcggccatgg cggccgggag catgcgacgt cgggcccaat tcccctatag 2586
tgagtogaat g 2597

<210> 49
<211> 2286
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (69)..(1727)

<400> 49
tctgtgtgca tgagccctg cggatccgc gacttctcg tcccttcttc ctgctgcaga 60
actcctct atg atg aag aag acc ttg aaa tgc atc cgc tgg tcg ctg ccg 110
Met Met Lys Lys Thr Leu Lys Cys Ile Arg Trp Ser Leu Pro
1 5 10
gaa atg gcc agc atc ggg ctg ctg ctg gcc atc cac ctg tgc ctc ttc 158
Glu Met Ala Ser Ile Gly Leu Leu Leu Ala Ile His Leu Cys Leu Phe
15 20 25 30
acc atg ttc gga atg ctg ctg ttc gct gga ggg aag cag gat gat ggg 206
Thr Met Phe Gly Met Leu Leu Phe Ala Gly Gly Lys Gln Asp Asp Gly
31 36 41 46
cag gac agg gag agg ctg acc tac ttc cag aac ctg cct gag tct ctg 254

Gln Asp Arg Glu Arg Leu Thr Tyr Phe Gln Asn Leu Pro Glu Ser Leu	
47 52 57 62	
act tcc ctc ctg gtg ctg ctg acc acg gcc aac aac ccc gat gtg atg	302
Thr Ser Leu Leu Val Leu Leu Thr Thr Ala Asn Asn Pro Asp Val Met	
63 68 73 78	
att cct gcg tat tcc aag aac cgg gcc tat gcc atc ttc ttc ata gtc	350
Ile Pro Ala Tyr Ser Lys Asn Arg Ala Tyr Ala Ile Phe Phe Ile Val	
79 84 89 94	
ttc act gtg ata gga agc ctg ttt ctg atg aac ctg ctg aca gcc atc	398
Phe Thr Val Ile Gly Ser Leu Phe Leu Met Asn Leu Leu Thr Ala Ile	
95 100 105 110	
atc tac agt cag ttc cgg ggc tac ctg atg aaa tct ctc cag acc tgc	446
Ile Tyr Ser Gln Phe Arg Gly Tyr Leu Met Lys Ser Leu Gln Thr Ser	
111 116 121 126	
ctg ttt cgg agg cgg ctg gga acc cgg gct gcc ttt gaa gtc cta tcc	494
Leu Phe Arg Arg Arg Leu Gly Thr Arg Ala Ala Phe Glu Val Leu Ser	
127 132 137 142	
tcc atg gtg ggg gag gga gga gcc ttc cct cag gca gtt ggg gtg aag	542
Ser Met Val Gly Glu Gly Gly Ala Phe Pro Gln Ala Val Gly Val Lys	
143 148 153 158	
ccc cag aac ttg ctg cag gtg ctt cag aag gtc cag ctg gac agc tcc	590
Pro Gln Asn Leu Leu Gln Val Leu Gln Lys Val Gln Leu Asp Ser Ser	
159 164 169 174	
cac aaa cag gcc atg atg gag aag gtg cgt tcc tac ggc agt gtt ctg	638
His Lys Gln Ala Met Met Glu Lys Val Arg Ser Tyr Gly Ser Val Leu	
175 180 185 190	
ctg tca gct gag gag ttt cag aag ctc ttc aac gag ctt gac aga agt	686
Leu Ser Ala Glu Glu Phe Gln Lys Leu Phe Asn Glu Leu Asp Arg Ser	
191 196 201 206	
gtg gtt aaa gag cac ccg ccg agg ccc gag tac cag tct ccg ttt ctg	734
Val Val Lys Glu His Pro Pro Arg Pro Glu Tyr Gln Ser Pro Phe Leu	
207 212 217 222	
cag agc gcc cag ttc ctc ttc ggc cac tac tac ttt gac tac ctg ggg	782
Gln Ser Ala Gln Phe Leu Phe Gly His Tyr Tyr Phe Asp Tyr Leu Gly	
223 228 233 238	
aac ctc atc gcc ctg gca aac ctg gtg tcc att tgc gtg ttc ctg gtg	830
Asn Leu Ile Ala Leu Ala Asn Leu Val Ser Ile Cys Val Phe Leu Val	
239 244 249 254	
ctg gat gca gat gtg ctg cct gct gag cgt gat gac ttc atc ctg ggg	878
Leu Asp Ala Asp Val Leu Pro Ala Glu Arg Asp Asp Phe Ile Leu Gly	
255 260 265 270	
att ctc aac tgc gtc ttc att gtg tac tac ctg ttg gag atg ctg ctc	926
Ile Leu Asn Cys Val Phe Ile Val Tyr Tyr Leu Leu Glu Met Leu Leu	

271	276	281	286	
aag gtc ttt gcc ctg	ggc ctg cga ggg tac	ctg tcc tac ccc agc aac		974
Lys Val Phe Ala Leu	Gly Leu Arg Gly Tyr	Leu Ser Tyr Pro Ser Asn		
287	292	297	302	
gtg ttt gac ggg ctc	ctc acc gtt gtc ctg	ctg gtt ttg gag atc tca		1022
Val Phe Asp Gly Leu	Leu Thr Val Val Leu	Leu Val Leu Glu Ile Ser		
303	308	313	318	
act ctg gct gtg tac	cga ttg cca cac cca	ggc tgg agg ccg gag atg		1070
Thr Leu Ala Val Tyr	Arg Leu Pro His Pro	Gly Trp Arg Pro Glu Met		
319	324	329	334	
gtg ggc ctg ctg tcg	ctg tgg gac atg acc	cgc atg ctg aac atg ctc		1118
Val Gly Leu Leu Ser	Leu Trp Asp Met Thr	Arg Met Leu Asn Met Leu		
335	340	345	350	
atc gtg ttc cgc ttc	ctg cgt atc atc ccc	agc atg aag ccg atg gcc		1166
Ile Val Phe Arg Phe	Leu Arg Ile Ile Pro	Ser Met Lys Pro Met Ala		
351	356	361	366	
gtg gtg gcc agt acc	gtc ctg ggc ctg gtg	cag aac atg cgt gcg ttt		1214
Val Val Ala Ser Thr	Val Leu Gly Leu Val	Gln Asn Met Arg Ala Phe		
367	372	377	382	
ggc ggg atc ctg gtg	gtg gtc tac tac gta	ttt gcc atc att ggg atc		1262
Gly Gly Ile Leu Val	Val Val Tyr Tyr Val	Phe Ala Ile Ile Gly Ile		
383	388	393	398	
aac ttg ttt aga ggc	gtc att gtg gct ctt	cct gga aac agc agc ctg		1310
Asn Leu Phe Arg Gly	Val Ile Val Ala Leu	Pro Gly Asn Ser Ser Leu		
399	404	409	414	
gcc cct gcc aat ggc	tcg gcg ccc tgt ggg	agc ttc gag cag ctg gag		1358
Ala Pro Ala Asn Gly	Ser Ala Pro Cys Gly	Ser Phe Glu Gln Leu Glu		
415	420	425	430	
tac tgg gcc aac aac	ttc gat gac ttt gcg	gct gcc ctg gtc act ctg		1406
Tyr Trp Ala Asn Asn	Phe Asp Asp Phe Ala	Ala Ala Leu Val Thr Leu		
431	436	441	446	
tgg aac ttg atg gtg	gtg aac aac tgg cag	gtg ttt ctg gat gca tat		1454
Trp Asn Leu Met Val	Val Asn Asn Trp Gln	Val Phe Leu Asp Ala Tyr		
447	452	457	462	
cgg cgc tac tca ggc	ccg tgg tcc aag atc	tat ttt gta ttg tgg tgg		1502
Arg Arg Tyr Ser Gly	Pro Trp Ser Lys Ile	Tyr Phe Val Leu Trp Trp		
463	468	473	478	
ctg gtg tcg tct gtc	atc tgg gtc aac ctg	ttt ctg gcc ctg att ctg		1550
Leu Val Ser Ser Val	Ile Trp Val Asn Leu	Phe Leu Ala Leu Ile Leu		
479	484	489	494	
gag aac ttc ctt cac	aag tgg gac ccc cgc	agc cac ctg cag ccc ctt		1598
Glu Asn Phe Leu His	Lys Trp Asp Pro Arg	Ser His Leu Gln Pro Leu		
495	500	505	510	

gct ggg acc cca gag gcc acc tac cag atg act gtg gag ctc ctg ttc	1646
Ala Gly Thr Pro Glu Ala Thr Tyr Gln Met Thr Val Glu Leu Leu Phe	
511 516 521 526	
agg gat att ctg gag gag ccc gag gag gat gag ctc aca gag agg ctg	1694
Arg Asp Ile Leu Glu Glu Pro Glu Glu Asp Glu Leu Thr Glu Arg Leu	
527 532 537 542	
agc cag cac ccg cac ctg tgg ctg tgc agg tga cgtccggg ctgccgtccc	1745
Ser Gln His Pro His Leu Trp Leu Cys Arg *	
543 548 553	
agcagggggcg gcaggagaga gaggctggcc tacacagggtg ccdgtcatgg aagaggcggc	1805
catgctgttg ccagccaggc aggaagagac ctttctctg acggaccact aagctgggga	1865
caggaaccaa gtcctttgcg tgtggcccaa caaccatcta cagaacagct gctgggtgctt	1925
cagggaggcg ccgtgccctc cgctttcttt tatagctgct tcagtggagaa ttccctcgtc	1985
gactccacag ggacctttca gacaaaaatg caagaagcag cggcctcccc tgtccctgct	2045
agtttccgtg gtgcctttgc tgccggcagc ccttggggac cacaggcctg accagggcct	2105
gcacaggtta accgtcagac ttccggggca ttcagggtggg gatgctggtg gtttgacatg	2165
gagagaacct tgactgtgtt ttattatttc atggcttgta tgagtgtgac tgggtgtgtt	2225
tctttagggt tctgattgcc agttattttc atcaataagt cttgcaaaga aaaaaaaaaa	2285
a	2286

<210> 50
 <211> 3114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (626) .. (2614)

<400> 50	
gttaccgctc cggaattccc gggtcgaccc acgcgtccgc ggacgcgtgg gcattgctga	60
aagctgcaat agaatatggc acggaagaag atgtagtaaa gtcaaagaaa acattcagaa	120
gtcaagcaat agtgaaccaa aatgcagaga cagaacttat gctggaagga gacgatgatg	180
cagtcagtct gctacaggag aaagaaattg acaaccttgc aggccagtg gttctcagca	240
cccctgccca gtcctcgct cccgtgggtg tggccaaggg gactctctcc atcaccacga	300
cagaaatcta cttcgaggta gatgaggatg actctgcctt caagaagatc gacacgaaag	360

ttcttgcata cactgaggga cttcacggaa aatggatgtt cagcgagata cgagctgtat	420
tttcaagacg ttaccttcta caaaacactg ctttggaagt atttatggca aaccgaacct	480
cagttatgtt taatttcctt gatcaagcaa cagtaaaaaa agttgtctat agcttgccctc	540
gggttggagt agggaccagc tatggtctgc cacaagccag gaggatatca ttggccactc	600
ctcgacagct ttataaattt ccaat atg act cag cgc tgg caa aga agg gaa	652
Met Thr Gln Arg Trp Gln Arg Arg Glu	
1 5	
att tca aac ttc gaa tat ttg atg ttc ctt aat act att gca gga cgg	700
Ile Ser Asn Phe Glu Tyr Leu Met Phe Leu Asn Thr Ile Ala Gly Arg	
10 15 20 25	
aca tat aat gat ctg aac caa tat cca gtg ttt ccg tgg gtg tta acc	748
Thr Tyr Asn Asp Leu Asn Gln Tyr Pro Val Phe Pro Trp Val Leu Thr	
26 31 36 41	
aac tat gaa tca gaa gag ttg gac ctg act ctt cca gga aac ttc agg	796
Asn Tyr Glu Ser Glu Glu Leu Asp Leu Thr Leu Pro Gly Asn Phe Arg	
42 47 52 57	
gat cta tca aag cca att ggt gct ttg aac ccc aag aga gct gtg ttt	844
Asp Leu Ser Lys Pro Ile Gly Ala Leu Asn Pro Lys Arg Ala Val Phe	
58 63 68 73	
tat gca gag cgt tat gag aca tgg gaa gat gat caa agc cca ccc tac	892
Tyr Ala Glu Arg Tyr Glu Thr Trp Glu Asp Asp Gln Ser Pro Pro Tyr	
74 79 84 89	
cat tat aat acc cat tat tca aca gca aca tct act tta tcc tgg ctt	940
His Tyr Asn Thr His Tyr Ser Thr Ala Thr Ser Thr Leu Ser Trp Leu	
90 95 100 105	
gtt cga att gaa cct ttc aca acc ttc ttc ctc aat gca aat gat gga	988
Val Arg Ile Glu Pro Phe Thr Thr Phe Phe Leu Asn Ala Asn Asp Gly	
106 111 116 121	
aaa ttt gat cat cca gat cga acc ttc tca tcc gtt gca agg tct tgg	1036
Lys Phe Asp His Pro Asp Arg Thr Phe Ser Ser Val Ala Arg Ser Trp	
122 127 132 137	
aga act agt cag aga gat act tct gat gta aag gaa cta att cca gag	1084
Arg Thr Ser Gln Arg Asp Thr Ser Asp Val Lys Glu Leu Ile Pro Glu	
138 143 148 153	
ttc tac tac cta cca gag atg ttt gtc aac agt aat gga tat aat ctt	1132
Phe Tyr Tyr Leu Pro Glu Met Phe Val Asn Ser Asn Gly Tyr Asn Leu	
154 159 164 169	
gga gtc aga gaa gat gaa gta gtg gta aat gat gtt gat ctt ccc cct	1180
Gly Val Arg Glu Asp Glu Val Val Val Asn Asp Val Asp Leu Pro Pro	
170 175 180 185	

tgg gca aaa aaa cct gaa gac ttt gtg cgg atc aac agg atg gcc cta	1228
Trp Ala Lys Lys Pro Glu Asp Phe Val Arg Ile Asn Arg Met Ala Leu	
186 191 196 201	
gaa agt gaa ttt gtt tct tgc caa ctt cat cag tgg atc gac ctt ata	1276
Glu Ser Glu Phe Val Ser Cys Gln Leu His Gln Trp Ile Asp Leu Ile	
202 207 212 217	
ttt ggc tat aag cag cga gga cca gaa gca gtt cgt gct ctg aat gtt	1324
Phe Gly Tyr Lys Gln Arg Gly Pro Glu Ala Val Arg Ala Leu Asn Val	
218 223 228 233	
ttt cac tac ttg act tat gaa ggc tct gtg aac ctg gat agt atc act	1372
Phe His Tyr Leu Thr Tyr Glu Gly Ser Val Asn Leu Asp Ser Ile Thr	
234 239 244 249	
gat cct gtg ctc agg gag gcc atg gag gca cag ata cag aac ttt gga	1420
Asp Pro Val Leu Arg Glu Ala Met Glu Ala Gln Ile Gln Asn Phe Gly	
250 255 260 265	
cag acg cca tct cag ttg ctt att gag cca cat ccg cct cgg agc tct	1468
Gln Thr Pro Ser Gln Leu Leu Ile Glu Pro His Pro Pro Arg Ser Ser	
266 271 276 281	
gcc atg cac ctg tgt ttc ctt cca cag agt ccg ctc atg ttt aaa gat	1516
Ala Met His Leu Cys Phe Leu Pro Gln Ser Pro Leu Met Phe Lys Asp	
282 287 292 297	
cag atg caa cag gat gtg ata atg gtg ctg aag ttt cct tca aat tct	1564
Gln Met Gln Gln Asp Val Ile Met Val Leu Lys Phe Pro Ser Asn Ser	
298 303 308 313	
cca gta acc cat gtg gca gcc aac act ctg ccc cac ttg acc atc ccc	1612
Pro Val Thr His Val Ala Ala Asn Thr Leu Pro His Leu Thr Ile Pro	
314 319 324 329	
gca gtg gtg aca gtg act tgc agc cga ctc ttt gca gtg aat aga tgg	1660
Ala Val Val Thr Val Thr Cys Ser Arg Leu Phe Ala Val Asn Arg Trp	
330 335 340 345	
cac aac aca gta ggc ctc aga gga gct cca gga tac tcc ttg gat caa	1708
His Asn Thr Val Gly Leu Arg Gly Ala Pro Gly Tyr Ser Leu Asp Gln	
346 351 356 361	
gcc cac cat ctt ccc att gaa atg gat cca tta ata gcc aat aat tca	1756
Ala His His Leu Pro Ile Glu Met Asp Pro Leu Ile Ala Asn Asn Ser	
362 367 372 377	
ggg gta aac aaa cgg cag atc aca gac ctc gtt gac cag agt ata caa	1804
Gly Val Asn Lys Arg Gln Ile Thr Asp Leu Val Asp Gln Ser Ile Gln	
378 383 388 393	
atc aat gca cat tgt ttt gtg gta aca gca gat aat cgc tat att ctt	1852
Ile Asn Ala His Cys Phe Val Val Thr Ala Asp Asn Arg Tyr Ile Leu	
394 399 404 409	
atc tgt gga ttc tgg gat aag agc ttc aga gtt tat tct aca gaa aca	1900

Ile Cys Gly Phe Trp Asp Lys Ser Phe Arg Val Tyr Ser Thr Glu Thr	
410 415 420 425	
ggg aaa ttg act cag att gta ttt ggc cat tgg gat gtg gtc act tgc	1948
Gly Lys Leu Thr Gln Ile Val Phe Gly His Trp Asp Val Val Thr Cys	
426 431 436 441	
ttg gcc agg tcc gag tca tac att ggt ggg gac tgc tac atc gtg tcc	1996
Leu Ala Arg Ser Glu Ser Tyr Ile Gly Gly Asp Cys Tyr Ile Val Ser	
442 447 452 457	
gga tct cga gat gcc acc ctg ctg ctc tgg tac tgg agt ggg cgg cac	2044
Gly Ser Arg Asp Ala Thr Leu Leu Leu Trp Tyr Trp Ser Gly Arg His	
458 463 468 473	
cat atc ata gga gac aac cct aac agc agt gac tat ccg gca cca aga	2092
His Ile Ile Gly Asp Asn Pro Asn Ser Ser Asp Tyr Pro Ala Pro Arg	
474 479 484 489	
gcc gtc ctc aca ggc cat gac cat gaa gtt gtc tgt gtt tct gtc tgt	2140
Ala Val Leu Thr Gly His Asp His Glu Val Val Cys Val Ser Val Cys	
490 495 500 505	
gca gaa ctt ggg ctt gtt atc agt ggt gct aaa gag ggc cct tgc ctt	2188
Ala Glu Leu Gly Leu Val Ile Ser Gly Ala Lys Glu Gly Pro Cys Leu	
506 511 516 521	
gtc cac acc atc act gga gat ttg ctg aga gcc ctt gaa gga cca gaa	2236
Val His Thr Ile Thr Gly Asp Leu Leu Arg Ala Leu Glu Gly Pro Glu	
522 527 532 537	
aac tgc tta ttc cca cgc ttg ata tct gtc tcc agc gaa ggc cac tgt	2284
Asn Cys Leu Phe Pro Arg Leu Ile Ser Val Ser Ser Glu Gly His Cys	
538 543 548 553	
atc ata tac tat gaa cga ggg cga ttc agt aat ttc agc att aat ggg	2332
Ile Ile Tyr Tyr Glu Arg Gly Arg Phe Ser Asn Phe Ser Ile Asn Gly	
554 559 564 569	
aaa ctt ttg gct caa atg gag atc aat gat tca aca cgg gcc att ctc	2380
Lys Leu Leu Ala Gln Met Glu Ile Asn Asp Ser Thr Arg Ala Ile Leu	
570 575 580 585	
ctg agc agt gac ggc cag aac ctg gtc acc gga ggg gac aat ggg gta	2428
Leu Ser Ser Asp Gly Gln Asn Leu Val Thr Gly Gly Asp Asn Gly Val	
586 591 596 601	
gta gag gtc tgg cag gcc tgt gac ttc aag caa ctg tac att tac cct	2476
Val Glu Val Trp Gln Ala Cys Asp Phe Lys Gln Leu Tyr Ile Tyr Pro	
602 607 612 617	
gga tgt gat gct ggc att aga gca atg gac ttg tcc cat gac cag agg	2524
Gly Cys Asp Ala Gly Ile Arg Ala Met Asp Leu Ser His Asp Gln Arg	
618 623 628 633	
act ctg atc act ggc atg gct tct ggt agc att gta gct ttt aat ata	2572
Thr Leu Ile Thr Gly Met Ala Ser Gly Ser Ile Val Ala Phe Asn Ile	

gct tca gat ctc aga gcc aat aaa aat cag gaa agt tag tagattcttc 346
 Ala Ser Asp Leu Arg Ala Asn Lys Asn Gln Glu Ser *
 81 86 91

ctgactctgg aatcttcata cctgaactt aaaccagtta cctacagtct accacccatt 406

taagaagagc aaagttacct cagctcctcc ggaggg 442

<210> 52
 <211> 3735
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1890)..(2096)

<220>
 <221> misc_feature
 <222> (1)...(3735)
 <223> n = a,t,c or g

<400> 52
 ctctgtggcc ccactcctcc ctcccatgtg tatgctntga gccgttccctt agttgagtag 60
 gtgattgacc ataccagcag cactgggtgcc aattaagcgg tctgcttggt tcacacagcc 120
 tttcattcct gttctagcat ggctctgtct taaatctgca tgcattgtatt tattccttaa 180
 tatattacct ctcttccttt cttccttttt acatttcttc ccatttttta ttgtttctct 240
 ctctctcact ctctcactca ttctctcttg cactttgtct tcggagctca ttgccatgga 300
 gtggcttggc tgtacgcac aaaaagccac ccgcaaactg ccaccccttg ccgtgcgggt 360
 ccacgtctca ctcatcact ccttcctgca ttcatagcat ccttccttcc tgcttgctct 420
 ctttttatta ggcatttatt cctctattag tggagtcagg tgcccttatg acaagtccta 480
 gcctaactct tctcgtggat ctaccattt atccatttgg ttgttatttc tttttaccgt 540
 tcctttctct cttctgtcat agctttccat acctcctgtc cttcattttc atgcagctgg 600
 ggtgccagg ggggaccca acaccctcat caggaggacc catggggcca tgtcttctca 660
 ttcacctcat ccttgcttat ttagatactc actgacttgt tcaacttagat gttcattatt 720
 taatggacag cctgtggttt tctagaagtg gaccagccat agcccttaat ctgtgatgat 780
 cttttgccac catcgatcgc attgccttct tttacatctt tatttaccac ccattaatgt 840
 atttctgtac ttaacatttg ttacattgtt tectatttct ttatttacca atattacctt 900

aaactttgaa gacagaaaat ctgcccatta tgttttccag acatttcgag ggggcgagcg	2346
gaggtcattg gagcttgaag cccatttgga aggctgggtcc ctcggcctgc gttttctcct	2406
tggccctttg aagggccccc cagctcacag ggcacttcca tcctagtctg ccgatttcga	2466
gctggagagg ggctggggtc ccacattcga ggtcccttcc cacgtaggca tccaggtgat	2526
ggcttccgcc caaaccagga aggagacgag aggcccgcca ggaagaagac ttgggtccgg	2586
gatggtgggc cccatcaggg cctcttccgc agcttccatc cgcagttctt cagccgacct	2646
agccgggcca cggccacgt gcctttgtga gcgtgcttcc acggagtaga gcgagtcagg	2706
aagcagtggg ttgaagagga aattggagggt gaggaaggaa gacagcaagt gtagacaggc	2766
ctttcaagaa gcttggtga tgcaaggaga gcccgtagac aagggtgcc tggagtgtgt	2826
ttggagaata aataagacaa gtaagacaag caagaggggt gggaaggac tgacctgtca	2886
aaccttttca acaaactttt gctgatcacc tcctctatgc cagatcctgc ctgaggcctc	2946
ttttatctca ttttaattct acaacaacct taggaggttg ctctcatcga cccattccc	3006
ccagaaaagg ataggaagat cttcagagag gtggggcgtg cctttggtga ttcagtagca	3066
tgctcattcc agaagcccac ccagggcctt ggagttgccg gcaggatgct ggccaagccc	3126
ttggcccagg tccccctcct gagaatttcc caaagggtac cttccattca ggacatcata	3186
aggggtgatga cagagtcagt cgacaaagac tgacaccccc ttggggaggg aaacactcca	3246
gtttgctagc aggtgaacac aagcaaagac ttataggaaa gtactcatag agtcaaagta	3306
tgagcatagc aaaggtcagg gcttaatgcc caatgcccc tcactagggc attggtttaa	3366
gtctttaggt aagagggaca gctggctggt cagttccggt cctcttcac ctttgccatc	3426
ctggtcctgg gggtcagtga gtggctgctt tgtatgttgg tgggatccag gaaaccgtgc	3486
tcctagtgcc ctggtgaggt gtagatgggc agcaggcccc ttggcagcag ctgagcatgg	3546
agaggaggtg gtccctgaag acaaggaggt ggacggatga tgtcatccct gaggagagac	3606
ccgggtgagg gatcctctcg tgggcgcccc agctctcctg aggagccgcc gccaaaggcca	3666
gcgagccaag gcgcgctccc tctctgccgg acgcgtgggt cgacccggga attccggagc	3726
ggtacctaa	3735

<210> 53
 <211> 2868
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (431)..(1924)

<220>

<221> misc_feature

<222> (1)...(2868)

<223> n = a,t,c or g

<400> 53

aaggatcctt aattaaatta atcccccccc cccccccgag cgcggcgcgc gcggcggttg 60

ggccgttggc tgttcggccc tgggatccgc cgccactccg cgatcagacc gctctgtgcc 120

gcgagccgcc gtgagcactc ggattcaagc cggcgccaac gagtcggggg gcatcgcccg 180

cagcgcccaa gctcatggcc ggctgagcgg gacgcgcct cgcctcagc caccgcccgc 240

gccgncgcct cctcctcctc agccggcggc ggcccgggcc cagcaaccat ggctgaagac 300

tactgggacg ggcgccctgc gcgaacagga ggagaaggag gtgcgcggc ctcaccccg 360

gccgccgccc caggcgccgc cgcgcgggcc ccgcggctct gaggttgctc gcgcgcccc 420

gccgatcgcc atg gat cgg atg aag aag atc aaa cgg cag ctg tca atg 469

Met Asp Arg Met Lys Lys Ile Lys Arg Gln Leu Ser Met

1 5 10

aca ctc cga ggt ggc cga ggc ata gac aag acc aat ggt gcc cct gag 517

Thr Leu Arg Gly Gly Arg Gly Ile Asp Lys Thr Asn Gly Ala Pro Glu

14 19 24 29

cag ata ggc ctg gat gag agt ggt ggt ggt ggc ggc agt gac cct gga 565

Gln Ile Gly Leu Asp Glu Ser Gly Gly Gly Gly Gly Ser Asp Pro Gly

30 35 40 45

gag gcc ccc aca cgt gct gct cct ggg gaa ctt cgt tct gca cgg ggc 613

Glu Ala Pro Thr Arg Ala Ala Pro Gly Glu Leu Arg Ser Ala Arg Gly

46 51 56 61

cca ctc agc tct gca cca gag att gtg cac gag gac ttg aag atg ggg 661

Pro Leu Ser Ser Ala Pro Glu Ile Val His Glu Asp Leu Lys Met Gly

62 67 72 77

tct gat ggg gag agt gac cag gct tca gcc acg tcc tcg gat gag gtg 709

Ser Asp Gly Glu Ser Asp Gln Ala Ser Ala Thr Ser Ser Asp Glu Val

78 83 88 93

cag tct cca gtg aga gtg cgt atg cgc aac cat ccc cca cgc aag atc 757

Gln Ser Pro Val Arg Val Arg Met Arg Asn His Pro Pro Arg Lys Ile

94 99 104 109

tcc act gag gac atc aac aag cgc cta tca cta cca gct gac atc cgg 805

Ser Thr Glu Asp Ile Asn Lys Arg Leu Ser Leu Pro Ala Asp Ile Arg

110 115 120 125

ctg cct gag ggc tac ctg gag aag ctg acc ctc aat agc ccc atc ttt	853
Leu Pro Glu Gly Tyr Leu Glu Lys Leu Thr Leu Asn Ser Pro Ile Phe	
126 131 136 141	
gac aag ccc ctc agc cgc cgc ctc cgt cgt gtc agc cta tct gag att	901
Asp Lys Pro Leu Ser Arg Arg Leu Arg Arg Val Ser Leu Ser Glu Ile	
142 147 152 157	
ggc ttt ggg aaa ctg gag acc tac att aag ctg gac aaa ctg ggc gag	949
Gly Phe Gly Lys Leu Glu Thr Tyr Ile Lys Leu Asp Lys Leu Gly Glu	
158 163 168 173	
ggc acc tat gcc acc gtc tac aaa ggc aaa agc aag ctc aca gac aac	997
Gly Thr Tyr Ala Thr Val Tyr Lys Gly Lys Ser Lys Leu Thr Asp Asn	
174 179 184 189	
ctt gtg gca ctc aag gag atc aga ctg gaa cat gaa gag ggg gca ccc	1045
Leu Val Ala Leu Lys Glu Ile Arg Leu Glu His Glu Glu Gly Ala Pro	
190 195 200 205	
tgc acc gcc atc cgg gaa gtg tcc ctg ctc aag gac ctc aaa cac gcc	1093
Cys Thr Ala Ile Arg Glu Val Ser Leu Leu Lys Asp Leu Lys His Ala	
206 211 216 221	
aac atc gtt acg cta cat gac att atc cac acg gag aag tcc ctc acc	1141
Asn Ile Val Thr Leu His Asp Ile Ile His Thr Glu Lys Ser Leu Thr	
222 227 232 237	
ctt gtc ttt gag tac ctg gac aag gac ctg aag cag tac ctg gat gac	1189
Leu Val Phe Glu Tyr Leu Asp Lys Asp Leu Lys Gln Tyr Leu Asp Asp	
238 243 248 253	
tgt ggg aac atc atc aac atg cac aac gtg aaa ctg ttc ctg ttc cag	1237
Cys Gly Asn Ile Ile Asn Met His Asn Val Lys Leu Phe Leu Phe Gln	
254 259 264 269	
ctg ctc cgt ggc ctg gcc tac tgc cac cgg cag aag gtg cta cac cga	1285
Leu Leu Arg Gly Leu Ala Tyr Cys His Arg Gln Lys Val Leu His Arg	
270 275 280 285	
gat ctc aag ccc cag aac ctg ctc atc aac gag agg gga gag ctc aag	1333
Asp Leu Lys Pro Gln Asn Leu Leu Ile Asn Glu Arg Gly Glu Leu Lys	
286 291 296 301	
ctg gct gac ttt ggc ctg gcc cga gcc aag tca atc cca aca aag aca	1381
Leu Ala Asp Phe Gly Leu Ala Arg Ala Lys Ser Ile Pro Thr Lys Thr	
302 307 312 317	
tac tcc aat gag gtg gtg aca ctg tgg tac cgg ccc cct gac atc ctg	1429
Tyr Ser Asn Glu Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Ile Leu	
318 323 328 333	
ctt ggg tcc acg gac tac tcc act cag att gac atg tgg ggt gtg ggc	1477
Leu Gly Ser Thr Asp Tyr Ser Thr Gln Ile Asp Met Trp Gly Val Gly	
334 339 344 349	

tgc atc ttc tat gag atg gcc aca ggc cgt ccc ctc ttt ccg ggc tcc	1525
Cys Ile Phe Tyr Glu Met Ala Thr Gly Arg Pro Leu Phe Pro Gly Ser	
350 355 360 365	
acg gtg gag gaa cag cta cac ttc atc ttc cgt atc tta gga acc cca	1573
Thr Val Glu Glu Gln Leu His Phe Ile Phe Arg Ile Leu Gly Thr Pro	
366 371 376 381	
act gag gag acg tgg cca ggc atc ctg tcc aac gag gag ttc aag aca	1621
Thr Glu Glu Thr Trp Pro Gly Ile Leu Ser Asn Glu Glu Phe Lys Thr	
382 387 392 397	
tac aac tac ccc aag tac cga gcc gag gcc ctt ttg agc cac gca ccc	1669
Tyr Asn Tyr Pro Lys Tyr Arg Ala Glu Ala Leu Leu Ser His Ala Pro	
398 403 408 413	
cga ctt gat agc gac ggg gcc gac ctc ctc acc aag ctg ttg cag ttt	1717
Arg Leu Asp Ser Asp Gly Ala Asp Leu Leu Thr Lys Leu Leu Gln Phe	
414 419 424 429	
gag ggt cga aat cgg atc tcc gca gag gat gcc atg aaa cat cca ttc	1765
Glu Gly Arg Asn Arg Ile Ser Ala Glu Asp Ala Met Lys His Pro Phe	
430 435 440 445	
ttc ctc agt ctg ggg gag cgg atc cac aaa ctt cct gac act act tcc	1813
Phe Leu Ser Leu Gly Glu Arg Ile His Lys Leu Pro Asp Thr Thr Ser	
446 451 456 461	
ata ttt gca cta aag gag att cag cta caa aag gag gcc agc ctt cgg	1861
Ile Phe Ala Leu Lys Glu Ile Gln Leu Gln Lys Glu Ala Ser Leu Arg	
462 467 472 477	
tct tcg tcg atg cct gac tca gtt gcc ggt gga cag cat ggc cgt gcc	1909
Ser Ser Ser Met Pro Asp Ser Val Ala Gly Gly Gln His Gly Arg Ala	
478 483 488 493	
agc ctc cca cac tga ggccaggtct acccccatc ataccagccc ccaggaccac	1964
Ser Leu Pro His *	
494	
tacccacagg ccagccagggt gccagagct agccaggtt ggggatctcg actcagacaa	2024
gatggtgaca atgccttgag tctgaggcat cctctgcctg ctttccctgcc tgccccacct	2084
gcctcatatt gtgtgggcct tttttgttt gtttcattca ttgttttttt ttttttaatt	2144
attttaaagt agatttttgt tttttttaa tgcaatatct ctgtatacag actggctggg	2204
cacaaccctt gogtgtggcc cttccacagt attttgtgca atgaagccct gctccagcc	2264
tttcagagac agggacacag cccctatttg gaacctgat catcaccaga cctggggatt	2324
ggctatggga aagcatgcca cagccactcg ccttccctacc cccgcccgcc atccccagtt	2384
gcagggggat ctggggacta ccagagactc tgggaaatgg acaaggtggg gggccccact	2444
ctttctctcc tgcagtcctg tagctggggc ctccttccct ctcaggggtct cccagccca	2504

gtcccccttgc tcccatccca ctcgggtgctg ttgggtaggg gccttgccag gaactgacca 2564
gctcagcgag gagccataat gtgcatatgt gcacaagcag ggttggggga ggggggtgtg 2624
aggggttgtg cccaggtgtt gccccctatc tcctggggag ggtgaggcag ggcagggaca 2684
gtctccaggg tcagtccttg gatgggtggt tacctcccct tcctccaccc taagccctgg 2744
ggccctgaaa tgggggtggga gggcaggggt gggagccctc ctagtggggt tgggggggtg 2804
ggttcctgaa tgcaccataa tcgctgtatg aaatattaaa aagtctaaag tgaaaaaaaa 2864
aaaa 2868

<210> 54
<211> 1699
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (193) .. (1533)

<400> 54
tcatttcagc gacgtggaat tcgatggaat gtccataccc ttcaccctca tccaagagca 60
gtgtgggctg ggatagggag gggacatggg tcataggctc ttctaggtag agccagggcc 120
ccggcgttgt gctttcccac ccttctagag tttctggagt ccctggagcc ggacctgccc 180
gccctgagag cc atg ggg ctc cac ctg tgg gct gca ggc cca gga acc 228
Met Gly Leu His Leu Trp Ala Ala Gly Pro Gly Thr
1 5 10
cac cct gct gga att agc gat ttg ctg gct gaa gtg tcc gct gaa gtg 276
His Pro Ala Gly Ile Ser Asp Leu Leu Ala Glu Val Ser Ala Glu Val
13 18 23 28
gat ggg cca gtg cca gga tac ctc tct tcc ccc cag agc ata aca gac 324
Asp Gly Pro Val Pro Gly Tyr Leu Ser Ser Pro Gln Ser Ile Thr Asp
29 34 39 44
acg tgc ctg tac atc ttc acc tct ggc acc acg ggc ctc ccc aag gct 372
Thr Cys Leu Tyr Ile Phe Thr Ser Gly Thr Thr Gly Leu Pro Lys Ala
45 50 55 60
gct cgg atc agt cat ctg aag atc ctg caa tgc cag ggc ttc tat cag 420
Ala Arg Ile Ser His Leu Lys Ile Leu Gln Cys Gln Gly Phe Tyr Gln
61 66 71 76
ctg tgt ggt gtc cac cag gaa gat gtg atc tac ctc gcc ctc cca ctc 468
Leu Cys Gly Val His Gln Glu Asp Val Ile Tyr Leu Ala Leu Pro Leu
77 82 87 92

tac cac atg tcc ggt tcc ctg ctg ggc atc gtg ggc tgc atg ggc att	516
Tyr His Met Ser Gly Ser Leu Leu Gly Ile Val Gly Cys Met Gly Ile	
93 98 103 108	
ggg gcc aca gtg gtg ctg aaa tcc aag ttc tcg gct ggt cag ttc tgg	564
Gly Ala Thr Val Val Leu Lys Ser Lys Phe Ser Ala Gly Gln Phe Trp	
109 114 119 124	
gaa gat tgc cag cag cac agg gtg acg gtg ttc cag tac att ggg gag	612
Glu Asp Cys Gln Gln His Arg Val Thr Val Phe Gln Tyr Ile Gly Glu	
125 130 135 140	
ctg tgc cga tac ctt gtc aac cag ccc ccg agc aag gca gaa cgt ggc	660
Leu Cys Arg Tyr Leu Val Asn Gln Pro Pro Ser Lys Ala Glu Arg Gly	
141 146 151 156	
cat aag gtc cgg ctg gca gtg ggc agc ggg ctg cgc cca gat acc tgg	708
His Lys Val Arg Leu Ala Val Gly Ser Gly Leu Arg Pro Asp Thr Trp	
157 162 167 172	
gag cgt ttt gtg cgg cgc ttc ggg ccc ctg cag gtg ctg gag aca tat	756
Glu Arg Phe Val Arg Arg Phe Gly Pro Leu Gln Val Leu Glu Thr Tyr	
173 178 183 188	
gga ctg aca gag ggc aac gtg gcc acc atc aac tac aca gga cag cgg	804
Gly Leu Thr Glu Gly Asn Val Ala Thr Ile Asn Tyr Thr Gly Gln Arg	
189 194 199 204	
ggc gct gtg ggg cgt gct tcc tgg ctt tac aag cat atc ttc ccc ttc	852
Gly Ala Val Gly Arg Ala Ser Trp Leu Tyr Lys His Ile Phe Pro Phe	
205 210 215 220	
tcc ttg att cgc tat gat gtc acc aca gga gag cca att cgg gac ccc	900
Ser Leu Ile Arg Tyr Asp Val Thr Thr Gly Glu Pro Ile Arg Asp Pro	
221 226 231 236	
cag ggg cac tgt atg gcc aca tct cca ggt gag cca ggg ctg ctg gtg	948
Gln Gly His Cys Met Ala Thr Ser Pro Gly Glu Pro Gly Leu Leu Val	
237 242 247 252	
gcc ccg gta agc cag cag tcc cca ttc ctg ggc tat gct ggc ggg cca	996
Ala Pro Val Ser Gln Gln Ser Pro Phe Leu Gly Tyr Ala Gly Gly Pro	
253 258 263 268	
gag ctg gcc cag ggg aag ttg cta aag gat gtc ttc cgg cct ggg gat	1044
Glu Leu Ala Gln Gly Lys Leu Leu Lys Asp Val Phe Arg Pro Gly Asp	
269 274 279 284	
gtt ttc ttc aac act ggg gac ctg ctg gtc tgc gat gac caa ggt ttt	1092
Val Phe Phe Asn Thr Gly Asp Leu Leu Val Cys Asp Asp Gln Gly Phe	
285 290 295 300	
ctc cgc ttc cat gat cgt act gga gac acc ttc agg tgg aag ggg gag	1140
Leu Arg Phe His Asp Arg Thr Gly Asp Thr Phe Arg Trp Lys Gly Glu	
301 306 311 316	

aat gtg gcc aca acc gag gtg gca gag gtc ttc gag gcc cta gat ttt	1188
Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp Phe	
317 322 327 332	
ctt cag gag gtg aac gtc tat gga gtc act gtg cca ggg cat gaa ggc	1236
Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His Glu Gly	
333 338 343 348	
agg gct gga atg gca gcc cta gtt ctg cgt ccc ccc cac gct ttg gac	1284
Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His Ala Leu Asp	
349 354 359 364	
ctt atg cag ctc tac acc cac gtg tct gag aac ttg cca cct tat gcc	1332
Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu Pro Pro Tyr Ala	
365 370 375 380	
cgg ccc cga ttc ctc agg ctc cag gag tct ttg gcc acc aca gag acc	1380
Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu Ala Thr Thr Glu Thr	
381 386 391 396	
ttc aaa cag cag aaa gtt cgg atg gca aat gag ggc ttc gac ccc agc	1428
Phe Lys Gln Gln Lys Val Arg Met Ala Asn Glu Gly Phe Asp Pro Ser	
397 402 407 412	
acc ctg tct gac cca ctg tac gtt ctg gac cag gct gta ggt gcc tac	1476
Thr Leu Ser Asp Pro Leu Tyr Val Leu Asp Gln Ala Val Gly Ala Tyr	
413 418 423 428	
ctg ccc ctc aca act gcc cgg tac agc gcc ctc ctg gca gga aac ctt	1524
Leu Pro Leu Thr Thr Ala Arg Tyr Ser Ala Leu Leu Ala Gly Asn Leu	
429 434 439 444	
cga atc tga gaacttc cacacctgag gcacctgaga gaggaactct gtgggggtggg	1580
Arg Ile *	
445	
ggccgttgca ggtgtactgg gctgtcaggg atcttttcta taccagaact gcggtcacta	1640
ttttgtaata aatgtggctg gagctgatcc agctgtctct gacctacaaa aaaaaaaaaa	1699

<210> 55
 <211> 7263
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (159)..(5057)

actgatcatc gaacggctga tgtatataac tatctattcg atgatgaaga taccacacca	60
aacccaaaaa aagagatctc tcgaggatcc gaattcgcg cgcgctcgac gccagcagtg	120

ctgttggaac tgctctgccca aaatttgcca tccgaggg	atg ctg aaa acc ttt	173
	Met Leu Lys Thr Phe	
	1	
ggg ctt cat gga gtc gtc tta gat gtt gat tca gtg aat gaa ctg gtg		221
Gly Leu His Gly Val Val Leu Asp Val Asp Ser Val Asn Glu Leu Val		
6 11 16 21		
cag gta gaa acg tac ctc cgc agt gaa ggt gtg ctg gtg cga tac tgg		269
Gln Val Glu Thr Tyr Leu Arg Ser Glu Gly Val Leu Val Arg Tyr Trp		
22 27 32 37		
tat cct att gac atg ttg gaa agg ccc cca gca ggc tac cga agg act		317
Tyr Pro Ile Asp Met Leu Glu Arg Pro Pro Ala Gly Tyr Arg Arg Thr		
38 43 48 53		
gcc acc aat ggg ctg gtc aca ctg gac aat acc aac ctt caa att cac		365
Ala Thr Asn Gly Leu Val Thr Leu Asp Asn Thr Asn Leu Gln Ile His		
54 59 64 69		
agg gag ctg ctg cgc tgc gag gct gcg ctg gcc agg ctg tac tgc cgc		413
Arg Glu Leu Leu Arg Cys Glu Ala Ala Leu Ala Arg Leu Tyr Cys Arg		
70 75 80 85		
atg gcc ctg ctc aat atc ttc gcc cgc aag ttg cct cac ttg ttc act		461
Met Ala Leu Leu Asn Ile Phe Ala Pro Lys Leu Pro His Leu Phe Thr		
86 91 96 101		
cgc ctc ttc cac atc cct gcc atc cgg gac att acc ctg gag cac ctg		509
Arg Leu Phe His Ile Pro Ala Ile Arg Asp Ile Thr Leu Glu His Leu		
102 107 112 117		
caa ctg ctg tcc aat cag ctc ctc gca cct cct ctc cca gac ggc acc		557
Gln Leu Leu Ser Asn Gln Leu Leu Ala Pro Pro Leu Pro Asp Gly Thr		
118 123 128 133		
atc agc tcc agc tgc atc ctc ctg gcg cag tct tta cag cat tgc atc		605
Ile Ser Ser Ser Ser Ile Leu Leu Ala Gln Ser Leu Gln His Cys Ile		
134 139 144 149		
cat tcc cag aac tgc tcc gcc acg gac ctc ttt tac cag ggc aac tcc		653
His Ser Gln Asn Cys Ser Ala Thr Asp Leu Phe Tyr Gln Gly Asn Ser		
150 155 160 165		
cag aca gtg aga gag tgg ctc aac gtg gcc atc acc cgg acc ctg cac		701
Gln Thr Val Arg Glu Trp Leu Asn Val Ala Ile Thr Arg Thr Leu His		
166 171 176 181		
cag ggc gag gag agc ctt tta gag ctg acg aaa cag atc tgc tct ttc		749
Gln Gly Glu Glu Ser Leu Leu Glu Leu Thr Lys Gln Ile Cys Ser Phe		
182 187 192 197		
ctg cag aca gca cca gag cag ttc ccc tcc gaa gag ttc cca att tcc		797
Leu Gln Thr Ala Pro Glu Gln Phe Pro Ser Glu Glu Phe Pro Ile Ser		
198 203 208 213		
gaa tcc aaa gtc aac atg gac gtg aat ttc ccc ggg gca gct ttt gtt		845

Glu Ser Lys Val Asn Met Asp Val Asn Phe Pro Gly Ala Ala Phe Val	
214 219 224 229	
gtt gtg tct tgt aaa gaa agt caa tct gga ttc cgc aaa gac tcc tct	893
Val Val Ser Cys Lys Glu Ser Gln Ser Gly Phe Arg Lys Asp Ser Ser	
230 235 240 245	
ctg tac aag gca ccg tgg gca cgg gtg ctc gta tat ggc ctc ggc cac	941
Leu Tyr Lys Ala Pro Trp Ala Arg Val Leu Val Tyr Gly Leu Gly His	
246 251 256 261	
aaa gtg aag cga aat ggc cag ctg aac ctc atc gag gcc gcc tgt tac	989
Lys Val Lys Arg Asn Gly Gln Leu Asn Leu Ile Glu Ala Ala Cys Tyr	
262 267 272 277	
ccg cgg gac gcg tcc cca gcc aac act ggg ctt gca cct ccc ccc acc	1037
Pro Arg Asp Ala Ser Pro Ala Asn Thr Gly Leu Ala Pro Pro Pro Thr	
278 283 288 293	
gct gac cag tac ccc tct gtg gtc ctc tcc aca gac agg gtc cac atc	1085
Ala Asp Gln Tyr Pro Ser Val Val Leu Ser Thr Asp Arg Val His Ile	
294 299 304 309	
aaa ctg ggg gtg tct cca cct cct gga gca gtc ctg gtg tta cat tcc	1133
Lys Leu Gly Val Ser Pro Pro Gly Ala Val Leu Val Leu His Ser	
310 315 320 325	
ctg ccc ctg gag ttc cca ctg gct atg gcc ttc gca gag cag ctg ctg	1181
Leu Pro Leu Glu Phe Pro Leu Ala Met Ala Phe Ala Glu Gln Leu Leu	
326 331 336 341	
tcc tgg aaa tca gag gac agt gaa ggg aag tcc gaa gat gag cct gac	1229
Ser Trp Lys Ser Glu Asp Ser Glu Gly Lys Ser Glu Asp Glu Pro Asp	
342 347 352 357	
acc att ccg aca tcc gtc ctc ctg cag gtg gtg gag ctg cta gga aac	1277
Thr Ile Pro Thr Ser Val Leu Leu Gln Val Val Glu Leu Leu Gly Asn	
358 363 368 373	
ttc ttg tgg acc acg gac atg gca gcc tgc gtg aag gag ctt gtt ttc	1325
Phe Leu Trp Thr Thr Asp Met Ala Ala Cys Val Lys Glu Leu Val Phe	
374 379 384 389	
cat ctc ctg gca gag ctc ctg cgc acg gtg cac acc ctg gag cag agg	1373
His Leu Leu Ala Glu Leu Leu Arg Thr Val His Thr Leu Glu Gln Arg	
390 395 400 405	
cgg cac ccc gct ggc ctg tcc tcc tca atc gcc ctc cag ctg aac ccc	1421
Arg His Pro Ala Gly Leu Ser Ser Ser Ile Ala Leu Gln Leu Asn Pro	
406 411 416 421	
tgc ctg gcc atg ctg atg gcc ttg cag tgc gag ctc cac aag ctg tac	1469
Cys Leu Ala Met Leu Met Ala Leu Gln Ser Glu Leu His Lys Leu Tyr	
422 427 432 437	
gac gag gag acg cag aac tgg gtc tca ggc ggc gcc tgc ggg ggc tcc	1517
Asp Glu Glu Thr Gln Asn Trp Val Ser Gly Gly Ala Cys Gly Gly Ser	

438	443	448	453	
ggg ggg gcg gcg gcc ggt gac cag ggc agg ttc tct acg tat ttt cat				1565
Gly Gly Ala Ala Ala Gly Asp Gln Gly Arg Phe Ser Thr Tyr Phe His				
454	459	464	469	
gca ctc atg gaa ggg tgc ctg gct gtg gcc gaa gtg acc ctg cct act				1613
Ala Leu Met Glu Gly Cys Leu Ala Val Ala Glu Val Thr Leu Pro Thr				
470	475	480	485	
aac atg agt gtc aca gcc agt ggg gtg acc tca gcg acc gcc cca aat				1661
Asn Met Ser Val Thr Ala Ser Gly Val Thr Ser Ala Thr Ala Pro Asn				
486	491	496	501	
ctc agt gac tcg tcc tcc tcc tcc tcg tcc tcc cca gga cag acc cca				1709
Leu Ser Asp Ser Ser Ser Ser Ser Ser Ser Ser Pro Gly Gln Thr Pro				
502	507	512	517	
cag agt ccc agc ctc ctc tcc aag agg aaa aaa gtc aag atg aag cgg				1757
Gln Ser Pro Ser Leu Leu Ser Lys Arg Lys Lys Val Lys Met Lys Arg				
518	523	528	533	
gaa aag gcc tcc tcg tcg ggc aag cgc cag tct tcc cgc acc gtg gac				1805
Glu Lys Ala Ser Ser Ser Gly Lys Arg Gln Ser Ser Arg Thr Val Asp				
534	539	544	549	
tcg gac ccc acc gtg ctc agc atc gga ggc agc aag ccc gag gac atg				1853
Ser Asp Pro Thr Val Leu Ser Ile Gly Gly Ser Lys Pro Glu Asp Met				
550	555	560	565	
ctg tgg ttc cac cgc gca ctc acc ctg ctc atc atc ctc cgc cac ctc				1901
Leu Trp Phe His Arg Ala Leu Thr Leu Leu Ile Ile Leu Arg His Leu				
566	571	576	581	
acc agg aag gac cca cag ggg ctg ggc gtg acg agt gac gcc atc gcc				1949
Thr Arg Lys Asp Pro Gln Gly Leu Gly Val Thr Ser Asp Ala Ile Ala				
582	587	592	597	
gat gcc tgc cag gcc ctg gtg ggc ccc acc gcc cac agc cgc ttg ctg				1997
Asp Ala Cys Gln Ala Leu Val Gly Pro Thr Ala His Ser Arg Leu Leu				
598	603	608	613	
gtg atc tcc ggg atc ccc acc cac ctg gac gag ggc gta gtc aga ggc				2045
Val Ile Ser Gly Ile Pro Thr His Leu Asp Glu Gly Val Val Arg Gly				
614	619	624	629	
gcc atc cgc aag gcc tgc aac gcc cac ggc ggg gtc ttc aaa gac gag				2093
Ala Ile Arg Lys Ala Cys Asn Ala His Gly Gly Val Phe Lys Asp Glu				
630	635	640	645	
atc tac atc ccg ctg cag gaa gaa gac acc aag aag cca aaa gac aag				2141
Ile Tyr Ile Pro Leu Gln Glu Glu Asp Thr Lys Lys Pro Lys Asp Lys				
646	651	656	661	
gcc gag ggc ggg gac ggg aaa gtt gag ccc gag aag aca ctg gcc ttc				2189
Ala Glu Gly Gly Asp Gly Lys Val Glu Pro Glu Lys Thr Leu Ala Phe				
662	667	672	677	

ccc ggc aca gac agc atg gag gtc agc acg tcc agc agc ctg acc ccc	2237
Pro Gly Thr Asp Ser Met Glu Val Ser Thr Ser Ser Ser Leu Thr Pro	
678 683 688 693	
gcc atg agc atc agc gcc tcc gcc tcc acc agc cag gcc tcc atc tgc	2285
Ala Met Ser Ile Ser Ala Ser Ala Ser Thr Ser Gln Ala Ser Ile Cys	
694 699 704 709	
agc tcg cag ggc atc tcc caa acc gtc agc gac ctc tct gtg gat ccg	2333
Ser Ser Gln Gly Ile Ser Gln Thr Val Ser Asp Leu Ser Val Asp Pro	
710 715 720 725	
ctg cct gcc ggc ctc gag ctg ccc atc cct ccg ggc ctg ttg gag ccc	2381
Leu Pro Ala Gly Leu Glu Leu Pro Ile Pro Pro Gly Leu Leu Glu Pro	
726 731 736 741	
cac gcg gtg tcc agc cag gaa agc ctg gac att tcc ctg tgc agc acc	2429
His Ala Val Ser Ser Gln Glu Ser Leu Asp Ile Ser Leu Cys Ser Thr	
742 747 752 757	
ggc agc ctg ggc agc ctg ggc agc ctg ggg gag ccc ctg gac aat gca	2477
Gly Ser Leu Gly Ser Leu Gly Ser Leu Gly Glu Pro Leu Asp Asn Ala	
758 763 768 773	
gag acg gcc tcg gtg tcg gac atg ggc tcc atg tac aca gtc act tcc	2525
Glu Thr Ala Ser Val Ser Asp Met Gly Ser Met Tyr Thr Val Thr Ser	
774 779 784 789	
ctg gac aac cag ccc ctc gcc gcc cgc ccc atc aaa ggc ttc gca gtc	2573
Leu Asp Asn Gln Pro Leu Ala Ala Arg Pro Ile Lys Gly Phe Ala Val	
790 795 800 805	
gtg gag ata aga tcc cga gcc aaa att gag aaa att cga gca agt tta	2621
Val Glu Ile Arg Ser Arg Ala Lys Ile Glu Lys Ile Arg Ala Ser Leu	
806 811 816 821	
ttt aac aat aat gac ttg att ggt ttg tca agt ttg gat ggt gaa gat	2669
Phe Asn Asn Asn Asp Leu Ile Gly Leu Ser Ser Leu Asp Gly Glu Asp	
822 827 832 837	
gaa ttg atg gaa atg tca aca gaa gag att cta acc gtg tct gta gta	2717
Glu Leu Met Glu Met Ser Thr Glu Glu Ile Leu Thr Val Ser Val Val	
838 843 848 853	
aat cag agt ctc ttt gat act caa ggg agc cca ggg tta gaa gat tat	2765
Asn Gln Ser Leu Phe Asp Thr Gln Gly Ser Pro Gly Leu Glu Asp Tyr	
854 859 864 869	
ttc aat gat aag tca att aaa ggg gag aag ctg gtg ccc gga gcc aga	2813
Phe Asn Asp Lys Ser Ile Lys Gly Glu Lys Leu Val Pro Gly Ala Arg	
870 875 880 885	
gag gtt ctg acg gag ata ttt aag agt tgt gcc cat tca gag cag acg	2861
Glu Val Leu Thr Glu Ile Phe Lys Ser Cys Ala His Ser Glu Gln Thr	
886 891 896 901	

ctg agc ctg aca cca gcg aag ccc atc aga gtc tct gac att tat ctt	2909
Leu Ser Leu Thr Pro Ala Lys Pro Ile Arg Val Ser Asp Ile Tyr Leu	
902 907 912 917	
agc aaa gag cag atc aac tcc cag acc cca ggc aac ctc ctc cac ctc	2957
Ser Lys Glu Gln Ile Asn Ser Gln Thr Pro Gly Asn Leu Leu His Leu	
918 923 928 933	
ttc ttc acc aat gtc cgg ccg cca aaa aag gtg ctg gag gat cag ctc	3005
Phe Phe Thr Asn Val Arg Pro Pro Lys Lys Val Leu Glu Asp Gln Leu	
934 939 944 949	
acc cag atc ctg agg aag tat ggc gtg cca aag ccc aag ttt gac aag	3053
Thr Gln Ile Leu Arg Lys Tyr Gly Val Pro Lys Pro Lys Phe Asp Lys	
950 955 960 965	
agc aag tac agc aag gcc ggg aag gag cag cac ccc gtg aag gtg gtg	3101
Ser Lys Tyr Ser Lys Ala Gly Lys Glu Gln His Pro Val Lys Val Val	
966 971 976 981	
agc acc aag cgg cct atc acc aag ccg ccc gcc aag gac aag gct gtg	3149
Ser Thr Lys Arg Pro Ile Thr Lys Pro Pro Ala Lys Asp Lys Ala Val	
982 987 992 997	
ctc aac agc gtc agc agg act gcc tta agt gag aag aag cca act gtg	3197
Leu Asn Ser Val Ser Arg Thr Ala Leu Ser Glu Lys Lys Pro Thr Val	
998 1003 1008 1013	
aag cca aaa tca cca gaa aag agc aaa cca gat gaa aag gac cca gaa	3245
Lys Pro Lys Ser Pro Glu Lys Ser Lys Pro Asp Glu Lys Asp Pro Glu	
1014 1019 1024 1029	
aag tca cct acc aaa aaa caa gaa gtc cct gag gaa aaa tac ctg acg	3293
Lys Ser Pro Thr Lys Lys Gln Glu Val Pro Glu Glu Lys Tyr Leu Thr	
1030 1035 1040 1045	
ctg gaa gga ttt cac aaa ttt gtt att gac cga gcc agg caa gat atc	3341
Leu Glu Gly Phe His Lys Phe Val Ile Asp Arg Ala Arg Gln Asp Ile	
1046 1051 1056 1061	
cgt agc gtc tgg agg gcg atc ttg tcc tgt ggt tac gat ctt cac ttt	3389
Arg Ser Val Trp Arg Ala Ile Leu Ser Cys Gly Tyr Asp Leu His Phe	
1062 1067 1072 1077	
gag agg tgc gca tgc atc gat gtc cga cat gca cag aag gcc tca aga	3437
Glu Arg Cys Ala Cys Ile Asp Val Arg His Ala Gln Lys Ala Ser Arg	
1078 1083 1088 1093	
aag tgg acc ctg gag atg gac gtg gca ctt gtg cag tac atc aac cag	3485
Lys Trp Thr Leu Glu Met Asp Val Ala Leu Val Gln Tyr Ile Asn Gln	
1094 1099 1104 1109	
cta tgc cgc cac ctc gcc atc aca ccc gca cgg ctc cat ccc cat gag	3533
Leu Cys Arg His Leu Ala Ile Thr Pro Ala Arg Leu His Pro His Glu	
1110 1115 1120 1125	
gtg tac ctg gac ccc gcg gat gct gct gac ccc aga gtg gcc tgt ctc	3581

Val Tyr Leu Asp Pro Ala Asp Ala Ala Asp Pro Arg Val Ala Cys Leu	
1126 1131 1136 1141	
ctg aac gtg ccc atc gag agc ctg cgc ctg cgc ttc gcc ttg ctg cag	3629
Leu Asn Val Pro Ile Glu Ser Leu Arg Leu Arg Phe Ala Leu Leu Gln	
1142 1147 1152 1157	
tcc ctc aac acc aca ctg gag acc ttc ttc ctg ccc ctg gtg gag ctg	3677
Ser Leu Asn Thr Thr Leu Glu Thr Phe Phe Leu Pro Leu Val Glu Leu	
1158 1163 1168 1173	
cgc cag aca ccc atg tat acc cac agc atc gcc gcc ctg ctg aag gag	3725
Arg Gln Thr Pro Met Tyr Thr His Ser Ile Ala Ala Leu Leu Lys Glu	
1174 1179 1184 1189	
gcc aaa ggg ctg atc ttc tat gac acg aag gtg acc gtg atg aat cga	3773
Ala Lys Gly Leu Ile Phe Tyr Asp Thr Lys Val Thr Val Met Asn Arg	
1190 1195 1200 1205	
gtg ctg aat gcc act gtg cag agg aca gcg gac cac gcg gcc cct gag	3821
Val Leu Asn Ala Thr Val Gln Arg Thr Ala Asp His Ala Ala Pro Glu	
1206 1211 1216 1221	
atc acc ttg gac cca ctg gaa att gtg gga ggg gaa atc aga gct tct	3869
Ile Thr Leu Asp Pro Leu Glu Ile Val Gly Gly Glu Ile Arg Ala Ser	
1222 1227 1232 1237	
gaa aac tcc tac ttc tgt cag gct gcc agg cag ctg gcc tca gtg ccg	3917
Glu Asn Ser Tyr Phe Cys Gln Ala Ala Arg Gln Leu Ala Ser Val Pro	
1238 1243 1248 1253	
tcg tct cag ctc tgc gtc aag ctg gcc agt ggc ggt gac ccc aca tat	3965
Ser Ser Gln Leu Cys Val Lys Leu Ala Ser Gly Gly Asp Pro Thr Tyr	
1254 1259 1264 1269	
gcc ttc aac atc cgc ttc act ggc gag gag gtc cat ggc acc agc ggc	4013
Ala Phe Asn Ile Arg Phe Thr Gly Glu Glu Val His Gly Thr Ser Gly	
1270 1275 1280 1285	
tct ttc cgc cac ttc ctg tgg cag gtg tgt aag gag ctg cag agt tcc	4061
Ser Phe Arg His Phe Leu Trp Gln Val Cys Lys Glu Leu Gln Ser Ser	
1286 1291 1296 1301	
tcg ctg tcg ctg ctg ctg ctg tgc ccc agc tca gct gtc aat aag aac	4109
Ser Leu Ser Leu Leu Leu Leu Cys Pro Ser Ser Ala Val Asn Lys Asn	
1302 1307 1312 1317	
aag ggc aag tat atc ctg acc ccg agc ccc atc acc tac ggg gag gag	4157
Lys Gly Lys Tyr Ile Leu Thr Pro Ser Pro Ile Thr Tyr Gly Glu Glu	
1318 1323 1328 1333	
cag ctg ctg cac ttc ctg ggg cag ctg ctg ggg att gca att cgg gca	4205
Gln Leu Leu His Phe Leu Gly Gln Leu Leu Gly Ile Ala Ile Arg Ala	
1334 1339 1344 1349	
gac gtc ccg ctg ccc ctg gac ctc ctg ccc tcc ttc tgg aag acg ctg	4253
Asp Val Pro Leu Pro Leu Asp Leu Leu Pro Ser Phe Trp Lys Thr Leu	

1350	1355	1360	1365	
gtg ggc gag ccc ttg gac cct gag caa gac ctg cag gaa gcg gat atc				4301
Val Gly Glu Pro Leu Asp Pro Glu Gln Asp Leu Gln Glu Ala Asp Ile				
1366	1371	1376	1381	
ctc acc tac aat tac gtc aag aag ttt gag agc atc aat gat gag acc				4349
Leu Thr Tyr Asn Tyr Val Lys Lys Phe Glu Ser Ile Asn Asp Glu Thr				
1382	1387	1392	1397	
gag ctg gag gcc ctg tgc gct gag atc gcc tcc cag cac ctg gcc acg				4397
Glu Leu Glu Ala Leu Cys Ala Glu Ile Ala Ser Gln His Leu Ala Thr				
1398	1403	1408	1413	
gag agc cct gac agc ccc aac aag ccc tgc tgc agg ttc acc tac ctg				4445
Glu Ser Pro Asp Ser Pro Asn Lys Pro Cys Cys Arg Phe Thr Tyr Leu				
1414	1419	1424	1429	
acc atg acg ggc gag gag gtg gag ctg tgc agc cgg ggc cgg cac atc				4493
Thr Met Thr Gly Glu Glu Val Glu Leu Cys Ser Arg Gly Arg His Ile				
1430	1435	1440	1445	
ctt gtg gcg tgg gag aac aag gac atc tac gcg gca gcc atc cgg agc				4541
Leu Val Ala Trp Glu Asn Lys Asp Ile Tyr Ala Ala Ala Ile Arg Ser				
1446	1451	1456	1461	
ctg cgg ctg cgg gag ctg cag aat gtg gag tgc gtg acg gcc gtg cgg				4589
Leu Arg Leu Arg Glu Leu Gln Asn Val Glu Cys Val Thr Ala Val Arg				
1462	1467	1472	1477	
gcc ggc ctg ggc tcc atc atc ccc ctg cag ctg ctg acc atg ctc agc				4637
Ala Gly Leu Gly Ser Ile Ile Pro Leu Gln Leu Leu Thr Met Leu Ser				
1478	1483	1488	1493	
cca ctg gag atg gag ctg cgc acc tgc ggc ctc ccc tac atc aac ctc				4685
Pro Leu Glu Met Glu Leu Arg Thr Cys Gly Leu Pro Tyr Ile Asn Leu				
1494	1499	1504	1509	
gag ttc ctc aag gcc cac acc atg tac caa gtg ggg ctg atg gag acg				4733
Glu Phe Leu Lys Ala His Thr Met Tyr Gln Val Gly Leu Met Glu Thr				
1510	1515	1520	1525	
gac cag cac atc gag ttc ttc tgg ggg gcc ctg gag atg ttc acc cag				4781
Asp Gln His Ile Glu Phe Phe Trp Gly Ala Leu Glu Met Phe Thr Gln				
1526	1531	1536	1541	
gag gag ctg tgc aag ttc atc aag ttt gcc tgc aac cag gag cgc atc				4829
Glu Glu Leu Cys Lys Phe Ile Lys Phe Ala Cys Asn Gln Glu Arg Ile				
1542	1547	1552	1557	
ccg ttc acc tgc ccc tgc aaa gat ggg ggt ccc gac act gcc cat gtg				4877
Pro Phe Thr Cys Pro Cys Lys Asp Gly Gly Pro Asp Thr Ala His Val				
1558	1563	1568	1573	
ccc ccg tac ccc atg aag atc gcc ccc cca gat ggc aca gca ggt tcc				4925
Pro Pro Tyr Pro Met Lys Ile Ala Pro Pro Asp Gly Thr Ala Gly Ser				
1574	1579	1584	1589	

cca gac tct cgc tac atc cgc gtg gag acc tgc atg ttc atg atc aag	4973
Pro Asp Ser Arg Tyr Ile Arg Val Glu Thr Cys Met Phe Met Ile Lys	
1590 1595 1600 1605	
ctt ccc cag tac tcc tct ctg gaa atc atg ctg gag aaa ctt cgt tgt	5021
Leu Pro Gln Tyr Ser Ser Leu Glu Ile Met Leu Glu Lys Leu Arg Cys	
1606 1611 1616 1621	
gcc att cac tac cgt gaa gac ccc ctc agt ggc tga tggg agggagcccc	5071
Ala Ile His Tyr Arg Glu Asp Pro Leu Ser Gly *	
1622 1627 1632	
agaattaggc tgtcactgag gcacccactc tgctggcttg ggaagccacc actgcggccc	5131
gtccctccag ggccctcggt gaggagttag caacattttg cttttccaaa ctttctgcca	5191
cattccaggg cctcctggaa gacttaacct tttgtctttg tacgtttcgt gatgggttg	5251
ttcttttgct gcctgtttgt ggtctatttg taggatagtt tagttcccag acagtttgtg	5311
tctaatttga tcttcttgga cattgtccct catggccacc agattctaata gccataaggc	5371
cccagctggt tccccatcac agaaccaccc agcaggaagc cgggggtaca atgacctcgg	5431
ccacacagag cgctcgtgct ttcagcagag cgccctccaca gacaagcctg tggccagccc	5491
tgccctccag cctcgagctg gagttgctcc agaggcagcc ccagcaggcc tccctccaca	5551
tagaggtggc tgggccaatt gcccaaacac gtgagacaca caggagctt tatgtgttca	5611
tcttcctgct ttagaacttg ctcccggctc tggtttttct gaggaaaagc ccacagtgg	5671
tccctgccc ctccataacc tccctatctg cgtctgtct ctttgggccc tggctgaca	5731
gttttcatct gaggcctcct cgaggcagg agacttaagg gttcatcccg acctagttc	5791
acagagccta gctgggtgca tcccagccgc agggggtgag aagacacca gagatggggg	5851
gacaatgctc aggtgggggc ctctccgag actctggttg agaggaaagc acatgattca	5911
agcctacccc aaaaaaagg agcacaaaat gctcagaaat ggccttctc cctgcagt	5971
acgtaggaca agggaaagg ccacacccat tttcaaaaga gtggactgag gtgctctgct	6031
caatttggg tctgcttttag tgaccagac actcaagtcc agatggagac tccagggggg	6091
tccttctgcc cctctggcca gcccaccca gcaactccca tcaccccatg taagtgtgta	6151
tgccagggt gagctgctc caggctcacc cactgcatct ttgccccaaa taggtctttg	6211
tccagtggta ctttgttcat gagcagaca ggccatcttg ttggacactg tcactttggg	6271
ccttgccagg tctcacagaa tcacatcgt gtatttattg tataatattg tgaatattg	6331
aagttttgag tgagtgtgt ctagaaggtt ttggagtgtg gatgctggtc caagaaagaa	6391

gatgtgccct ggctgctgg aaagattgtg aattctagag atagagccgt tagcatccat 6451
ctcctccctg taactcttag gaaatgcac aaggaccatt atagaaagga tcccctgacc 6511
taaggatgaa atcgacctag ggttaatcat gacagctgca tcagttgtat tggatgcaag 6571
tcaactctgg aggtgagtgc ccgcaagcag ttccctgct ttgaaagaag atggtcagcc 6631
cgctgcctcc ccagcggcca cagctccttt gagtgtgggg ggtcacagcc aggatgtatt 6691
cctgacaata aggatccttt tattttcatt tctgcataat gaaagagcct ttcgatttat 6751
tagaagtggg ttttccctcc tacatcttta aattcttggg tctctttagt cctcatccct 6811
tgaatggact tgtcagctac ctcccagga ggagttcaga agcttctgtt ggccatcact 6871
tgagtagatg acaagctgta aggtatctgc tgctaacgtg gctgcttctc cgagagcaca 6931
ttgagggtcca gacagatcca aaccttggcc ctaaaaaatg tgtgctgtaa agttacttga 6991
tgtatattta ttataattat ttatggttgc atttaacaaa cttttcattc aatctgatgc 7051
tatttacacc atgctgtgta aaggaagctc actaaaggaa aaaagtcaca ccaataaata 7111
accttcatct aattttgatt taccttaaga gttgtgtgat catctactct tgctgagcaa 7171
gttcaaaggc tggcatgctt ggatggctct gatatttaag tgctgccaag tggctaggaa 7231
ttaagtgtt totaattata aaaaaaaaaa aa 7263

<210> 56
<211> 1159
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (183)..(1064)

<400> 56
atttggccct cgaggccaag aattcggcac gagcgggttct cgacgtgccg ccaatcttcg 60
aacgcaggtc tgtgatcatc cgcagactcc gaaaaagggg tcgaggaacg cgctgctcc 120
cctcgtcgca gtttccagcc cgacgagctt gttttgtccc ggactcgggtg cccctgtaga 180
ca atg gcc ctc gtg tct gcc gat tcc cgc att gca gaa ctt ctc aca 227
Met Ala Leu Val Ser Ala Asp Ser Arg Ile Ala Glu Leu Leu Thr
1 5 10
gag ctc cat cag ctg atc aaa caa acc cag gaa gag cgt tcg cgg agc 275
Glu Leu His Gln Leu Ile Lys Gln Thr Gln Glu Glu Arg Ser Arg Ser
16 21 26 31

gaa cac aac tta gtg aac atc cag aag acc cat gag cgg atg cag aca	323
Glu His Asn Leu Val Asn Ile Gln Lys Thr His Glu Arg Met Gln Thr	
32 37 42 47	
gag aac aag att tct ccc tat tac cgg aca aag ctg cgt ggc ctc tac	371
Glu Asn Lys Ile Ser Pro Tyr Tyr Arg Thr Lys Leu Arg Gly Leu Tyr	
48 53 58 63	
aca acc gcc aag gcc gat gca gag gct gag tgc aac atc ctt cgg aaa	419
Thr Thr Ala Lys Ala Asp Ala Glu Ala Glu Cys Asn Ile Leu Arg Lys	
64 69 74 79	
gct ctg gac aag atc gcg gaa atc aag tct ctg ttg gaa gag agg cgg	467
Ala Leu Asp Lys Ile Ala Glu Ile Lys Ser Leu Leu Glu Glu Arg Arg	
80 85 90 95	
att gcg gcc aag att gcc ggt ctc tac aat gac tcg gag cca ccc cgg	515
Ile Ala Ala Lys Ile Ala Gly Leu Tyr Asn Asp Ser Glu Pro Pro Arg	
96 101 106 111	
aag acc atg cgc aga ggg gtg ctg atg acc ctg ctg cag cag tcg gcc	563
Lys Thr Met Arg Arg Gly Val Leu Met Thr Leu Leu Gln Gln Ser Ala	
112 117 122 127	
atg acc ctg ccc ctg tgg atc ggg aag cct ggt gac aag ccc cca ccc	611
Met Thr Leu Pro Leu Trp Ile Gly Lys Pro Gly Asp Lys Pro Pro Pro	
128 133 138 143	
ctc tgt ggg gcc atc cct gcc tca gga gac tac gtg gcc aga cct gga	659
Leu Cys Gly Ala Ile Pro Ala Ser Gly Asp Tyr Val Ala Arg Pro Gly	
144 149 154 159	
gac aag gtg gct gcc cgg gtg aag gcc gtg gat ggg gac gag cag tgg	707
Asp Lys Val Ala Ala Arg Val Lys Ala Val Asp Gly Asp Glu Gln Trp	
160 165 170 175	
atc ctg gcc gag gtg gtc agt tac agc cat gcc acc aac aag tat gag	755
Ile Leu Ala Glu Val Val Ser Tyr Ser His Ala Thr Asn Lys Tyr Glu	
176 181 186 191	
gta gat gac atc gat gaa gaa ggc aaa gag aga cac acc ctg agc cgg	803
Val Asp Asp Ile Asp Glu Glu Gly Lys Glu Arg His Thr Leu Ser Arg	
192 197 202 207	
cgc cgt gtc atc ccg ctg ccc cag tgg aag gcc aac ccg gag acg gac	851
Arg Arg Val Ile Pro Leu Pro Gln Trp Lys Ala Asn Pro Glu Thr Asp	
208 213 218 223	
cct gag gcc ttg ttc cag aag gag cag ctc gtg ctg gcc ctg tat ccc	899
Pro Glu Ala Leu Phe Gln Lys Glu Gln Leu Val Leu Ala Leu Tyr Pro	
224 229 234 239	
cag act acc tgc ttc tac cgc gcc ctg atc cat gcg ccc cca cag cgg	947
Gln Thr Thr Cys Phe Tyr Arg Ala Leu Ile His Ala Pro Pro Gln Arg	
240 245 250 255	
ccc cag gat gac tac tcg gtc ctg ttt gaa gac acc tcc tat gca gat	995

Pro Gln Asp Asp Tyr Ser Val Leu Phe Glu Asp Thr Ser Tyr Ala Asp
 256 261 266 271

ggc tat tcc cct ccc ctc aat gtg gct cag aga tac gtg gtg gct tgt 1043
 Gly Tyr Ser Pro Pro Leu Asn Val Ala Gln Arg Tyr Val Val Ala Cys
 272 277 282 287

aag gaa ccc aag aaa aag tga tg ccgcctggca gactcgccat cccccaacga 1096
 Lys Glu Pro Lys Lys Lys *
 288 293

cacagggcag gacagcagag gacgtgctgg gattaaacac attccccctc taaaaaaaaa 1156

aaa 1159

<210> 57
 <211> 6260
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (192) ..(5339)

<400> 57
 atgtaccgct ccggaattcc cgggtcgacg atttcgtaga atatggccgc cgggtgtggt 60
 gagggcgacg cgcttgcaagt cgcgtctct tgcttccccg tcctctgaca tcgcttgacg 120
 ccgagcgggc ccgttccgcc ggagctgagg accaggtatt caaataaagt taattgcagc 180
 tttctgtgaa a atg tca gtt ttg ata tca cag agc gtc ata aat tat gta 230
 Met Ser Val Leu Ile Ser Gln Ser Val Ile Asn Tyr Val
 1 5 10

gag gaa gaa aac att cct gct ctg aaa gct ctt ctt gaa aaa tgc aaa 278
 Glu Glu Glu Asn Ile Pro Ala Leu Lys Ala Leu Leu Glu Lys Cys Lys
 14 19 24 29

gat gta gat gag aga aat gag tgt ggc cag act cca ctg atg ata gct 326
 Asp Val Asp Glu Arg Asn Glu Cys Gly Gln Thr Pro Leu Met Ile Ala
 30 35 40 45

gcc gaa caa ggc aat ctg gaa ata gtg aag gaa tta att aag aat gga 374
 Ala Glu Gln Gly Asn Leu Glu Ile Val Lys Glu Leu Ile Lys Asn Gly
 46 51 56 61

gct aac tgc aat ctg gaa gat ttg gat aat tgg aca gca ctt ata tct 422
 Ala Asn Cys Asn Leu Glu Asp Leu Asp Asn Trp Thr Ala Leu Ile Ser
 62 67 72 77

gca tcg aaa gaa ggg cat gtg cac atc gta gag gaa cta ctg aaa tgt 470
 Ala Ser Lys Glu Gly His Val His Ile Val Glu Glu Leu Leu Lys Cys
 78 83 88 93

ggg gtt aac ttg gag cac cgt gat atg gga gga tgg aca gct ctt atg	518
Gly Val Asn Leu Glu His Arg Asp Met Gly Gly Trp Thr Ala Leu Met	
94 99 104 109	
tggt gca tgt tac aaa ggc cgt act gac gta gta gag ttg ctt ctt tct	566
Trp Ala Cys Tyr Lys Gly Arg Thr Asp Val Val Glu Leu Leu Leu Ser	
110 115 120 125	
cat ggt gcc aat cca agt gtc act ggt ctg cag tac agt gtt tac cca	614
His Gly Ala Asn Pro Ser Val Thr Gly Leu Gln Tyr Ser Val Tyr Pro	
126 131 136 141	
atc att tgg gca gca ggg aga ggc cat gca gat ata gtt cat ctt tta	662
Ile Ile Trp Ala Ala Gly Arg Gly His Ala Asp Ile Val His Leu Leu	
142 147 152 157	
ctg caa aat ggt gct aaa gtc aac tgc tct gat aag tat gga acc acc	710
Leu Gln Asn Gly Ala Lys Val Asn Cys Ser Asp Lys Tyr Gly Thr Thr	
158 163 168 173	
cct tta gtt tgg gct gca cga aag ggt cat ttg gaa tgt gtg aaa cat	758
Pro Leu Val Trp Ala Ala Arg Lys Gly His Leu Glu Cys Val Lys His	
174 179 184 189	
tta ttg gcc atg gga gct gat gtg gat caa gaa gga gct aat tca atg	806
Leu Leu Ala Met Gly Ala Asp Val Asp Gln Glu Gly Ala Asn Ser Met	
190 195 200 205	
act gca ctt att gtg gca gtg aaa gga ggt tac aca cag tca gta aaa	854
Thr Ala Leu Ile Val Ala Val Lys Gly Gly Tyr Thr Gln Ser Val Lys	
206 211 216 221	
gaa att ttg aag agg aat cca aat gta aac tta aca gat aaa gat gga	902
Glu Ile Leu Lys Arg Asn Pro Asn Val Asn Leu Thr Asp Lys Asp Gly	
222 227 232 237	
aat aca gct ttg atg att gca tca aag gag gga cat acg gag att gtg	950
Asn Thr Ala Leu Met Ile Ala Ser Lys Glu Gly His Thr Glu Ile Val	
238 243 248 253	
cag gat ctg ctc gac gct gga aca tat gtg aac ata cct gac agg agt	998
Gln Asp Leu Leu Asp Ala Gly Thr Tyr Val Asn Ile Pro Asp Arg Ser	
254 259 264 269	
ggg gat act gtg ttg att ggc gct gtc aga ggt ggt cat gtt gaa att	1046
Gly Asp Thr Val Leu Ile Gly Ala Val Arg Gly Gly His Val Glu Ile	
270 275 280 285	
gtt cga gcg ctt ctc caa aaa tat gct gat ata gac att aga gga cag	1094
Val Arg Ala Leu Leu Gln Lys Tyr Ala Asp Ile Asp Ile Arg Gly Gln	
286 291 296 301	
gat aat aaa act gct ttg tat tgg gct gtt gag aaa gga aat gca aca	1142
Asp Asn Lys Thr Ala Leu Tyr Trp Ala Val Glu Lys Gly Asn Ala Thr	
302 307 312 317	

atg gtg aga gat atc tta cag tgc aat cct gac act gaa ata tgc aca	1190
Met Val Arg Asp Ile Leu Gln Cys Asn Pro Asp Thr Glu Ile Cys Thr	
318 323 328 333	
aag gat ggt gaa acg cca ctt ata aag gct acc aag atg aga aac att	1238
Lys Asp Gly Glu Thr Pro Leu Ile Lys Ala Thr Lys Met Arg Asn Ile	
334 339 344 349	
gaa gtg gtg gag ctg ctg cta gat aaa ggt gct aaa gtg tct gct gta	1286
Glu Val Val Glu Leu Leu Leu Asp Lys Gly Ala Lys Val Ser Ala Val	
350 355 360 365	
gat aag aaa gga gat act ccc ttg cat att gct att cgt gga agg agc	1334
Asp Lys Lys Gly Asp Thr Pro Leu His Ile Ala Ile Arg Gly Arg Ser	
366 371 376 381	
cgg aaa ctg gca gaa ctg ctt tta aga aat ccc aaa gat ggg cga tta	1382
Arg Lys Leu Ala Glu Leu Leu Leu Arg Asn Pro Lys Asp Gly Arg Leu	
382 387 392 397	
ctt tat agg ccc aac aaa gca ggc gag act cct tat aat att gac tgt	1430
Leu Tyr Arg Pro Asn Lys Ala Gly Glu Thr Pro Tyr Asn Ile Asp Cys	
398 403 408 413	
agc cat cag aag agt att tta act caa ata ttt gga gcc aga cac ttg	1478
Ser His Gln Lys Ser Ile Leu Thr Gln Ile Phe Gly Ala Arg His Leu	
414 419 424 429	
tct cct act gaa aca gac ggt gac atg ctt gga tat gat tta tat agc	1526
Ser Pro Thr Glu Thr Asp Gly Asp Met Leu Gly Tyr Asp Leu Tyr Ser	
430 435 440 445	
agt gcc ctg gca gat att ctc agt gag cct acc atg cag cca ccc att	1574
Ser Ala Leu Ala Asp Ile Leu Ser Glu Pro Thr Met Gln Pro Pro Ile	
446 451 456 461	
tgt gtg ggg tta tat gca cag tgg gga agt ggg aaa tct ttc tta ctc	1622
Cys Val Gly Leu Tyr Ala Gln Trp Gly Ser Gly Lys Ser Phe Leu Leu	
462 467 472 477	
aag aaa cta gaa gac gaa atg aaa acc ttc gcc gga caa cag att gag	1670
Lys Lys Leu Glu Asp Glu Met Lys Thr Phe Ala Gly Gln Gln Ile Glu	
478 483 488 493	
cct ctc ttt cag ttc tca tgg ctc ata gtg ttt ctt acc ctg cta ctt	1718
Pro Leu Phe Gln Phe Ser Trp Leu Ile Val Phe Leu Thr Leu Leu Leu	
494 499 504 509	
tgt gga ggg ctt ggt tta ttg ttt gcc ttc acg gtc cac cca aat ctt	1766
Cys Gly Gly Leu Gly Leu Leu Phe Ala Phe Thr Val His Pro Asn Leu	
510 515 520 525	
gga ata gca gtg tca ctg agc ttc ttg gct ctc tta tat ata ttc ttt	1814
Gly Ile Ala Val Ser Leu Ser Phe Leu Ala Leu Leu Tyr Ile Phe Phe	
526 531 536 541	
att gtc att tac ttt ggt gga cga aga gaa gga gag agt tgg aat tgg	1862

Ile Val Ile Tyr Phe	Gly Gly Arg Arg Glu	Gly Glu Ser Trp Asn Trp	
542	547	552	557
gcc tgg gtc ctc agc act aga ttg gca aga cat att gga tat ttg gaa			1910
Ala Trp Val Leu Ser Thr Arg Leu Ala Arg His Ile Gly Tyr Leu Glu			
558	563	568	573
ctc ctc ctt aaa ttg atg ttt gtg aat cca cct gag ttg cca gag cag			1958
Leu Leu Leu Lys Leu Met Phe Val Asn Pro Pro Glu Leu Pro Glu Gln			
574	579	584	589
act act aaa gct tta cct gtg agg ttt ttg ttt aca gat tac aat aga			2006
Thr Thr Lys Ala Leu Pro Val Arg Phe Leu Phe Thr Asp Tyr Asn Arg			
590	595	600	605
ctg tcc agt gta ggt gga gaa act tct ctg gct gaa atg att gca acc			2054
Leu Ser Ser Val Gly Gly Glu Thr Ser Leu Ala Glu Met Ile Ala Thr			
606	611	616	621
ctc tcg gat gct tgt gaa aga gag ttt ggc ttt ttg gca acc agg ctt			2102
Leu Ser Asp Ala Cys Glu Arg Glu Phe Gly Phe Leu Ala Thr Arg Leu			
622	627	632	637
ttt cga gta ttc aag act gaa gat act cag ggt aaa aag aaa tgg aaa			2150
Phe Arg Val Phe Lys Thr Glu Asp Thr Gln Gly Lys Lys Lys Trp Lys			
638	643	648	653
aaa aca tgt tgt ctc cca tct ttt gtc atc ttc ctt ttt atc att ggc			2198
Lys Thr Cys Cys Leu Pro Ser Phe Val Ile Phe Leu Phe Ile Ile Gly			
654	659	664	669
tgc att ata tct gga att act ctt ctg gct ata ttt aga gtt gac cca			2246
Cys Ile Ile Ser Gly Ile Thr Leu Leu Ala Ile Phe Arg Val Asp Pro			
670	675	680	685
aag cat ctg act gta aat gct gtc ctc ata tca atc gca tct gta gtg			2294
Lys His Leu Thr Val Asn Ala Val Leu Ile Ser Ile Ala Ser Val Val			
686	691	696	701
gga ttg gcc ttt gtg ttg aac tgt cgt aca tgg tgg caa gtg ctg gac			2342
Gly Leu Ala Phe Val Leu Asn Cys Arg Thr Trp Trp Gln Val Leu Asp			
702	707	712	717
tcg ctc ctg aat tcc caa aga aaa cgc ctc cat aat gca gcc tcc aaa			2390
Ser Leu Leu Asn Ser Gln Arg Lys Arg Leu His Asn Ala Ala Ser Lys			
718	723	728	733
ctg cac aaa ttg aaa agt gaa gga ttc atg aaa gtt ctt aaa tgt gaa			2438
Leu His Lys Leu Lys Ser Glu Gly Phe Met Lys Val Leu Lys Cys Glu			
734	739	744	749
gtg gaa ttg atg gcc agg atg gca aaa acc att gac agc ttc act cag			2486
Val Glu Leu Met Ala Arg Met Ala Lys Thr Ile Asp Ser Phe Thr Gln			
750	755	760	765
aat cag aca agg ctg gtg gtc atc atc gat gga tta gat gcc tgt gag			2534
Asn Gln Thr Arg Leu Val Val Ile Ile Asp Gly Leu Asp Ala Cys Glu			

766	771	776	781	
cag gac aaa gtc ctt	cag atg ctg gac act	gtc cga gtt ctg ttt tca		2582
Gln Asp Lys Val Leu	Gln Met Leu Asp Thr	Val Arg Val Leu Phe Ser		
782	787	792	797	
aaa ggc ccg ttc att	gcc att ttt gca agt	gat cca cat att atc ata		2630
Lys Gly Pro Phe Ile	Ala Ile Phe Ala Ser	Asp Pro His Ile Ile Ile		
798	803	808	813	
aag gca att aac cag	aac ctc aat agt gtg	ctt cgg gat tca aat ata		2678
Lys Ala Ile Asn Gln	Asn Leu Asn Ser Val	Leu Arg Asp Ser Asn Ile		
814	819	824	829	
aat ggc cat gac tac	atg cgc aac ata gtc	cac ttg cct gtg ttc ctt		2726
Asn Gly His Asp Tyr	Met Arg Asn Ile Val	His Leu Pro Val Phe Leu		
830	835	840	845	
aat agt cgt gga cta	agc aat gca aga aaa	ttt ctc gta act tca gca		2774
Asn Ser Arg Gly Leu	Ser Asn Ala Arg Lys	Phe Leu Val Thr Ser Ala		
846	851	856	861	
aca aat gga gac gtt	cca tgc tca gat act	aca ggg ata cag gaa gat		2822
Thr Asn Gly Asp Val	Pro Cys Ser Asp Thr	Thr Gly Ile Gln Glu Asp		
862	867	872	877	
gct gac aga aga gtt	tca cag aac agc ctt	ggg gag atg aca aaa ctt		2870
Ala Asp Arg Arg Val	Ser Gln Asn Ser Leu	Gly Glu Met Thr Lys Leu		
878	883	888	893	
ggc agc aag aca gcc	ctc aat aga cgg gac	act tac cga aga agg cag		2918
Gly Ser Lys Thr Ala	Leu Asn Arg Arg Asp	Thr Tyr Arg Arg Arg Gln		
894	899	904	909	
atg cag agg acc atc	act cgc cag atg tcc	ttt gat ctt aca aaa ctg		2966
Met Gln Arg Thr Ile	Thr Arg Gln Met Ser	Phe Asp Leu Thr Lys Leu		
910	915	920	925	
ctg gtt acc gag gac	tgg ttc agt gac atc	agt ccc cag acc atg aga		3014
Leu Val Thr Glu Asp	Trp Phe Ser Asp Ile	Ser Pro Gln Thr Met Arg		
926	931	936	941	
aga tta ctt aat att	gtt tct gtg aca gga	cga tta ctg aga gcc aat		3062
Arg Leu Leu Asn Ile	Val Ser Val Thr Gly	Arg Leu Leu Arg Ala Asn		
942	947	952	957	
cag att agt ttc aac	tgg gac agg ctt gct	agc tgg atc aac ctt act		3110
Gln Ile Ser Phe Asn	Trp Asp Arg Leu Ala	Ser Trp Ile Asn Leu Thr		
958	963	968	973	
gag cag tgg cca tac	cgg act tca tgg ctc	ata tta tat ttg gaa gag		3158
Glu Gln Trp Pro Tyr	Arg Thr Ser Trp Leu	Ile Leu Tyr Leu Glu Glu		
974	979	984	989	
act gaa ggt att cca	gat caa atg aca tta	aaa acc atc tac gaa aga		3206
Thr Glu Gly Ile Pro	Asp Gln Met Thr Leu	Lys Thr Ile Tyr Glu Arg		
990	995	1000	1005	

ata tca aag aat att cca aca act aag gat gtt gag cca ctt ctt gaa	3254
Ile Ser Lys Asn Ile Pro Thr Thr Lys Asp Val Glu Pro Leu Leu Glu	
1006 1011 1016 1021	
att gat gga gat ata aga aat ttt gaa gtg ttt ttg tct tca agg acc	3302
Ile Asp Gly Asp Ile Arg Asn Phe Glu Val Phe Leu Ser Ser Arg Thr	
1022 1027 1032 1037	
cca gtt ctt gtg gct cga gat gta aaa gtc ttt ttg cca tgc act gta	3350
Pro Val Leu Val Ala Arg Asp Val Lys Val Phe Leu Pro Cys Thr Val	
1038 1043 1048 1053	
aac cta gat ccc aaa cta cgg gaa att att gca gat gtt cgt gct gcc	3398
Asn Leu Asp Pro Lys Leu Arg Glu Ile Ile Ala Asp Val Arg Ala Ala	
1054 1059 1064 1069	
aga gag cag atc agt att gga gga ctg gcg tac ccc ccg ctc cct cta	3446
Arg Glu Gln Ile Ser Ile Gly Gly Leu Ala Tyr Pro Pro Leu Pro Leu	
1070 1075 1080 1085	
cat gag ggt cct cct agg gcg cca tca ggg tac agc cag ccc cca tcc	3494
His Glu Gly Pro Pro Arg Ala Pro Ser Gly Tyr Ser Gln Pro Pro Ser	
1086 1091 1096 1101	
gtg tgc tct tcc acg tcc ttc aat ggg ccc ttc gca ggt gga gtg gtg	3542
Val Cys Ser Ser Thr Ser Phe Asn Gly Pro Phe Ala Gly Gly Val Val	
1102 1107 1112 1117	
tca cca cag cct cac agc agc tat tac agc ggc atg acg ggc cct cag	3590
Ser Pro Gln Pro His Ser Ser Tyr Tyr Ser Gly Met Thr Gly Pro Gln	
1118 1123 1128 1133	
cat ccc ttc tac aac agg ggg tca ggc cca gcc cca ggc cca gtg gta	3638
His Pro Phe Tyr Asn Arg Gly Ser Gly Pro Ala Pro Gly Pro Val Val	
1134 1139 1144 1149	
tta ctg aat tca ctg aat gtg gat gca gta tgt gag aag ctg aaa caa	3686
Leu Leu Asn Ser Leu Asn Val Asp Ala Val Cys Glu Lys Leu Lys Gln	
1150 1155 1160 1165	
ata gaa ggg ctg gac cag agt atg ctg cct cag tat tgt acc acg atc	3734
Ile Glu Gly Leu Asp Gln Ser Met Leu Pro Gln Tyr Cys Thr Thr Ile	
1166 1171 1176 1181	
aaa aag gca aac ata aat ggc cgt gtg tta gct cag tgt aac att gat	3782
Lys Lys Ala Asn Ile Asn Gly Arg Val Leu Ala Gln Cys Asn Ile Asp	
1182 1187 1192 1197	
gag ctg aag aaa gag atg aat atg aat ttt gga gac tgg cac ctt ttc	3830
Glu Leu Lys Lys Glu Met Asn Met Asn Phe Gly Asp Trp His Leu Phe	
1198 1203 1208 1213	
aga agc aca gta cta gaa atg aga aac gca gaa agc cac gtg gtc cct	3878
Arg Ser Thr Val Leu Glu Met Arg Asn Ala Glu Ser His Val Val Pro	
1214 1219 1224 1229	

gaa gac cca cgt ttc ctc agt gag agc agc agt ggc cca gcc ccg cac	3926
Glu Asp Pro Arg Phe Leu Ser Glu Ser Ser Ser Gly Pro Ala Pro His	
1230 1235 1240 1245	
ggt gag cct gct cgc cgc gct tcc cac aac gag ctg cct cac acc gag	3974
Gly Glu Pro Ala Arg Arg Ala Ser His Asn Glu Leu Pro His Thr Glu	
1246 1251 1256 1261	
ctc tcc agc cag acg ccc tac aca ctc aac ttc agc ttc gaa gag ctg	4022
Leu Ser Ser Gln Thr Pro Tyr Thr Leu Asn Phe Ser Phe Glu Glu Leu	
1262 1267 1272 1277	
aac acg ctt ggc ctg gat gaa ggt gcc cct cgt cac agt aat cta agt	4070
Asn Thr Leu Gly Leu Asp Glu Gly Ala Pro Arg His Ser Asn Leu Ser	
1278 1283 1288 1293	
tgg cag tca caa act cgc aga acc cca agt ctt tcg agt ctc aat tcc	4118
Trp Gln Ser Gln Thr Arg Arg Thr Pro Ser Leu Ser Ser Leu Asn Ser	
1294 1299 1304 1309	
cag gat tcc agt att gaa att tca aag ctt act gat aag gtg cag gcc	4166
Gln Asp Ser Ser Ile Glu Ile Ser Lys Leu Thr Asp Lys Val Gln Ala	
1310 1315 1320 1325	
gag tat aga gat gcc tat aga gaa tac att gct cag atg tcc cag tta	4214
Glu Tyr Arg Asp Ala Tyr Arg Glu Tyr Ile Ala Gln Met Ser Gln Leu	
1326 1331 1336 1341	
gaa ggg ggc ccc ggg tct aca acc att agt ggc aga tct tct cca cat	4262
Glu Gly Gly Pro Gly Ser Thr Thr Ile Ser Gly Arg Ser Ser Pro His	
1342 1347 1352 1357	
agc aca tat tac atg ggt cag agt tca tca ggg ggc tct att cat tca	4310
Ser Thr Tyr Tyr Met Gly Gln Ser Ser Ser Gly Gly Ser Ile His Ser	
1358 1363 1368 1373	
aac cta gag caa gaa aag ggg aag gat agt gaa cca aag ccc gat gat	4358
Asn Leu Glu Gln Glu Lys Gly Lys Asp Ser Glu Pro Lys Pro Asp Asp	
1374 1379 1384 1389	
ggg agg aag tcc ttt cta atg aag agg gga gat gtt atc gat tat tca	4406
Gly Arg Lys Ser Phe Leu Met Lys Arg Gly Asp Val Ile Asp Tyr Ser	
1390 1395 1400 1405	
tca tca ggg gtt tcc acc aac gat gct tcc ccc ctg gat cct atc act	4454
Ser Ser Gly Val Ser Thr Asn Asp Ala Ser Pro Leu Asp Pro Ile Thr	
1406 1411 1416 1421	
gaa gaa gat gaa aaa tca gat cag tca ggc agt aag ctt ctc cca ggc	4502
Glu Glu Asp Glu Lys Ser Asp Gln Ser Gly Ser Lys Leu Leu Pro Gly	
1422 1427 1432 1437	
aag aaa tct tcc gaa agg tca agc ctc ttc cag aca gat ttg aag ctt	4550
Lys Lys Ser Ser Glu Arg Ser Ser Leu Phe Gln Thr Asp Leu Lys Leu	
1438 1443 1448 1453	
aag gga agt ggg ctg cgc tat caa aaa ctc cca agt gac gag gat gaa	4598

Lys Gly Ser Gly Leu Arg Tyr Gln Lys Leu Pro Ser Asp Glu Asp Glu	
1454 1459 1464 1469	
tct ggc aca gaa gaa tca gat aac act cca ctg ctc aaa gat gac aaa	4646
Ser Gly Thr Glu Glu Ser Asp Asn Thr Pro Leu Leu Lys Asp Asp Lys	
1470 1475 1480 1485	
gac aga aaa gcc gaa ggg aaa gta gag aga gtg ccg aag tct cca gaa	4694
Asp Arg Lys Ala Glu Gly Lys Val Glu Arg Val Pro Lys Ser Pro Glu	
1486 1491 1496 1501	
cac agt gct gag ccg atc aga acc ttc att aaa gcc aaa gag tat tta	4742
His Ser Ala Glu Pro Ile Arg Thr Phe Ile Lys Ala Lys Glu Tyr Leu	
1502 1507 1512 1517	
tcg gat gcg ctc ctt gac aaa aag gat tca tcg gat tca gga gtg aga	4790
Ser Asp Ala Leu Leu Asp Lys Lys Asp Ser Ser Asp Ser Gly Val Arg	
1518 1523 1528 1533	
tcc agt gaa agt tct ccc aat cac tct ctg cac aat gaa gtg gcg gat	4838
Ser Ser Glu Ser Ser Pro Asn His Ser Leu His Asn Glu Val Ala Asp	
1534 1539 1544 1549	
gac tcc cag ctt gaa aag gca aat ctc ata gag ctg gaa gat gac agt	4886
Asp Ser Gln Leu Glu Lys Ala Asn Leu Ile Glu Leu Glu Asp Asp Ser	
1550 1555 1560 1565	
cac agc gga aag cgg gga atc cca cat agc ctg agt ggc ctg caa gat	4934
His Ser Gly Lys Arg Gly Ile Pro His Ser Leu Ser Gly Leu Gln Asp	
1566 1571 1576 1581	
cca att ata gct cgg atg tcc att tgt tca gaa gac aag aaa agc cct	4982
Pro Ile Ile Ala Arg Met Ser Ile Cys Ser Glu Asp Lys Lys Ser Pro	
1582 1587 1592 1597	
tcc gaa tgc agc ttg ata gcc agc agc cct gaa gaa aac tgg cct gca	5030
Ser Glu Cys Ser Leu Ile Ala Ser Ser Pro Glu Glu Asn Trp Pro Ala	
1598 1603 1608 1613	
tgc cag aaa gcc tac aac ctg aac cga act ccc agc acc gtg act ctg	5078
Cys Gln Lys Ala Tyr Asn Leu Asn Arg Thr Pro Ser Thr Val Thr Leu	
1614 1619 1624 1629	
aac aac aat agt gct cca gcc aac aga gcc aat caa aat ttc gat gag	5126
Asn Asn Asn Ser Ala Pro Ala Asn Arg Ala Asn Gln Asn Phe Asp Glu	
1630 1635 1640 1645	
atg gag gga att agg gag act tct caa gtc att ttg agg cct agt tcc	5174
Met Glu Gly Ile Arg Glu Thr Ser Gln Val Ile Leu Arg Pro Ser Ser	
1646 1651 1656 1661	
agt ccc aac cca acc act att cag aat gag aat cta aaa agc atg aca	5222
Ser Pro Asn Pro Thr Thr Ile Gln Asn Glu Asn Leu Lys Ser Met Thr	
1662 1667 1672 1677	
cat aag cga agc caa cgt tca agt tac aca agg ctc tcc aaa gat cct	5270
His Lys Arg Ser Gln Arg Ser Ser Tyr Thr Arg Leu Ser Lys Asp Pro	

1678	1683	1688	1693	
ccg gag ctc cat gca gca gcc tct tct gag agc aca ggc ttt gga gaa				5318
Pro Glu Leu His Ala Ala Ala Ser Ser Glu Ser Thr Gly Phe Gly Glu				
1694	1699	1704	1709	
gaa aga gaa agc att ctt tga ga aaaacaagca aaggagaaga gtgttactgt				5371
Glu Arg Glu Ser Ile Leu *				
1710	1715			
acccttatga cagaattgtc ctggattttg actccatcca cgcccatcac ctttctacat				5431
tttgctgaca gataactaac cgatgatgag gccgaggtaa aagagacatc tgcagtgtga				5491
cagaagggag catgagaagc atggctcacc agccagcctc tgtggtcttt gtaattagaa				5551
gcttcagaac tcactaatac tactgtacct ttcatggcg cattacccca taaaactttt				5611
tgagacgagg tgagatctga gtataaagat aggtcagaag tatttttaaag ggcttaatgt				5671
gccaaaaaga aaaaaagcta gagacccttt ttgcaaacat ttggtgacca cacatttgag				5731
ggaagacgtg gcgttaggtg aagcagaagc aaacctgct cttaggggct cacctaggtg				5791
agtgcacagc ctgtgacgct acagggagag gctgagtaaa ccgagatcca gcgttctgta				5851
tggcaggggt attgcttatc acagaggttc tgaagagtag gaagtacata atgaagaggg				5911
ctttaaaaat tgccaacaaa gtgagtcacc agggctggca gtagtgtgac ggggctgtcc				5971
tgagctgtta ggagagtaga tgcggggagg gctggtgacc tccgtgggtt tatatgtcgg				6031
aaactcttct ctccaaatcc caggcctggc ttccagcacc atccagctgt gcccaagaag				6091
ccacctggt ctgttctcca actcttttaa atggtgocca acttttctaa gtgagcttag				6151
caatgagcag aaaaaaaaaac atgaattctt tttctggaaa atcagggaga catgggtaat				6211
aataggtact aataaatatt tatagatgag tgaatgagga aataattac				6260

<210> 58
 <211> 3116
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (522) .. (3116)

<400> 58	
tacgctgcg cgaccggtcc ggaattcccg ggtcgaccca cgcgtcogaa cccaatccac	60
cttactacca gacaacctta tccgaacctt ttacccaaat aaagcatagg cgatagaaat	120

tgaaacctgg cgcaatagat ataggaccgc aagggataga tgaaaaaag ttgcctgtga 180
 aggagcgaat aatgatccag atgagtctat gagttctaga atttcaaaca cggaagatc 240
 tcataaggat gctcacacag ttgaagaaga gtctctgacc ttatcaaggg aggatgcaga 300
 gcaggttgca ttataagtag acctaaatca aaagaaaaga aggaggaaga agcaagatgg 360
 agctaataaa ctgggagtaa acaatctttt agaaaatgcc actgttcagg cgggtccttc 420
 taaaggagaa aaacacaaga ataaatgtca ggctataagg cctgagctaa aggaaggtga 480
 atgcagtaag gagcagatgc tttcctgcac acaaaacata g atg gca ttg tgg 533
 Met Ala Leu Trp

1

gtt ttg ccg tcc act gaa aaa gtt gag agg aga act gac ccc atc ctt 581
 Val Leu Pro Ser Thr Glu Lys Val Glu Arg Arg Thr Asp Pro Ile Leu
 5 10 15 20

tca tta agt aat caa caa gat gcc aca tca gta gca act gag tct tca 629
 Ser Leu Ser Asn Gln Gln Asp Ala Thr Ser Val Ala Thr Glu Ser Ser
 21 26 31 36

gaa tca agc act tca gat ttg cct tca ttc gaa gtt gga att aga gca 677
 Glu Ser Ser Thr Ser Asp Leu Pro Ser Phe Glu Val Gly Ile Arg Ala
 37 42 47 52

ttg tgt gag gtg aat aat gct gag ggt agt tgt ata gaa gaa aga aat 725
 Leu Cys Glu Val Asn Asn Ala Glu Gly Ser Cys Ile Glu Glu Arg Asn
 53 58 63 68

gtt gac cta aaa aat aat tca ctg gaa att gat caa aca gaa aat gtt 773
 Val Asp Leu Lys Asn Asn Ser Leu Glu Ile Asp Gln Thr Glu Asn Val
 69 74 79 84

aaa cca atg ttg aga ggt cgc ttc caa aga cct aaa ccc aat ttg tca 821
 Lys Pro Met Leu Arg Gly Arg Phe Gln Arg Pro Lys Pro Asn Leu Ser
 85 90 95 100

agg gct ggg aag aaa tca gtt ctt tca caa ggc aaa aca gag tca gag 869
 Arg Ala Gly Lys Lys Ser Val Leu Ser Gln Gly Lys Thr Glu Ser Glu
 101 106 111 116

agc aag aat tca cat tca aaa act tca gtt gaa aag aac cac gtg gaa 917
 Ser Lys Asn Ser His Ser Lys Thr Ser Val Glu Lys Asn His Val Glu
 117 122 127 132

aaa gat aaa atg aat aca ttg gac att ttg aga atg gag act aca gag 965
 Lys Asp Lys Met Asn Thr Leu Asp Ile Leu Arg Met Glu Thr Thr Glu
 133 138 143 148

aga gag aat cca gaa gct gaa act gta tct gtt ttg ggt gaa aaa aat 1013
 Arg Glu Asn Pro Glu Ala Glu Thr Val Ser Val Leu Gly Glu Lys Asn
 149 154 159 164

tgt ctg cag gaa ggg agt caa cta aag gct tta aga cct gta caa gtg 1061

Cys	Leu	Gln	Glu	Gly	Ser	Gln	Leu	Lys	Ala	Leu	Arg	Pro	Val	Gln	Val	
165					170					175					180	
agg	ggc	cga	ttg	caa	aag	cca	aag	cca	aat	gca	ggg	aaa	gct	gct	gaa	1109
Arg	Gly	Arg	Leu	Gln	Lys	Pro	Lys	Pro	Asn	Ala	Gly	Lys	Ala	Ala	Glu	
181					186					191					196	
aga	aaa	gaa	att	ctc	ata	tca	cag	gaa	gaa	att	ggg	gcc	aat	gta	gag	1157
Arg	Lys	Glu	Ile	Leu	Ile	Ser	Gln	Glu	Glu	Ile	Gly	Ala	Asn	Val	Glu	
197					202					207					212	
aag	aat	gaa	aat	gaa	tcc	tgt	gct	gat	aga	gat	act	cct	caa	cac	atg	1205
Lys	Asn	Glu	Asn	Glu	Ser	Cys	Ala	Asp	Arg	Asp	Thr	Pro	Gln	His	Met	
213					218					223					228	
gaa	gat	caa	tcg	cgt	aaa	gat	ttt	gaa	gag	gaa	gat	gtc	ata	tta	cag	1253
Glu	Asp	Gln	Ser	Arg	Lys	Asp	Phe	Glu	Glu	Glu	Asp	Val	Ile	Leu	Gln	
229					234					239					244	
cct	gag	aaa	aat	gat	tct	ttt	caa	aat	gtg	cag	cca	gat	gag	ccc	aag	1301
Pro	Glu	Lys	Asn	Asp	Ser	Phe	Gln	Asn	Val	Gln	Pro	Asp	Glu	Pro	Lys	
245					250					255					260	
gtt	ctt	aat	gaa	tgt	cta	agc	gtt	caa	gag	aat	aat	aag	gca	aat	aaa	1349
Val	Leu	Asn	Glu	Cys	Leu	Ser	Val	Gln	Glu	Asn	Asn	Lys	Ala	Asn	Lys	
261					266					271					276	
ctt	aac	caa	gtc	cca	att	cta	agg	act	cga	ttt	cag	aaa	cca	aag	cca	1397
Leu	Asn	Gln	Val	Pro	Ile	Leu	Arg	Thr	Arg	Phe	Gln	Lys	Pro	Lys	Pro	
277					282					287					292	
aat	ata	gga	aga	gga	act	gga	agg	agt	gaa	att	tcc	tca	aag	gaa	gag	1445
Asn	Ile	Gly	Arg	Gly	Thr	Gly	Arg	Ser	Glu	Ile	Ser	Ser	Lys	Glu	Glu	
293					298					303					308	
gta	cta	gag	aag	att	ctt	gtc	tct	ggg	gaa	atg	gcg	gca	gca	ttg	aga	1493
Val	Leu	Glu	Lys	Ile	Leu	Val	Ser	Gly	Glu	Met	Ala	Ala	Ala	Leu	Arg	
309					314					319					324	
gaa	act	gta	aga	ctg	gac	acc	tca	cca	aag	gag	atg	gta	cca	gca	gag	1541
Glu	Thr	Val	Arg	Leu	Asp	Thr	Ser	Pro	Lys	Glu	Met	Val	Pro	Ala	Glu	
325					330					335					340	
att	aat	act	aaa	gaa	atg	cag	tca	gat	tta	aaa	gaa	act	gga	aga	aga	1589
Ile	Asn	Thr	Lys	Glu	Met	Gln	Ser	Asp	Leu	Lys	Glu	Thr	Gly	Arg	Arg	
341					346					351					356	
gcc	att	tct	ccc	agg	gag	aag	att	cta	gat	gtg	att	gat	gac	acc	ata	1637
Ala	Ile	Ser	Pro	Arg	Glu	Lys	Ile	Leu	Asp	Val	Ile	Asp	Asp	Thr	Ile	
357					362					367					372	
gaa	atg	gag	aca	ggg	ctg	aaa	gca	atg	gga	aga	gag	att	tgt	cta	agg	1685
Glu	Met	Glu	Thr	Gly	Leu	Lys	Ala	Met	Gly	Arg	Glu	Ile	Cys	Leu	Arg	
373					378					383					388	
gag	aag	acg	cca	gag	gtg	att	gat	gcc	act	gag	gaa	ata	gac	aaa	gat	1733
Glu	Lys	Thr	Pro	Glu	Val	Ile	Asp	Ala	Thr	Glu	Glu	Ile	Asp	Lys	Asp	

389	394	399	404	
ttg gaa gaa gct gga aga aga gaa ata tcc cca cag aaa aat ggc cca				1781
Leu Glu Glu Ala Gly Arg Arg Glu Ile Ser Pro Gln Lys Asn Gly Pro				
405	410	415	420	
gag gag gtt aag cct cta ggt gaa gtg gag aca gat ttg aaa gca act				1829
Glu Glu Val Lys Pro Leu Gly Glu Val Glu Thr Asp Leu Lys Ala Thr				
421	426	431	436	
gga aat gag agt tcc cca agg gag aag aca cca gag gtg act gat gcc				1877
Gly Asn Glu Ser Ser Pro Arg Glu Lys Thr Pro Glu Val Thr Asp Ala				
437	442	447	452	
act gag gaa ata gac aaa aat ttg gaa gaa act gga aga aga aaa ata				1925
Thr Glu Glu Ile Asp Lys Asn Leu Glu Glu Thr Gly Arg Arg Lys Ile				
453	458	463	468	
tcc cca agg gaa aat ggc cca gag gag gtc aag cct gta gat gaa atg				1973
Ser Pro Arg Glu Asn Gly Pro Glu Glu Val Lys Pro Val Asp Glu Met				
469	474	479	484	
gag aca gat ttg aac gca act gga aga gag agt tct cca agg gag aag				2021
Glu Thr Asp Leu Asn Ala Thr Gly Arg Glu Ser Ser Pro Arg Glu Lys				
485	490	495	500	
aca cca gag gtg att gat gct act gag gaa ata gat ttg gaa gaa act				2069
Thr Pro Glu Val Ile Asp Ala Thr Glu Glu Ile Asp Leu Glu Glu Thr				
501	506	511	516	
gaa aga gaa gta tcc cca cag gaa aat gga cta gag gag gtc aag cct				2117
Glu Arg Glu Val Ser Pro Gln Glu Asn Gly Leu Glu Glu Val Lys Pro				
517	522	527	532	
cta ggt gaa atg gag acg gat ttg aaa gca act gga aga gac agt ttc				2165
Leu Gly Glu Met Glu Thr Asp Leu Lys Ala Thr Gly Arg Asp Ser Phe				
533	538	543	548	
cca agg ggg aag aca cca gag gtg att gat gcc att gag gaa ata gag				2213
Pro Arg Gly Lys Thr Pro Glu Val Ile Asp Ala Ile Glu Glu Ile Glu				
549	554	559	564	
ata gat ttg gaa gaa act gaa aga gaa ata tcc cca cag gaa aat ggc				2261
Ile Asp Leu Glu Glu Thr Glu Arg Glu Ile Ser Pro Gln Glu Asn Gly				
565	570	575	580	
cta gag gag gtt aag cct cta ggt gaa atg caa aca gat ttg aaa gca				2309
Leu Glu Glu Val Lys Pro Leu Gly Glu Met Gln Thr Asp Leu Lys Ala				
581	586	591	596	
acc gga agg gag att tcc cca agg gag aag aca cca gag gtg att gat				2357
Thr Gly Arg Glu Ile Ser Pro Arg Glu Lys Thr Pro Glu Val Ile Asp				
597	602	607	612	
gcc act gag gaa ata gac aaa gat ctg gaa gaa act gga aga aga gaa				2405
Ala Thr Glu Glu Ile Asp Lys Asp Leu Glu Glu Thr Gly Arg Arg Glu				
613	618	623	628	

ata tcc cca gag gaa aat ggc cca gag gag gtc aag cct gta gat gaa	2453
Ile Ser Pro Glu Glu Asn Gly Pro Glu Glu Val Lys Pro Val Asp Glu	
629 634 639 644	
atg gag aca gac ttg aaa aca act gga aga gag ggt tcc tca agg gag	2501
Met Glu Thr Asp Leu Lys Thr Thr Gly Arg Glu Gly Ser Ser Arg Glu	
645 650 655 660	
aag aca cga gag gtg att gat gct gct gag gta ata gag aca gat ttg	2549
Lys Thr Arg Glu Val Ile Asp Ala Ala Glu Val Ile Glu Thr Asp Leu	
661 666 671 676	
gaa gaa act gaa aga gaa ata tcg cca cag gaa aat ggc cca gag gag	2597
Glu Glu Thr Glu Arg Glu Ile Ser Pro Gln Glu Asn Gly Pro Glu Glu	
677 682 687 692	
gtc aag cct gta ggt aaa atg gag aca gat ttg aaa gaa att aga gaa	2645
Val Lys Pro Val Gly Lys Met Glu Thr Asp Leu Lys Glu Ile Arg Glu	
693 698 703 708	
gaa att tcc caa agg gaa aag gtg cta gca gag ttc agt gct ata agg	2693
Glu Ile Ser Gln Arg Glu Lys Val Leu Ala Glu Phe Ser Ala Ile Arg	
709 714 719 724	
gaa aag gag att gat ttg aaa gaa act gga aaa aga gac att ccc atg	2741
Glu Lys Glu Ile Asp Leu Lys Glu Thr Gly Lys Arg Asp Ile Pro Met	
725 730 735 740	
atg gag aaa gta tca gga aag atg gct gtt gtt gaa gaa atg gag gca	2789
Met Glu Lys Val Ser Gly Lys Met Ala Val Val Glu Glu Met Glu Ala	
741 746 751 756	
gat ttg aaa gaa act gga aaa gaa aat ttt aga gag aga gga tct gaa	2837
Asp Leu Lys Glu Thr Gly Lys Glu Asn Phe Arg Glu Arg Gly Ser Glu	
757 762 767 772	
gag atc tgt gtt act gag gaa aag gtg gca gaa ttg aaa caa act gga	2885
Glu Ile Cys Val Thr Glu Glu Lys Val Ala Glu Leu Lys Gln Thr Gly	
773 778 783 788	
aaa aca gac att tct cca agg gaa aac gag cta gag gag acc agt acc	2933
Lys Thr Asp Ile Ser Pro Arg Glu Asn Glu Leu Glu Glu Thr Ser Thr	
789 794 799 804	
tca aga caa act gac aca cat tta atg cag agc ggt agc aat gac ttc	2981
Ser Arg Gln Thr Asp Thr His Leu Met Gln Ser Gly Ser Asn Asp Phe	
805 810 815 820	
agt gct atg cct tca cta gat att cag gta tgt att ttt ctg tcc ttt	3029
Ser Ala Met Pro Ser Leu Asp Ile Gln Val Cys Ile Phe Leu Ser Phe	
821 826 831 836	
aaa agt ttt ttg aat gct ttt tca gag gaa ata aat aat tcc atg att	3077
Lys Ser Phe Leu Asn Ala Phe Ser Glu Glu Ile Asn Asn Ser Met Ile	
837 842 847 852	

att ttg tcc tta agt cca aca aca ttt aaa aat ctc taa 3116
 Ile Leu Ser Leu Ser Pro Thr Thr Phe Lys Asn Leu *
 853 858 863

<210> 59
 <211> 1380
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (57) .. (1193)

<400> 59
 ttgctgcggt ccgcccggaa tccaactcga cccacgcgtc cgggtcaacc gtcaaa 56
 atg tcc aaa gaa cct ctc att ctc tgg ctg atg att gag ttt tgg tgg 104
 Met Ser Lys Glu Pro Leu Ile Leu Trp Leu Met Ile Glu Phe Trp Trp
 1 5 10 15
 ctt tac ctg aca cca gtc act tca gag act gtt gtg acg gag gtt ttg 152
 Leu Tyr Leu Thr Pro Val Thr Ser Glu Thr Val Val Thr Glu Val Leu
 17 22 27 32
 ggt cac cgg gtg act ttg ccc tgt ctg tac tca tcc tgg tct cac aac 200
 Gly His Arg Val Thr Leu Pro Cys Leu Tyr Ser Ser Trp Ser His Asn
 33 38 43 48
 agc aac agc atg tgc tgg ggg aaa gac cag tgc ccc tac tcc ggt tgc 248
 Ser Asn Ser Met Cys Trp Gly Lys Asp Gln Cys Pro Tyr Ser Gly Cys
 49 54 59 64
 aag gag gcg ctc atc cgc act gat gga atg agg gtg acc tca aga aag 296
 Lys Glu Ala Leu Ile Arg Thr Asp Gly Met Arg Val Thr Ser Arg Lys
 65 70 75 80
 tca gca aaa tat aga ctt cag ggg act atc ccg aga ggt gat gtc tcc 344
 Ser Ala Lys Tyr Arg Leu Gln Gly Thr Ile Pro Arg Gly Asp Val Ser
 81 86 91 96
 ttg acc atc tta aac ccc agt gaa agt gac agc ggt gtg tac tgc tgc 392
 Leu Thr Ile Leu Asn Pro Ser Glu Ser Asp Ser Gly Val Tyr Cys Cys
 97 102 107 112
 cgc ata gaa gtg cct ggc tgg ttc aac gat gta aag ata aac gtg cgc 440
 Arg Ile Glu Val Pro Gly Trp Phe Asn Asp Val Lys Ile Asn Val Arg
 113 118 123 128
 ctg aat cta cag aga gcc tca aca acc acg cac aga aca gca acc acc 488
 Leu Asn Leu Gln Arg Ala Ser Thr Thr Thr His Arg Thr Ala Thr Thr
 129 134 139 144
 acc aca cgc aga aca aca aca aca agc ccc acc acc acc cga caa atg 536
 Thr Thr Arg Arg Thr Thr Thr Thr Ser Pro Thr Thr Thr Arg Gln Met

550	555	560	
gat gtt cac ggc tca gtg ctg tcc ctg gcc tcc agt gcc tcc tcc acc			2085
Asp Val His Gly Ser Val Leu Ser Leu Ala Ser Ser Ala Ser Ser Thr			
565	570	575	
tac tcc tca caa atc cgg aag ctt cgt agg gaa ctg gaa tca tcc cag			2133
Tyr Ser Ser Gln Ile Arg Lys Leu Arg Arg Glu Leu Glu Ser Ser Gln			
580	585	590	
gaa aaa gtg gcc acc ttg acg tct cag ctt tct gcc aat gct aat ctg			2181
Glu Lys Val Ala Thr Leu Thr Ser Gln Leu Ser Ala Asn Ala Asn Leu			
595	600	605	610
gtg gct gct ttt gag cag agc ctg gtg aat atg aca tcc cgc ctg cga			2229
Val Ala Ala Phe Glu Gln Ser Leu Val Asn Met Thr Ser Arg Leu Arg			
615	620	625	
cac ctg gca gag acg gcc gag gag aag gac act gag ctg ctg gat ttg			2277
His Leu Ala Glu Thr Ala Glu Glu Lys Asp Thr Glu Leu Leu Asp Leu			
630	635	640	
cga gaa acc ata gac ttt ctg aag aaa aag aac tct gag gcc cag gca			2325
Arg Glu Thr Ile Asp Phe Leu Lys Lys Lys Asn Ser Glu Ala Gln Ala			
645	650	655	
gtc att cag gga gcc ctt aat gcc tca gaa acc aca ccc aaa ggt agg			2373
Val Ile Gln Gly Ala Leu Asn Ala Ser Glu Thr Thr Pro Lys Gly Arg			
660	665	670	
aca tcc agc cac aga ttg aga ggg aac agg gag cag gaa agt aag agt			2421
Thr Ser Ser His Arg Leu Arg Gly Asn Arg Glu Gln Glu Ser Lys Ser			
675	680	685	690
att aca gat ttt tat ctg ggc cca tag			2448
Ile Thr Asp Phe Tyr Leu Gly Pro			
695			

<210> 65
 <211> 2155
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (143)..(2032)

<220>
 <221> misc_feature
 <222> (1)...(2155)
 <223> n = a,t,c or g

ttctgaacga cattgctagg accacgatta cgccaagntn nggacgaggg ggactttgag	60
atgtgtgaat attcatcagc atttgcttgt ggaacgctca cctctgcttt ttactcttgc	120

gattgaggat gggggcatga cactccagtg tcaaaataag tcttagtaga tttccttggt 1271
tcataaaaaa gactcactta ttccatggat gtcattgatc caggcttgct ttagtttcat 1331
gaatgaaggg tacttttagag accacaactt ctctgtcaaa aaaaaaaaaa 1380

<210> 60
<211> 1748
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (529)..(1308)

<400> 60
cttggcacgc ataggggagg ctgatgtata taactatcta ttogatgatg aagatacccc 60
accaaaccga aaaaaagaga tctctcgagg atccgaattc ggggcgcgct cgaggcggcg 120
gtggcggcag cgggttggtcc tgcctctccg ccacctccac cgcggttat cccctggctg 180
gcggcggttg gcggggcgggg gacagtagtt gtagacgccc gccctgcct cagagaagat 240
accacattga atgaacaaag actgaacttt gtttacagat accttttata aaagatgtct 300
gtggagtagt gttacagttc aaataacaaa ggattttgca ttatgagatg agtgagagtg 360
gagaattgga caaaaattga tttttgatct ctgaattgtg gtttttagct caccagttat 420
tgtgtagtct cactatttga aaattcatgc tgaaaaactg agtgaatatg atcagatttc 480
tccaccaaatt tctcagcctg ataaggaaaa tcccgttttg tcaacctg atg aag cat 537
Met Lys His
1

tca aag aag aca tat gac tct ttt caa gat gaa ctt gaa gat tat att 585
Ser Lys Lys Thr Tyr Asp Ser Phe Gln Asp Glu Leu Glu Asp Tyr Ile
4 9 14 19

aaa gta cag aaa gcc aga ggc tta gag cca aag act tgt ttc aga aag 633
Lys Val Gln Lys Ala Arg Gly Leu Glu Pro Lys Thr Cys Phe Arg Lys
20 25 30 35

atg aaa ggg gac tat ttg gaa acc tgg ggg tac aaa gga gag gtt aat 681
Met Lys Gly Asp Tyr Leu Glu Thr Trp Gly Tyr Lys Gly Glu Val Asn
36 41 46 51

tcc aga ccc acg tat aga atg ttt gac cag aga ctc cca tct gaa acc 729
Ser Arg Pro Thr Tyr Arg Met Phe Asp Gln Arg Leu Pro Ser Glu Thr
52 57 62 67

atc cag acc tac cca aga tca tgc aat att cca caa aca gtg gaa aat 777

Ile	Gln	Thr	Tyr	Pro	Arg	Ser	Cys	Asn	Ile	Pro	Gln	Thr	Val	Glu	Asn		
68					73					78					83		
cgg	ttg	cct	cag	tgg	tta	cca	gcc	cat	gac	agc	aga	ttg	aga	cta	gac		825
Arg	Leu	Pro	Gln	Trp	Leu	Pro	Ala	His	Asp	Ser	Arg	Leu	Arg	Leu	Asp		
84					89					94					99		
tct	ctg	agc	tac	tgt	cag	ttc	acg	agg	gac	tgt	ttc	tca	gaa	aaa	cca		873
Ser	Leu	Ser	Tyr	Cys	Gln	Phe	Thr	Arg	Asp	Cys	Phe	Ser	Glu	Lys	Pro		
100					105					110					115		
gta	ccc	ctg	aac	ttt	aat	caa	caa	gaa	tat	att	tgt	ggc	tca	cat	ggt		921
Val	Pro	Leu	Asn	Phe	Asn	Gln	Gln	Glu	Tyr	Ile	Cys	Gly	Ser	His	Gly		
116					121					126					131		
gta	gaa	cat	aga	gtt	tac	aag	cac	ttc	tcc	tca	gat	aac	agt	acc	agt		969
Val	Glu	His	Arg	Val	Tyr	Lys	His	Phe	Ser	Ser	Asp	Asn	Ser	Thr	Ser		
132					137					142					147		
act	cat	caa	gcc	agt	cac	aaa	cag	ata	cat	cag	aag	agg	aaa	agg	cac		1017
Thr	His	Gln	Ala	Ser	His	Lys	Gln	Ile	His	Gln	Lys	Arg	Lys	Arg	His		
148					153					158					163		
cca	gag	gaa	ggc	aga	gaa	aaa	tca	gag	gag	gag	cgg	tct	aag	cat	aag		1065
Pro	Glu	Glu	Gly	Arg	Glu	Lys	Ser	Glu	Glu	Glu	Arg	Ser	Lys	His	Lys		
164					169					174					179		
aga	aaa	aaa	agc	tgc	gag	gaa	att	gac	tta	gac	aaa	cac	aag	agc	atc		1113
Arg	Lys	Lys	Ser	Cys	Glu	Glu	Ile	Asp	Leu	Asp	Lys	His	Lys	Ser	Ile		
180					185					190					195		
caa	aga	aag	aaa	aca	gag	gtg	gaa	ata	gaa	acc	gta	cat	gtc	agt	aca		1161
Gln	Arg	Lys	Lys	Thr	Glu	Val	Glu	Ile	Glu	Thr	Val	His	Val	Ser	Thr		
196					201					206					211		
gaa	aag	ctt	aag	aat	cga	aag	gag	aaa	aaa	agc	cga	gat	gta	gtc	tct		1209
Glu	Lys	Leu	Lys	Asn	Arg	Lys	Glu	Lys	Lys	Ser	Arg	Asp	Val	Val	Ser		
212					217					222					227		
aag	aaa	gag	gaa	cgt	aag	cgt	aca	aaa	aag	aaa	aag	gaa	caa	ggc	caa		1257
Lys	Lys	Glu	Glu	Arg	Lys	Arg	Thr	Lys	Lys	Lys	Lys	Glu	Gln	Gly	Gln		
228					233					238					243		
gaa	agg	aca	gag	gag	gaa	atg	ctt	tgg	gac	cag	tct	att	ctt	gga	ttt		1305
Glu	Arg	Thr	Glu	Glu	Glu	Met	Leu	Trp	Asp	Gln	Ser	Ile	Leu	Gly	Phe		
244					249					254					259		
tga	agct	ttcaa	agttg	gttct	cccaa	agttaa	attg	aaaaa	atagg	tgagag	cttg						1362
*																	
260																	
gttttatgat	atccgtgttc	ataccacttt	tcttatgtga	ataggttctt	taacttctaa												1422
caaaggccta	gtaaacaaag	tgtttagcat	gcttgctctc	caacacagaa	attgcttttc												1482
ctcattttct	aaaagcatta	ttacattttt	tgaacatata	gtgtaatttc	ctttaatgaa												1542

agtgactctg cttttattca tcaaattgot ttgatggtgg aaatattttc tgttgggagg 1602
 ttatttattt taaattggag gattaatgac ctttgcacaa tctgtttctt gattgggttt 1662
 gttatagttt tgagttgggt attttatggt cattgggttt tctctgtgaa gcaatttttt 1722
 tctcctttat tagatctaac ttgcag 1748

<210> 61
 <211> 2765
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (123)..(2291)

<400> 61
 tcactatagg gaaagctggt acgcctgcag gtaccggtcc ggaattcccg ggtcgaccca 60
 cgcgcccggc ttttctgct cttccctgca cttcccagaa ccaaagaatg tgaaggggggt 120
 cc atg gag ggc tca cgt ccc cgc gcc ccg agc ggc cac tta gcg ccg 167
 Met Glu Gly Ser Arg Pro Arg Ala Pro Ser Gly His Leu Ala Pro
 1 5 10
 tcg ccg ccg gct ttc gac ggc gag ctg gat ctg cag cga tac tcc aac 215
 Ser Pro Pro Ala Phe Asp Gly Glu Leu Asp Leu Gln Arg Tyr Ser Asn
 16 21 26 31
 ggg cca gcc gtg agc gca ggg tcg ctc ggg atg gga gcg gtg agc tgg 263
 Gly Pro Ala Val Ser Ala Gly Ser Leu Gly Met Gly Ala Val Ser Trp
 32 37 42 47
 tct gag agt cgt gca ggc gaa cgg cgc ttc ccc tgc cct gta tgc ggg 311
 Ser Glu Ser Arg Ala Gly Glu Arg Arg Phe Pro Cys Pro Val Cys Gly
 48 53 58 63
 aag cgc ttc cgc ttc aac tct atc ctt gct ttg cac ctg cgg gcg cac 359
 Lys Arg Phe Arg Phe Asn Ser Ile Leu Ala Leu His Leu Arg Ala His
 64 69 74 79
 cca gga gcc cag gcc ttc cag tgc cct cac tgc ggc cac cgc gcg gcg 407
 Pro Gly Ala Gln Ala Phe Gln Cys Pro His Cys Gly His Arg Ala Ala
 80 85 90 95
 cag cgg gct ctg ctg cgc tcg cac ctg cgc aca cac cag ccc gag cgc 455
 Gln Arg Ala Leu Leu Arg Ser His Leu Arg Thr His Gln Pro Glu Arg
 96 101 106 111
 cca cgt agt cct gct gca cgc ctg ttg ctg gag ttg gaa gag cgc gcg 503
 Pro Arg Ser Pro Ala Ala Arg Leu Leu Leu Glu Leu Glu Glu Arg Ala
 112 117 122 127

cta cta cgc gag gcc cga ctg ggg aga gcc cga agc tca ggg ggc atg Leu Leu Arg Glu Ala Arg Leu Gly Arg Ala Arg Ser Ser Gly Gly Met 128 133 138 143	551
cag gcc acc cct gcc act gag ggt ctg gcg cgg ccc cag gct cct tca Gln Ala Thr Pro Ala Thr Glu Gly Leu Ala Arg Pro Gln Ala Pro Ser 144 149 154 159	599
tcg tcc gcc ttc cgt tgc ccc tac tgc aaa ggc aag ttt cgc acc tcg Ser Ser Ala Phe Arg Cys Pro Tyr Cys Lys Gly Lys Phe Arg Thr Ser 160 165 170 175	647
gcg gag cgc gaa cgc cac ctg cac atc ctg cat agg ccc tgg aag tgc Ala Glu Arg Glu Arg His Leu His Ile Leu His Arg Pro Trp Lys Cys 176 181 186 191	695
ggc ctg tgc agt ttc ggc tcc agc cag gag gag gag ctg ctg cac cac Gly Leu Cys Ser Phe Gly Ser Ser Gln Glu Glu Glu Leu Leu His His 192 197 202 207	743
agc ctg acg gcc cac ggg gct ccc gag cgt ccc ctg gcg gcc acc tcc Ser Leu Thr Ala His Gly Ala Pro Glu Arg Pro Leu Ala Ala Thr Ser 208 213 218 223	791
gct gcg cct ccg cct cag cct cag cct cag cct cca ccc cag ccc gaa Ala Ala Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Pro Gln Pro Glu 224 229 234 239	839
ccc aga tca gtc ccc cag ccg gag ccg gag ccg gag ccc gaa cgt gag Pro Arg Ser Val Pro Gln Pro Glu Pro Glu Pro Glu Pro Glu Arg Glu 240 245 250 255	887
gca acc ccg acc cca gct cct gcc gct ccc gag gag ccc cca gcg cct Ala Thr Pro Thr Pro Ala Pro Ala Ala Pro Glu Glu Pro Pro Ala Pro 256 261 266 271	935
ccg gag ttc cgc tgc caa gtg tgc ggc cag agc ttt aca cag tct tgg Pro Glu Phe Arg Cys Gln Val Cys Gly Gln Ser Phe Thr Gln Ser Trp 272 277 282 287	983
ttt ctc aag ggc cac atg cgt aag cac aag gcc tcc ttc gat cat gcg Phe Leu Lys Gly His Met Arg Lys His Lys Ala Ser Phe Asp His Ala 288 293 298 303	1031
tgt ccg gtg tgc ggc cgc tgc ttc aag gag ccc tgg ttc ctt aag aac Cys Pro Val Cys Gly Arg Cys Phe Lys Glu Pro Trp Phe Leu Lys Asn 304 309 314 319	1079
cac atg aag gtg cac gcc agc aag ctg ggc cca ctg cgt gcc ccg ggg His Met Lys Val His Ala Ser Lys Leu Gly Pro Leu Arg Ala Pro Gly 320 325 330 335	1127
cct gcc tcc ggg cct gcc cgc gcc ccc cag cct cct gac ctc ggc ctg Pro Ala Ser Gly Pro Ala Arg Ala Pro Gln Pro Pro Asp Leu Gly Leu 336 341 346 351	1175
ctg gcc tat gag ccg ttg ggc cca gcg ctc ctc ttg gcc ccg gct ccc	1223

Leu Ala Tyr Glu Pro	Leu Gly Pro Ala Leu	Leu Leu Leu Ala Pro Ala Pro	
352	357	362	367
acc ccg gcc gag cgc cgt gag ccc ccg agc ctc ttg ggc tac ctg agc			1271
Thr Pro Ala Glu Arg Arg Glu Pro Pro Ser Leu Leu Gly Tyr Leu Ser			
368	373	378	383
ctg cga gct ggc gag ggc cgg ccc aac ggc gag ggt gct gag ccc ggt			1319
Leu Arg Ala Gly Glu Gly Arg Pro Asn Gly Glu Gly Ala Glu Pro Gly			
384	389	394	399
ccc ggc cgc agc ttc gga ggc ttc cgc ccg ctg tcc tct gct ctc ccg			1367
Pro Gly Arg Ser Phe Gly Gly Phe Arg Pro Leu Ser Ser Ala Leu Pro			
400	405	410	415
gcc cgg gct cgc cgg cac cgt gcg gag gag cct gag gaa gaa gag gag			1415
Ala Arg Ala Arg Arg His Arg Ala Glu Glu Pro Glu Glu Glu Glu Glu			
416	421	426	431
gtg gtg gag gcc cag gag gaa acc tgg gcc cgg ggc agg tcg ctg ggc			1463
Val Val Glu Ala Gln Glu Glu Thr Trp Ala Arg Gly Arg Ser Leu Gly			
432	437	442	447
tct ctg gct tcc ctg cac ccg cgc ccg ggt gag gga ccg ggg cac tct			1511
Ser Leu Ala Ser Leu His Pro Arg Pro Gly Glu Gly Pro Gly His Ser			
448	453	458	463
gcc tct gct gct ggg gcc cag gca aga tcg acc gcc acg cag gaa gag			1559
Ala Ser Ala Ala Gly Ala Gln Ala Arg Ser Thr Ala Thr Gln Glu Glu			
464	469	474	479
aat ggg ctg ttg gtt gga ggg acc ccg cct gaa ggg ggc cgg ggc gcc			1607
Asn Gly Leu Leu Val Gly Gly Thr Arg Pro Glu Gly Gly Arg Gly Ala			
480	485	490	495
acc ggc aag gat tgt cct ttc tgc gga aaa tct ttc cgc tca gca cat			1655
Thr Gly Lys Asp Cys Pro Phe Cys Gly Lys Ser Phe Arg Ser Ala His			
496	501	506	511
cac ctc aaa gtg cat ctg cga gtg cac aca ggc gag cgg ccc tac aag			1703
His Leu Lys Val His Leu Arg Val His Thr Gly Glu Arg Pro Tyr Lys			
512	517	522	527
tgt ccg cac tgc gac tac gcg ggc acc cag tcc ggc tcg ctc aag tat			1751
Cys Pro His Cys Asp Tyr Ala Gly Thr Gln Ser Gly Ser Leu Lys Tyr			
528	533	538	543
cac cta cag cgc cac cac cgg gag cag agg agc ggg gcc ggc ccc ggg			1799
His Leu Gln Arg His His Arg Glu Gln Arg Ser Gly Ala Gly Pro Gly			
544	549	554	559
cca ccc ccg gag cca ccg cct cct tcc cag ccg ggt tcg gcc ccg caa			1847
Pro Pro Pro Glu Pro Pro Pro Pro Ser Gln Arg Gly Ser Ala Pro Gln			
560	565	570	575
tct gga gcc aag ccg tct ccg cag cct gcg acc tgg gtg gag ggc gcc			1895
Ser Gly Ala Lys Pro Ser Pro Gln Pro Ala Thr Trp Val Glu Gly Ala			

576	581	586	591	
tca agt ccc cgg cct cct tct agc ggt gct ggg ccg ggg tcc cgt cgg				1943
Ser Ser Pro Arg Pro Pro Ser Ser Gly Ala Gly Pro Gly Ser Arg Arg				
592	597	602	607	
aag ccc gcc agc cct ggg agg acc ctg cgc aac ggg cga ggc ggt gag				1991
Lys Pro Ala Ser Pro Gly Arg Thr Leu Arg Asn Gly Arg Gly Gly Glu				
608	613	618	623	
gcc gaa ccc ctg gac ctg tcc ttg cgg gca ggg ccg gga ggc gag gcc				2039
Ala Glu Pro Leu Asp Leu Ser Leu Arg Ala Gly Pro Gly Gly Glu Ala				
624	629	634	639	
ggg cct ggg ggt gcc ctc cac cgc tgc ctc ttc tgc ccg ttc gcc act				2087
Gly Pro Gly Gly Ala Leu His Arg Cys Leu Phe Cys Pro Phe Ala Thr				
640	645	650	655	
gga gcc cca gag ctc atg gcc ttg cac ctt caa gtg cac cac agc cgc				2135
Gly Ala Pro Glu Leu Met Ala Leu His Leu Gln Val His His Ser Arg				
656	661	666	671	
cgg gct agg ggc cgc cgg cca ccc cag gct gac gcg tcc ccg ccc tat				2183
Arg Ala Arg Gly Arg Arg Pro Pro Gln Ala Asp Ala Ser Pro Pro Tyr				
672	677	682	687	
gcc cga gta cca tca gga gag acc cct ccc agt cct tcg cag gaa ggg				2231
Ala Arg Val Pro Ser Gly Glu Thr Pro Pro Ser Pro Ser Gln Glu Gly				
688	693	698	703	
gag gag ggc tcc ggg ctg tcc aga ccc gga gag gca ggg ctg ggg ggg				2279
Glu Glu Gly Ser Gly Leu Ser Arg Pro Gly Glu Ala Gly Leu Gly Gly				
704	709	714	719	
caa gaa cgg tag tgg gccctcaggg gcgattagct tagtgagctt accccgccgg				2334
Gln Glu Arg *				
720				
agcggggggag cgctagaggt agttgggtag agaagccagc aggggggcagc gtgggaccca				2394
tatcccagcc ccaggcggac cagaggtgga aggcgcggcg ggcgtaggag ggtgggctgg				2454
cggtacccac ccagcccaag ggagtcacag tgccttagaa gtggcagagg tgagggtcaa				2514
agaacgggggt ccctgggctg gcagagaagg tttgtgtccc tggtgaggag ccactctgcc				2574
agtctttgct ggtccatagg cgtgagagtt tttttttgta caaggggtga ggggtgggggg				2634
cactgtaccc ttctagcccc atcagggggc ctgtagacgt cgctatTTTTT ggtacgattc				2694
ctgtcatccc tattgcagag tctgtgtccc aataaacagg tgtcttgagg cccaaaaaaa				2754
aaaaaaaaa a				2765

<210> 62
 <211> 805
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (29) .. (643)

<400> 62
 ctagccagtg tgttgtaatt ccgcagcc atg gcc tgg acc gct ctc ctt ctg 52
 Met Ala Trp Thr Ala Leu Leu Leu
 1 5

agc ctc ctt gct cac ttt aca ggt tct gtg gcc tcc tac gag gtg act 100
 Ser Leu Leu Ala His Phe Thr Gly Ser Val Ala Ser Tyr Glu Val Thr
 9 14 19 24

cag tca ctc tca gtg tca gtg gcc ctg gga cag acg gcc agg att acc 148
 Gln Ser Leu Ser Val Ser Val Ala Leu Gly Gln Thr Ala Arg Ile Thr
 25 30 35 40

tgt ggg gga gac aac att gga agt aaa aat gta cac tgg tac caa cag 196
 Cys Gly Gly Asp Asn Ile Gly Ser Lys Asn Val His Trp Tyr Gln Gln
 41 46 51 56

aag cca ggc cag gcc cct gta ttg gtc atc tat agg gat acc aac cgg 244
 Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Arg Asp Thr Asn Arg
 57 62 67 72

ccc cct ggg atc cct gag cga ttc tct ggc tcc aac tcg ggg aac acg 292
 Pro Pro Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr
 73 78 83 88

gcc acc ctg acc atc agc aga gcc caa gcc ggg gat gag gct gac tat 340
 Ala Thr Leu Thr Ile Ser Arg Ala Gln Ala Gly Asp Glu Ala Asp Tyr
 89 94 99 104

ttc tgt cag gtg tgg gac agt agc gcg tat gtg gtt ttc ggc gga ggg 388
 Phe Cys Gln Val Trp Asp Ser Ser Ala Tyr Val Val Phe Gly Gly Gly
 105 110 115 120

acc cag ctg acc gtc ctc ggt cag ccc aag gct gcc ccc tcg gtc act 436
 Thr Gln Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 121 126 131 136

ctg ttc cca ccc tcc tct gag gag ctt caa gcc aac aag gcc aca ctg 484
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 137 142 147 152

gtg tgt ctc ata agt gat ttt tac ccg gga gcc ggg aca gtg gcc tgg 532
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Gly Thr Val Ala Trp
 153 158 163 168

aag gca aaa aga agc ccc gtc aag gcg gga agg gga aac aac caa acc 580
 Lys Ala Lys Arg Ser Pro Val Lys Ala Gly Arg Gly Asn Asn Gln Thr
 169 174 179 184

ttt caa aaa aag gaa aga aca agg acc gcg ggc agc cat ctt acc tgg	628
Phe Gln Lys Lys Glu Arg Thr Arg Thr Ala Gly Ser His Leu Thr Trp	
185 190 195 200	
acc ccg acc ccc tga gccaggggac agccccacta aaacacttcc ggttccctcg	683
Thr Pro Thr Pro *	
201	
tttccccctt gaaagtgttc ccccggggta aaaaaacctg ggccccctta caaaaaaggt	743
tggtgggtgt ttctttcccc tcccccccc ccccggggg gagtgtttga acgtctcgtc	803
tc	805

<210> 63
 <211> 1566
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (133) .. (1095)

<400> 63	
ggccgcaccc gccgagccgt gaaaaaagta catctcctgg aagggatgct ttttagctga	60
gctctggtgg atgagaggag ctageccttga aaaacttgat actgatggac attgtgtggg	120
ccagaggcag gg atg gtt ggc tat gac ccc aaa cca gat ggc agg aat	168
Met Val Gly Tyr Asp Pro Lys Pro Asp Gly Arg Asn	
1 5 10	
aac acc aag ttc cag gtg gca gtg gct ggg tct gtg tct gga ctt gtt	216
Asn Thr Lys Phe Gln Val Ala Val Ala Gly Ser Val Ser Gly Leu Val	
13 18 23 28	
act cgg gcg ctg atc agt ccc ttc gac gtc atc aag atc cgt ttc cag	264
Thr Arg Ala Leu Ile Ser Pro Phe Asp Val Ile Lys Ile Arg Phe Gln	
29 34 39 44	
ctt cag cat gag cgc ctg tct cgc agt gac ccc agc gca aag tac cat	312
Leu Gln His Glu Arg Leu Ser Arg Ser Asp Pro Ser Ala Lys Tyr His	
45 50 55 60	
ggc atc ctc cag ggc tct agg cag att ctg cag gag gag ggt ccg aca	360
Gly Ile Leu Gln Gly Ser Arg Gln Ile Leu Gln Glu Glu Gly Pro Thr	
61 66 71 76	
gct ttc tgg aaa gga cac gtc cca gct cag att ctc tcc ata ggc tat	408
Ala Phe Trp Lys Gly His Val Pro Ala Gln Ile Leu Ser Ile Gly Tyr	
77 82 87 92	
gga gct gtc caa ttc ttg tca ttt gaa atg ctg acg gag ctg gtc cac	456

Gly	Ala	Val	Gln	Phe	Leu	Ser	Phe	Glu	Met	Leu	Thr	Glu	Leu	Val	His	
93					98					103					108	
aga	ggc	agc	gtg	tac	gac	gcc	cgg	gaa	ttc	tca	gtg	cac	ttt	gta	tgt	504
Arg	Gly	Ser	Val	Tyr	Asp	Ala	Arg	Glu	Phe	Ser	Val	His	Phe	Val	Cys	
109					114					119					124	
ggg	ggc	ctg	gct	gcc	tgt	atg	gcc	acc	ctc	act	gtg	cac	ccc	gtg	gat	552
Gly	Gly	Leu	Ala	Ala	Cys	Met	Ala	Thr	Leu	Thr	Val	His	Pro	Val	Asp	
125					130					135					140	
gtt	ctg	cgc	acc	cgc	ttt	gca	gct	cag	ggg	gag	ccc	aag	gtc	tat	aat	600
Val	Leu	Arg	Thr	Arg	Phe	Ala	Ala	Gln	Gly	Glu	Pro	Lys	Val	Tyr	Asn	
141					146					151					156	
acg	ctg	cgc	cac	gcc	gtg	ggg	acc	atg	tat	agg	agc	gaa	ggc	ccc	cag	648
Thr	Leu	Arg	His	Ala	Val	Gly	Thr	Met	Tyr	Arg	Ser	Glu	Gly	Pro	Gln	
157					162					167					172	
gtt	ttc	tac	aaa	ggc	ttg	gct	ccc	acc	ttg	atc	gcc	atc	ttc	ccc	tac	696
Val	Phe	Tyr	Lys	Gly	Leu	Ala	Pro	Thr	Leu	Ile	Ala	Ile	Phe	Pro	Tyr	
173					178					183					188	
gcc	ggg	ctg	cag	ttc	tct	tgc	tac	agc	tcc	ttg	aag	cac	ctg	tac	aag	744
Ala	Gly	Leu	Gln	Phe	Ser	Cys	Tyr	Ser	Ser	Leu	Lys	His	Leu	Tyr	Lys	
189					194					199					204	
tgg	gcc	ata	cca	gcc	gaa	gga	aag	aaa	aat	gag	aac	ctc	caa	aac	ctg	792
Trp	Ala	Ile	Pro	Ala	Glu	Gly	Lys	Lys	Asn	Glu	Asn	Leu	Gln	Asn	Leu	
205					210					215					220	
ctt	tgt	ggc	agt	gga	gct	ggg	gtc	atc	agc	aag	acc	ctg	aca	tat	ccg	840
Leu	Cys	Gly	Ser	Gly	Ala	Gly	Val	Ile	Ser	Lys	Thr	Leu	Thr	Tyr	Pro	
221					226					231					236	
ctg	gac	ctc	ttc	aag	aag	cgg	cta	cag	gtt	gga	ggg	ttt	gag	cat	gcc	888
Leu	Asp	Leu	Phe	Lys	Lys	Arg	Leu	Gln	Val	Gly	Gly	Phe	Glu	His	Ala	
237					242					247					252	
aga	gct	gcc	ttt	ggc	cag	gta	cgg	aga	tac	aag	ggc	ctc	atg	gac	tgt	936
Arg	Ala	Ala	Phe	Gly	Gln	Val	Arg	Arg	Tyr	Lys	Gly	Leu	Met	Asp	Cys	
253					258					263					268	
gcc	aag	cag	gtg	ctg	caa	aag	gaa	ggc	gcc	ctg	ggc	ttc	ttc	aag	ggc	984
Ala	Lys	Gln	Val	Leu	Gln	Lys	Glu	Gly	Ala	Leu	Gly	Phe	Phe	Lys	Gly	
269					274					279					284	
ctg	tcc	ccc	agc	ttg	ctg	aag	gct	gcc	ctc	tcc	aca	ggc	ttc	atg	ttc	1032
Leu	Ser	Pro	Ser	Leu	Leu	Lys	Ala	Ala	Leu	Ser	Thr	Gly	Phe	Met	Phe	
285					290					295					300	
ttc	tgc	tat	gaa	ttc	ttc	tgt	aat	gtc	ttc	cac	tgc	atg	aac	agg	aca	1080
Phe	Ser	Tyr	Glu	Phe	Phe	Cys	Asn	Val	Phe	His	Cys	Met	Asn	Arg	Thr	
301					306					311					316	
gcc	agc	cag	cgc	tga	gcgcaggaag	gaacccaggt	cttccttga	ggcagcctcc								1135
Ala	Ser	Gln	Arg	*												

317

```

tgaaggaagg aagattcagt ctccactgag aggtgccgtc tggcccttcc ctgcaggcca 1195
gctgccccaa gcggggtagc agccttgaac ccaccagct gggacaccac cagaaggctcc 1255
agggctctcc ccatgagaga atcagagggg atgcaggacg tggctatgg tgagccaacg 1315
acacagtgag aaggagcagg aagttgctgt ttctcctctg accagcccac actccaaagg 1375
aaacagacgc catctacac ctatcagccc tgctgccag gagaacagaa cacactcctg 1435
gtctggatgg ggctgctgct tgagtgcaga gggctgcggg aggccctttg caggagtcag 1495
gtccctacac ttggcctggt tttccaacct atttaataga cattaaagct aaacacacaa 1555
aaaaaaaaa a 1566

```

```

<210> 64
<211> 2448
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (352)..(2448)

```

```

<400> 64
ttgggagtaa agagcccgtc cgcagcctgc atcgccgggg ctcgggacat aagtcacgg 60
cggggaaatg gggctctgtc actttaagta cagctggagc cctgggatga aagcagctcc 120
atcagtagtg gactcagcga tgcctcagac aatctcagtt cagaagaatt caatgccagc 180
tctcactca actccctccc aagtactccc actgcttctc gcaggaactc aacaatagtg 240
ctacgcacag actcatagaa gcgctcactg gcagaaagtg ggctgagctg gtttagtgaa 300
tcagaggaga aagcccctaa aaaactggag tacgacagtg gtagcctgaa g atg gaa 357
Met Glu
1

```

```

cct ggg act tct aag tgg cgg agg gag cgg cct gag agc tgt gat gat 405
Pro Gly Thr Ser Lys Trp Arg Arg Glu Arg Pro Glu Ser Cys Asp Asp
3 8 13 18

```

```

tca tcc aag ggt gga gaa ctg aaa aag ccc atc agc ctg ggc cac cct 453
Ser Ser Lys Gly Gly Glu Leu Lys Lys Pro Ile Ser Leu Gly His Pro
19 24 29 34

```

```

ggg tcc ctg aag aag ggc aag acc cca cct gtg gct gta act tcc ccc 501
Gly Ser Leu Lys Lys Gly Lys Thr Pro Pro Val Ala Val Thr Ser Pro
35 40 45 50

```

atc act cac aca gcc cag agt gcc ctc aaa gtc gca ggc aaa cct gag	549
Ile Thr His Thr Ala Gln Ser Ala Leu Lys Val Ala Gly Lys Pro Glu	
51 56 61 66	
ggc aaa gct aca gac aag ggt aag ctt gca gtg aag aat act ggg ctc	597
Gly Lys Ala Thr Asp Lys Gly Lys Leu Ala Val Lys Asn Thr Gly Leu	
67 72 77 82	
caa cgc tcc tcc tct gat gct ggt cgg gac cgc ctg agt gat gct aag	645
Gln Arg Ser Ser Ser Asp Ala Gly Arg Asp Arg Leu Ser Asp Ala Lys	
83 88 93 98	
aag ccc ccc tcg ggc att gct cgc ccc tcc act tcg gga tcc ttt ggc	693
Lys Pro Pro Ser Gly Ile Ala Arg Pro Ser Thr Ser Gly Ser Phe Gly	
99 104 109 114	
tac aag aag cct cct cct gcc aca ggc aca gcc act gtc atg caa act	741
Tyr Lys Lys Pro Pro Pro Ala Thr Gly Thr Ala Thr Val Met Gln Thr	
115 120 125 130	
ggt ggt tca gcc act ctc agc aag atc cag aag tcc tca ggc atc cct	789
Gly Gly Ser Ala Thr Leu Ser Lys Ile Gln Lys Ser Ser Gly Ile Pro	
131 136 141 146	
gtc aag cca gta aat ggg cgc aag act agc tta gat gtt tcc aac agt	837
Val Lys Pro Val Asn Gly Arg Lys Thr Ser Leu Asp Val Ser Asn Ser	
147 152 157 162	
gca gag cca gga ttc ctg gct cct gga gcc cgt tct aac atc cag tac	885
Ala Glu Pro Gly Phe Leu Ala Pro Gly Ala Arg Ser Asn Ile Gln Tyr	
163 168 173 178	
cgc agc ctg ccc cgg cca gcc aag tca agt tct atg agc gtg acc ggc	933
Arg Ser Leu Pro Arg Pro Ala Lys Ser Ser Ser Met Ser Val Thr Gly	
179 184 189 194	
ggg cgg ggt gga cct cgc cct gtg agc agc agc att gac ccc agt ctc	981
Gly Arg Gly Gly Pro Arg Pro Val Ser Ser Ser Ile Asp Pro Ser Leu	
195 200 205 210	
ctc agc acc aag cag gga ggc ctt acg cct tcc aga ctg aag gag cct	1029
Leu Ser Thr Lys Gln Gly Gly Leu Thr Pro Ser Arg Leu Lys Glu Pro	
211 216 221 226	
acc aag gta gcc agt ggg cgg acc act cca gcc cct gtc aat cag aca	1077
Thr Lys Val Ala Ser Gly Arg Thr Thr Pro Ala Pro Val Asn Gln Thr	
227 232 237 242	
gat cgg gaa aag gag aag gcc aaa gcc aag gca gtg gcc ttg gac tca	1125
Asp Arg Glu Lys Glu Lys Ala Lys Ala Lys Ala Val Ala Leu Asp Ser	
243 248 253 258	
gac aac atc tcc ttg aag agt att ggc tcc cca gaa agt act ccc aag	1173
Asp Asn Ile Ser Leu Lys Ser Ile Gly Ser Pro Glu Ser Thr Pro Lys	
259 264 269 274	
aac caa gca agc cac ccc aca gcc acc aag ctg gca gag ctg cca cca	1221

Asn Gln Ala Ser His Pro Thr Ala Thr Lys Leu Ala Glu Leu Pro Pro	
275 280 285 290	
acc cct ctc agg gcc aca gcg aag agc ttt gtc aaa cca ccc tca cta	1269
Thr Pro Leu Arg Ala Thr Ala Lys Ser Phe Val Lys Pro Pro Ser Leu	
291 296 301 306	
gcc aat ctt gac aag gtc aac tcc aac agt ctg gat cta cca tca tcc	1317
Ala Asn Leu Asp Lys Val Asn Ser Asn Ser Leu Asp Leu Pro Ser Ser	
307 312 317 322	
agt gat acc acc cat gct tca aag gtc cca gat ctg cat gct aca agc	1365
Ser Asp Thr Thr His Ala Ser Lys Val Pro Asp Leu His Ala Thr Ser	
323 328 333 338	
tca gca tct ggg ggc cct ctc cct tcc tgc ttc acc ccc agt ccg gca	1413
Ser Ala Ser Gly Gly Pro Leu Pro Ser Cys Phe Thr Pro Ser Pro Ala	
339 344 349 354	
ccc atc ctc aat att aac tca gcc agc ttc tcc cag ggc ctg gag cta	1461
Pro Ile Leu Asn Ile Asn Ser Ala Ser Phe Ser Gln Gly Leu Glu Leu	
355 360 365 370	
atg agt ggt ttc agt gtg cca aaa gag acc cgc atg tac ccc aaa ctc	1509
Met Ser Gly Phe Ser Val Pro Lys Glu Thr Arg Met Tyr Pro Lys Leu	
371 376 381 386	
tca ggc ctg cac agg agc atg gag tcc ctc cag atg cca atg agc ctc	1557
Ser Gly Leu His Arg Ser Met Glu Ser Leu Gln Met Pro Met Ser Leu	
387 392 397 402	
ccc agt gcc ttc ccc agc agt act ccc gtc ccc acc cca cct gct ccc	1605
Pro Ser Ala Phe Pro Ser Ser Thr Pro Val Pro Thr Pro Pro Ala Pro	
403 408 413 418	
cct gct gct ccc aca gaa gaa gag acg gaa gag ctg act tgg agt gga	1653
Pro Ala Ala Pro Thr Glu Glu Glu Thr Glu Glu Leu Thr Trp Ser Gly	
419 424 429 434	
agc ccc aga gct ggg caa ctg gac agt aat cag cgg gat cgg aac act	1701
Ser Pro Arg Ala Gly Gln Leu Asp Ser Asn Gln Arg Asp Arg Asn Thr	
435 440 445 450	
ctt ccc aag aaa ggg ctc agg tac cag ctt cag tcc cag gag gag acc	1749
Leu Pro Lys Lys Gly Leu Arg Tyr Gln Leu Gln Ser Gln Glu Glu Thr	
451 456 461 466	
aag gag agg cga cat tcc cat acc att ggt ggg ctg cct gaa tcc gat	1797
Lys Glu Arg Arg His Ser His Thr Ile Gly Gly Leu Pro Glu Ser Asp	
467 472 477 482	
gac cag tca gag ctg cct tct ccc cct gca ctt ccc atg tct ctg agt	1845
Asp Gln Ser Glu Leu Pro Ser Pro Pro Ala Leu Pro Met Ser Leu Ser	
483 488 493 498	
gca aag ggc caa ctt acc aac ata gtg agt ccc act gcg gcc acc acg	1893
Ala Lys Gly Gln Leu Thr Asn Ile Val Ser Pro Thr Ala Ala Thr Thr	

499	504	509	514	
cca aga atc acc cgc tcc aac agc atc ccc acc cac gag gcg gcc ttc				1941
Pro Arg Ile Thr Arg Ser Asn Ser Ile Pro Thr His Glu Ala Ala Phe				
515	520	525	530	
gag ctg tac agc ggc tcc caa atg ggg agc acc ctg tcc ctg gcc gag				1989
Glu Leu Tyr Ser Gly Ser Gln Met Gly Ser Thr Leu Ser Leu Ala Glu				
531	536	541	546	
aga ccc aag gga atg att cgg tca gga tcc ttc cga gac ccc acg gac				2037
Arg Pro Lys Gly Met Ile Arg Ser Gly Ser Phe Arg Asp Pro Thr Asp				
547	552	557	562	
gat gtt cac ggc tca gtg ctg tcc ctg gcc tcc agt gcc tcc tcc acc				2085
Asp Val His Gly Ser Val Leu Ser Leu Ala Ser Ser Ala Ser Ser Thr				
563	568	573	578	
tac tcc tca caa atc cgg aag ctt cgt agg gaa ctg gaa tca tcc cag				2133
Tyr Ser Ser Gln Ile Arg Lys Leu Arg Arg Glu Leu Glu Ser Ser Gln				
579	584	589	594	
gaa aaa gtg gcc acc ttg acg tct cag ctt tct gcc aat gct aat ctg				2181
Glu Lys Val Ala Thr Leu Thr Ser Gln Leu Ser Ala Asn Ala Asn Leu				
595	600	605	610	
gtg gct gct ttt gag cag agc ctg gtg aat atg aca tcc cgc ctg cga				2229
Val Ala Ala Phe Glu Gln Ser Leu Val Asn Met Thr Ser Arg Leu Arg				
611	616	621	626	
cac ctg gca gag acg gcc gag gag aag gac act gag ctg ctg gat ttg				2277
His Leu Ala Glu Thr Ala Glu Glu Lys Asp Thr Glu Leu Leu Asp Leu				
627	632	637	642	
cga gaa acc ata gac ttt ctg aag aaa aag aac tct gag gcc cag gca				2325
Arg Glu Thr Ile Asp Phe Leu Lys Lys Lys Asn Ser Glu Ala Gln Ala				
643	648	653	658	
gtc att cag gga gcc ctt aat gcc tca gaa acc aca ccc aaa ggt agg				2373
Val Ile Gln Gly Ala Leu Asn Ala Ser Glu Thr Thr Pro Lys Gly Arg				
659	664	669	674	
aca tcc agc cac aga ttg aga ggg aac agg gag cag gaa agt aag agt				2421
Thr Ser Ser His Arg Leu Arg Gly Asn Arg Glu Gln Glu Ser Lys Ser				
675	680	685	690	
att aca gat ttt tat ctg ggc cca tag				2448
Ile Thr Asp Phe Tyr Leu Gly Pro *				
691	696			

<210> 65
 <211> 2155
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (143)..(2032)

<220>

<221> misc_feature

<222> (1)...(2155)

<223> n = a,t,c or g

<400> 65

ttctgaacga cattgctagg accacgatta cgccaagntn nggacgaggg ggacttttgag 60

atgtgtgaat attcatcagc atttgcttgt ggaacgctca cctctgcttt ttactcttgc 120

cgaaaactgt attgatcaag tg atg aaa cta cag aat ctg ttt gta gat gat 172
Met Lys Leu Gln Asn Leu Phe Val Asp Asp
1 5

tca ggt cga tat ttg gct att caa ttc cat ctg gaa tgt gca tat gtg 220
Ser Gly Arg Tyr Leu Ala Ile Gln Phe His Leu Glu Cys Ala Tyr Val
11 16 21 26

ttt tta tat tat tat gag tac aga aaa gca aaa gat cag ttg gat att 268
Phe Leu Tyr Tyr Tyr Glu Tyr Arg Lys Ala Lys Asp Gln Leu Asp Ile
27 32 37 42

gct aag gac atc agc caa tta caa att gat ttg aca ggt gct ttg gga 316
Ala Lys Asp Ile Ser Gln Leu Gln Ile Asp Leu Thr Gly Ala Leu Gly
43 48 53 58

aaa aga aca cgg ttc cag gaa aat tat gtg gca caa ctg att cta gat 364
Lys Arg Thr Arg Phe Gln Glu Asn Tyr Val Ala Gln Leu Ile Leu Asp
59 64 69 74

gta aga agg gaa ggg gat gtc ctt tca aat tgt gaa ttc act cca gca 412
Val Arg Arg Glu Gly Asp Val Leu Ser Asn Cys Glu Phe Thr Pro Ala
75 80 85 90

ccc act cct cag gaa cat tta acc aag aat ctt gag ctc aat gat gac 460
Pro Thr Pro Gln Glu His Leu Thr Lys Asn Leu Glu Leu Asn Asp Asp
91 96 101 106

acc att ctg aat gac ata aag tta gca gat tgt gaa cag ttc cag atg 508
Thr Ile Leu Asn Asp Ile Lys Leu Ala Asp Cys Glu Gln Phe Gln Met
107 112 117 122

cgg gat ctg tgt gct gaa gag atc gct att att ctt gga atc tgc act 556
Pro Asp Leu Cys Ala Glu Glu Ile Ala Ile Ile Leu Gly Ile Cys Thr
123 128 133 138

aat ttt caa aag aat aac cca gtg cac aca tta act gaa gtg gag ctt 604
Asn Phe Gln Lys Asn Asn Pro Val His Thr Leu Thr Glu Val Glu Leu
139 144 149 154

ctg gca ttt aca tca tgt ttg ctt tca caa cca aag ttc tgg gcc att 652

Leu Ala Phe Thr Ser Cys Leu Leu Ser Gln Pro Lys Phe Trp Ala Ile	
155 160 165 170	
cag aca tca gcc ttg atc ctc cgg aca aaa ctt gag aaa gga agt act	700
Gln Thr Ser Ala Leu Ile Leu Arg Thr Lys Leu Glu Lys Gly Ser Thr	
171 176 181 186	
cgc cga gtg gaa cgg gca atg agg cag aca cag gct ctt gca gac caa	748
Arg Arg Val Glu Arg Ala Met Arg Gln Thr Gln Ala Leu Ala Asp Gln	
187 192 197 202	
ttt gaa gat aaa act aca tct gta ttg gaa cgc ctg aag att ttc tat	796
Phe Glu Asp Lys Thr Thr Ser Val Leu Glu Arg Leu Lys Ile Phe Tyr	
203 208 213 218	
tgc tgt caa gta cca cct cac tgg gcc att cag cgc caa ctt gca agt	844
Cys Cys Gln Val Pro Pro His Trp Ala Ile Gln Arg Gln Leu Ala Ser	
219 224 229 234	
ttg ctc ttt gag ttg gga tgt acc agt tca gcc ctt cag ata ttt gaa	892
Leu Leu Phe Glu Leu Gly Cys Thr Ser Ser Ala Leu Gln Ile Phe Glu	
235 240 245 250	
aag cta gaa atg tgg gaa gat gtt gtc att tgt tat gaa aga gcc ggg	940
Lys Leu Glu Met Trp Glu Asp Val Val Ile Cys Tyr Glu Arg Ala Gly	
251 256 261 266	
cag cac gga aag gca gaa gaa atc ctt aga caa gag ctg gag aaa aaa	988
Gln His Gly Lys Ala Glu Glu Ile Leu Arg Gln Glu Leu Glu Lys Lys	
267 272 277 282	
gaa acg cct agt tta tac tgc ttg ctt gga gat gtc ctc gga gac cat	1036
Glu Thr Pro Ser Leu Tyr Cys Leu Leu Gly Asp Val Leu Gly Asp His	
283 288 293 298	
tct tgc tat gac aag gcc tgg gag ttg tcc cgg tac cgc agt gct cgt	1084
Ser Cys Tyr Asp Lys Ala Trp Glu Leu Ser Arg Tyr Arg Ser Ala Arg	
299 304 309 314	
gct cag cgc tcc aaa gcc ctc ctt cat ctt cgg aat aag gag ttt caa	1132
Ala Gln Arg Ser Lys Ala Leu Leu His Leu Arg Asn Lys Glu Phe Gln	
315 320 325 330	
gag tgt gta gag tgc ttc gaa cgc tgc gtt aag att aat ccc atg cag	1180
Glu Cys Val Glu Cys Phe Glu Arg Ser Val Lys Ile Asn Pro Met Gln	
331 336 341 346	
ctc ggg gtg tgg ttt tct ctc ggt tgt gcc tat ttg gcc ttg gaa gac	1228
Leu Gly Val Trp Phe Ser Leu Gly Cys Ala Tyr Leu Ala Leu Glu Asp	
347 352 357 362	
tat caa ggt tca gca aag gca ttt cag cgc tgt gtg act cta gaa ccc	1276
Tyr Gln Gly Ser Ala Lys Ala Phe Gln Arg Cys Val Thr Leu Glu Pro	
363 368 373 378	
gat aat gct gaa gct tgg aac aat ttg tca act tcc tat atc cga tta	1324
Asp Asn Ala Glu Ala Trp Asn Asn Leu Ser Thr Ser Tyr Ile Arg Leu	

379	384	389	394	
aaa caa aaa gta aaa gct ttt aga act tta caa gaa gct ctc aag tgt				1372
Lys Gln Lys Val Lys Ala Phe Arg Thr Leu Gln Glu Ala Leu Lys Cys				
395	400	405	410	
aac tat gaa cac tgg cag att tgg gaa aac tac atc ctc acc agc act				1420
Asn Tyr Glu His Trp Gln Ile Trp Glu Asn Tyr Ile Leu Thr Ser Thr				
411	416	421	426	
gac gtt ggg gaa ttt tca gaa gcc att aaa gct tat cac cgg ctc ttg				1468
Asp Val Gly Glu Phe Ser Glu Ala Ile Lys Ala Tyr His Arg Leu Leu				
427	432	437	442	
gac tta cgt gac aaa tac aaa gat gtt cag gtc ctt aaa att cta gtc				1516
Asp Leu Arg Asp Lys Tyr Lys Asp Val Gln Val Leu Lys Ile Leu Val				
443	448	453	458	
agg gca gtg att gat ggg atg act gat cga agt gga gat gtt gca act				1564
Arg Ala Val Ile Asp Gly Met Thr Asp Arg Ser Gly Asp Val Ala Thr				
459	464	469	474	
ggc ctc aaa gga aag ctg cag gag tta ttt ggc aga gtg act tca aga				1612
Gly Leu Lys Gly Lys Leu Gln Glu Leu Phe Gly Arg Val Thr Ser Arg				
475	480	485	490	
gtg aca aat gat gga gaa atc tgg agg ctg tat gcc cac gta tat gga				1660
Val Thr Asn Asp Gly Glu Ile Trp Arg Leu Tyr Ala His Val Tyr Gly				
491	496	501	506	
aat ggg cag agt gaa aag cct gat gaa aat gaa aag gca ttc cag tgc				1708
Asn Gly Gln Ser Glu Lys Pro Asp Glu Asn Glu Lys Ala Phe Gln Cys				
507	512	517	522	
ctc tca aag gca tac aag tgt gac acc cag tcc aat tgt tgg gag aaa				1756
Leu Ser Lys Ala Tyr Lys Cys Asp Thr Gln Ser Asn Cys Trp Glu Lys				
523	528	533	538	
gat att aca tca ttt aag gaa gtt gtt caa aga gcc tta gga ctt gca				1804
Asp Ile Thr Ser Phe Lys Glu Val Val Gln Arg Ala Leu Gly Leu Ala				
539	544	549	554	
cat gtg gcc ata aaa tgc agt aaa aac aaa tcc agt tcc caa gaa gct				1852
His Val Ala Ile Lys Cys Ser Lys Asn Lys Ser Ser Ser Gln Glu Ala				
555	560	565	570	
gta caa atg ctt tct tct gtt cga ctc aat tta cgg ggc ttg tta tct				1900
Val Gln Met Leu Ser Ser Val Arg Leu Asn Leu Arg Gly Leu Leu Ser				
571	576	581	586	
aaa gca aag caa ctt ttt aca gat gtg gca act gga gaa atg tcc agg				1948
Lys Ala Lys Gln Leu Phe Thr Asp Val Ala Thr Gly Glu Met Ser Arg				
587	592	597	602	
gaa tta gct gat gac ata aca gct atg gac acc tta gtg aca gag ctc				1996
Glu Leu Ala Asp Asp Ile Thr Ala Met Asp Thr Leu Val Thr Glu Leu				
603	608	613	618	

caa gac cta agc aac cag ttt cga aat cag tat tga ttct gctggaagca 2046
 Gln Asp Leu Ser Asn Gln Phe Arg Asn Gln Tyr *
 619 624 629

gattctggaa aaggtgcttt cacctgctgg taaaagatac atctgtatat ctgaaatgca 2106

agatattgat ttttaaaata aatttgtttt atgacttaaa aaaaaaaaaa 2155

<210> 66
 <211> 2471
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (56)..(2224)

<220>
 <221> misc_feature
 <222> (1)...(2471)
 <223> n = a,t,c or g

<400> 66
 gcacgagagc tccgcagccc ttgccacctt cctgcacct gccctgcccg gcctc atg 58
 Met
 1

tac cgc gcg ctg tac gcg ttc cgc tcg gcg gag ccc aac gcg ctg gcg 106
 Tyr Arg Ala Leu Tyr Ala Phe Arg Ser Ala Glu Pro Asn Ala Leu Ala
 2 7 12 17

ttc gcc gcg ggc gag acc ttc ctg gtg cta gag cga agc agc gcg cac 154
 Phe Ala Ala Gly Glu Thr Phe Leu Val Leu Glu Arg Ser Ser Ala His
 18 23 28 33

tgg tgg ctg gcc gcg cgg gcg cgc agt ggt gag acg ggc tac gtg ccg 202
 Trp Trp Leu Ala Ala Arg Ala Arg Ser Gly Glu Thr Gly Tyr Val Pro
 34 39 44 49

cca gcc tac ctg cgc cgc ctg cag ggc ctg gag cag gat gtc ctc cag 250
 Pro Ala Tyr Leu Arg Arg Leu Gln Gly Leu Glu Gln Asp Val Leu Gln
 50 55 60 65

gcc att gac cgg gcc atc gag gct gta cac aac aca gcc atg cgg gat 298
 Ala Ile Asp Arg Ala Ile Glu Ala Val His Asn Thr Ala Met Arg Asp
 66 71 76 81

ggc ggc aag tac agc ctg gaa cag cgt gga gtc ctc cag aag ctg atc 346
 Gly Gly Lys Tyr Ser Leu Glu Gln Arg Gly Val Leu Gln Lys Leu Ile
 82 87 92 97

cac cac cgg aaa gag acc ctg tca cgc aga ggc cct tca gcc tcc agt 394
 His His Arg Lys Glu Thr Leu Ser Arg Arg Gly Pro Ser Ala Ser Ser

98	103	108	113	
gtt gca gtt atg acc tca tca acc agt gac cac cac ttg gat gct gct				442
Val Ala Val Met Thr Ser Ser Thr Ser Asp His His Leu Asp Ala Ala				
114	119	124	129	
gca gcc agg cag ccc aat ggg gtg tgt cga gct ggg ttc gag cgg cag				490
Ala Ala Arg Gln Pro Asn Gly Val Cys Arg Ala Gly Phe Glu Arg Gln				
130	135	140	145	
cac agc cta ccc agt tct gag cat ctt ggg gca gat gga ggc ctc tac				538
His Ser Leu Pro Ser Ser Glu His Leu Gly Ala Asp Gly Gly Leu Tyr				
146	151	156	161	
cag atc cca ctt cca tct tcc cag atc cca cca cag cct cgc cga gca				586
Gln Ile Pro Leu Pro Ser Ser Gln Ile Pro Pro Gln Pro Arg Arg Ala				
162	167	172	177	
gca ccc acc aca ccg ccc cca cca gtg aag cgc cga gac cgc gag gcc				634
Ala Pro Thr Thr Pro Pro Pro Pro Val Lys Arg Arg Asp Arg Glu Ala				
178	183	188	193	
ctg atg gcc tct ggg agt ggt ggc cac aac acc atg ccc tcc ggg ggt				682
Leu Met Ala Ser Gly Ser Gly Gly His Asn Thr Met Pro Ser Gly Gly				
194	199	204	209	
aac tct gtg tcc agc ggc tcc tca gtc agc agc acc tcc ctg gac acg				730
Asn Ser Val Ser Ser Gly Ser Ser Val Ser Ser Thr Ser Leu Asp Thr				
210	215	220	225	
ctc tat acc agc tcc agc cca tct gaa cca ggc tcc agc tgc tca ccc				778
Leu Tyr Thr Ser Ser Ser Pro Ser Glu Pro Gly Ser Ser Cys Ser Pro				
226	231	236	241	
aca ccc cca cct gtg ccc cgc cga ggc acc cac acc acc gtg tcc caa				826
Thr Pro Pro Pro Val Pro Arg Arg Gly Thr His Thr Thr Val Ser Gln				
242	247	252	257	
gtc cag ccc cct ccc tcc aag gca tca gca cct gaa ccc cct gca gaa				874
Val Gln Pro Pro Pro Ser Lys Ala Ser Ala Pro Glu Pro Pro Ala Glu				
258	263	268	273	
gaa gaa gtg gca act ggt aca acc tca gcc tct gat gac ctg gaa gcc				922
Glu Glu Val Ala Thr Gly Thr Thr Ser Ala Ser Asp Asp Leu Glu Ala				
274	279	284	289	
ctg ggt aca ctg agc ctg ggg acc aca gag gag aag gca gca gct gag				970
Leu Gly Thr Leu Ser Leu Gly Thr Thr Glu Glu Lys Ala Ala Ala Glu				
290	295	300	305	
gcg gct gtg ccc agg acc att ggg gcc gag ctg atg gag ctg gtg cgg				1018
Ala Ala Val Pro Arg Thr Ile Gly Ala Glu Leu Met Glu Leu Val Arg				
306	311	316	321	
aga aac act ggc ctg agc cac gaa tta tgc cgg gtg gcc atc ggc atc				1066
Arg Asn Thr Gly Leu Ser His Glu Leu Cys Arg Val Ala Ile Gly Ile				
322	327	332	337	

ata gtg ggt cac atc cag gcc tcg gtg ccg gcc agc tca cca gtc atg Ile Val Gly His Ile Gln Ala Ser Val Pro Ala Ser Ser Pro Val Met 338 343 348 353	1114
gag cag gtc ctc ctc tca ctc gta gag ggc aag gac ctc agc atg gcc Glu Gln Val Leu Leu Ser Leu Val Glu Gly Lys Asp Leu Ser Met Ala 354 359 364 369	1162
ctg ccc tca ggg cag gtc tgc cac gac cag cag agg ctg gag gtg atc Leu Pro Ser Gly Gln Val Cys His Asp Gln Gln Arg Leu Glu Val Ile 370 375 380 385	1210
ttt gca gac ctg gct cgc cgg aag gac gac gcc cag cag cgc agt tgg Phe Ala Asp Leu Ala Arg Arg Lys Asp Asp Ala Gln Gln Arg Ser Trp 386 391 396 401	1258
gca cta tat gag gat gag ggt gtc atc cgc tgc tac cta gag gag ctg Ala Leu Tyr Glu Asp Glu Gly Val Ile Arg Cys Tyr Leu Glu Glu Leu 402 407 412 417	1306
ctg cat att ctg act gat gca gac cct gaa gtt tgc aag aaa atg tgc Leu His Ile Leu Thr Asp Ala Asp Pro Glu Val Cys Lys Lys Met Cys 418 423 428 433	1354
aag aga aac gag ttc gag tct gtc ctg gcc ttg gtg gcc tat tac caa Lys Arg Asn Glu Phe Glu Ser Val Leu Ala Leu Val Ala Tyr Tyr Gln 434 439 444 449	1402
atg gaa cac cga gca tca ctg cgg ctg ctg ctc ctc aag tgc ttt ggc Met Glu His Arg Ala Ser Leu Arg Leu Leu Leu Leu Lys Cys Phe Gly 450 455 460 465	1450
gcc atg tgc agc ctg gat gca gcc atc atc tcc acg ctt gtg tca tcc Ala Met Cys Ser Leu Asp Ala Ala Ile Ile Ser Thr Leu Val Ser Ser 466 471 476 481	1498
gtg ctg cct gta gag ctg gcg agg gac atg cag aca gac acg cag gac Val Leu Pro Val Glu Leu Ala Arg Asp Met Gln Thr Asp Thr Gln Asp 482 487 492 497	1546
cac cag aaa ctc tgt tac tct gcc ctc atc ctg gcc atg gtc ttc tcc His Gln Lys Leu Cys Tyr Ser Ala Leu Ile Leu Ala Met Val Phe Ser 498 503 508 513	1594
atg gga gag gca gtg ccc tat gca cac tat gag cac ctg ggc acg cct Met Gly Glu Ala Val Pro Tyr Ala His Tyr Glu His Leu Gly Thr Pro 514 519 524 529	1642
ttc gcc cag ttc cta ctg aac atc gtc gag gat ggg ctg ccc ttg gac Phe Ala Gln Phe Leu Leu Asn Ile Val Glu Asp Gly Leu Pro Leu Asp 530 535 540 545	1690
acc aca gag cag ctg ccg gac ctc tgc gtg aac ctg ctt ctg gct ctc Thr Thr Glu Gln Leu Pro Asp Leu Cys Val Asn Leu Leu Leu Ala Leu 546 551 556 561	1738

aac ctg cac ctg cca gct gct gac cag aat gtc atc atg gct gcc ctg	1786
Asn Leu His Leu Pro Ala Ala Asp Gln Asn Val Ile Met Ala Ala Leu	
562 567 572 577	
agc aaa cac gcc aat gtc aag atc ttc tcc gag aag ctg ttg ttg ctc	1834
Ser Lys His Ala Asn Val Lys Ile Phe Ser Glu Lys Leu Leu Leu Leu	
578 583 588 593	
ctg aac aga ggg gat gac cct gtg cgc atc ttc aaa cat gag cca cag	1882
Leu Asn Arg Gly Asp Asp Pro Val Arg Ile Phe Lys His Glu Pro Gln	
594 599 604 609	
cca cca cac tot gtc ctc aag ttc ctg cag gac gtg ttt ggc agc ccg	1930
Pro Pro His Ser Val Leu Lys Phe Leu Gln Asp Val Phe Gly Ser Pro	
610 615 620 625	
gcc aca gct gcc atc ttc tac cac aca gac atg atg gct ctc att gac	1978
Ala Thr Ala Ala Ile Phe Tyr His Thr Asp Met Met Ala Leu Ile Asp	
626 631 636 641	
atc act gtg cgg cac atc gca gac ctg tca cca gga gac aag ctg cgc	2026
Ile Thr Val Arg His Ile Ala Asp Leu Ser Pro Gly Asp Lys Leu Arg	
642 647 652 657	
atg gag tac ctc tcc ctg atg cat gct ata gtc cgc acc aca ccc tac	2074
Met Glu Tyr Leu Ser Leu Met His Ala Ile Val Arg Thr Thr Pro Tyr	
658 663 668 673	
ctg cag cac cgc cac cgg cta ccc gac ctg cag gcc ata ctg cga cgc	2122
Leu Gln His Arg His Arg Leu Pro Asp Leu Gln Ala Ile Leu Arg Arg	
674 679 684 689	
atc ctg aat gag gag gag acc tca ccc cag tgc cag atg gac cgc atg	2170
Ile Leu Asn Glu Glu Glu Thr Ser Pro Gln Cys Gln Met Asp Arg Met	
690 695 700 705	
att gtc cga gag atg tgc aag gaa ttc ctg gtg ctg ggg gag gct ccc	2218
Ile Val Arg Glu Met Cys Lys Glu Phe Leu Val Leu Gly Glu Ala Pro	
706 711 716 721	
agc tag caccttgctg tctcccttc cctgcagctc cagtcagtgt gcaggggact	2274
Ser *	
722	
caggggcttg gcctaagaa tgttttgcac tgacagtggg aggggataag gtggcangaa	2334
ggaacctgag caggaccccc acctgaagta gaacttaaga gaggggcca gtgtangatt	2394
ggggaccatg gtctgggagc tgttctgggg cangggggaa tatgcaagct aaaagcccct	2454
ctataccctg gtagggc	2471

<210> 67
<211> 2590

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (386) .. (2194)

<400> 67

cggtactagc agctgggagt actgtgagcc tgccaccaca tctggcgact ttgtgtatat	60
gacgtagaga aggggggtaca gcatgtcgtc caggttggtc ttgaactcct gacctcaggt	120
gatccagcca ctttggcctc acaaagtgtc gggattatag gcaagagcga tggcgcccgg	180
cccactcagc aggattccta gaatgggcac gagctctgcc ctcattcacag tccaaaagtg	240
agcacctgcc tggagctgcc cagaaacagc cttgtggggg ggggttggtg tctgacctcc	300
ctccccgggg gccttcgcag gcttctctgc tgggtgcttct gtgcctgtgg gtctggattc	360
ctccagggcc tgatcctggg tgcag atg cag ctg gaa gcc ctg aac ctg ctg	412
Met Gln Leu Glu Ala Leu Asn Leu Leu	
1 5	
cac aca cta gtc tgg gca cgg agt ctc tgc cgt gcc gga gct gtg cag	460
His Thr Leu Val Trp Ala Arg Ser Leu Cys Arg Ala Gly Ala Val Gln	
10 15 20 25	
aca cag gag cgg ctg tca ggc agt gcc agc cct gag caa gtg cca gct	508
Thr Gln Glu Arg Leu Ser Gly Ser Ala Ser Pro Glu Gln Val Pro Ala	
26 31 36 41	
ggg gag tgc tgt gct ctg cag gag tat gag gcc gcc gtg gag cag ctc	556
Gly Glu Cys Cys Ala Leu Gln Glu Tyr Glu Ala Ala Val Glu Gln Leu	
42 47 52 57	
aag agc gag cag atc cgg gcg cag gct gag gag agg agg aag acc ctg	604
Lys Ser Glu Gln Ile Arg Ala Gln Ala Glu Glu Arg Arg Lys Thr Leu	
58 63 68 73	
agc gag gag acc cgg cag cac cag gcc agg gcc cag tat caa gac aag	652
Ser Glu Glu Thr Arg Gln His Gln Ala Arg Ala Gln Tyr Gln Asp Lys	
74 79 84 89	
ctg gcc cgg cag cgc tac gag gac caa ctg aag cag cag caa ctt ctc	700
Leu Ala Arg Gln Arg Tyr Glu Asp Gln Leu Lys Gln Gln Gln Leu Leu	
90 95 100 105	
aat gag gag aat tta cgg aag cag gag gag tcc gtg cag aag cag gaa	748
Asn Glu Glu Asn Leu Arg Lys Gln Glu Glu Ser Val Gln Lys Gln Glu	
106 111 116 121	
gcc atg cgg cga gcc acc gtg gag cgg gag atg gag ctg cgg cac aag	796
Ala Met Arg Arg Ala Thr Val Glu Arg Glu Met Glu Leu Arg His Lys	
122 127 132 137	
aat gag atg ctg cga gtg gag acc gag gcc cgg gcg cgc gcc aag gcc	844

Asn Glu Met Leu Arg Val Glu Thr Glu Ala Arg Ala Arg Ala Lys Ala	
138 143 148 153	
gag cgg gag aat gca gac atc atc cgc gag cag atc cgc ctg aag gcg	892
Glu Arg Glu Asn Ala Asp Ile Ile Arg Glu Gln Ile Arg Leu Lys Ala	
154 159 164 169	
tcc gag cac cgt cag acc gtc ttg gag tcc atc agg acg gct ggc acc	940
Ser Glu His Arg Gln Thr Val Leu Glu Ser Ile Arg Thr Ala Gly Thr	
170 175 180 185	
ttg ttt ggg gaa gga ttc cgt gcc ttt gtg aca gac cgg gac aaa gtg	988
Leu Phe Gly Glu Gly Phe Arg Ala Phe Val Thr Asp Arg Asp Lys Val	
186 191 196 201	
aca gcc acg gtg gct ggg ctg acg ctg ctg gct gtc ggg gtc tac tca	1036
Thr Ala Thr Val Ala Gly Leu Thr Leu Leu Ala Val Gly Val Tyr Ser	
202 207 212 217	
gcc aag aat gcg aca gcc gtc act ggc cgc ttc atc gag gct cgg ctg	1084
Ala Lys Asn Ala Thr Ala Val Thr Gly Arg Phe Ile Glu Ala Arg Leu	
218 223 228 233	
ggg aag ccg tcc cta gtg agg gag acg tcc cgc atc acg gtg ctg gag	1132
Gly Lys Pro Ser Leu Val Arg Glu Thr Ser Arg Ile Thr Val Leu Glu	
234 239 244 249	
gcg ctg cgg cac ccc atc cag gtc agc cgg cgg ctc ctc agt cga ccc	1180
Ala Leu Arg His Pro Ile Gln Val Ser Arg Arg Leu Leu Ser Arg Pro	
250 255 260 265	
cag gac gtg ctg gag ggt gtt gtg ctt agt ccc agc ctg gaa gca cgg	1228
Gln Asp Val Leu Glu Gly Val Val Leu Ser Pro Ser Leu Glu Ala Arg	
266 271 276 281	
gtg cgc gac atc gcc ata gca acc agg aac acc aag aag aac cgg ggc	1276
Val Arg Asp Ile Ala Ile Ala Thr Arg Asn Thr Lys Lys Asn Arg Gly	
282 287 292 297	
ctg tac agg cac atc ctg ctg tat ggg cca cca ggc acc ggg aag acg	1324
Leu Tyr Arg His Ile Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr	
298 303 308 313	
ctg ttt gcc aag aaa ctc gcc ctg cac tca ggc atg gac tac gcc atc	1372
Leu Phe Ala Lys Lys Leu Ala Leu His Ser Gly Met Asp Tyr Ala Ile	
314 319 324 329	
atg aca ggc ggg gac gtg gcc ccc atg ggg cgg gaa ggc gtg acc gcc	1420
Met Thr Gly Gly Asp Val Ala Pro Met Gly Arg Glu Gly Val Thr Ala	
330 335 340 345	
atg cac aag ctc ttt gac tgg gcc aat acc agc cgg cgc ggc ctc ctg	1468
Met His Lys Leu Phe Asp Trp Ala Asn Thr Ser Arg Arg Gly Leu Leu	
346 351 356 361	
ctc ttc atg gat gaa gca gac gcc ttc ctt cgg aag cga gcc act gag	1516
Leu Phe Met Asp Glu Ala Asp Ala Phe Leu Arg Lys Arg Ala Thr Glu	

362	367	372	377	
gag ata agc aag gac ctc aga gcc aca ctg aac gcc ttc ctg tac cac				1564
Glu Ile Ser Lys Asp Leu Arg Ala Thr Leu Asn Ala Phe Leu Tyr His				
378	383	388	393	
atg ggc caa cac agc aac aaa ttc atg ctg gtc ctg gcc agc aat ctg				1612
Met Gly Gln His Ser Asn Lys Phe Met Leu Val Leu Ala Ser Asn Leu				
394	399	404	409	
cct gag cag ttc gac tgt gcc atc aac agc cgc att gac gtg atg gtc				1660
Pro Glu Gln Phe Asp Cys Ala Ile Asn Ser Arg Ile Asp Val Met Val				
410	415	420	425	
cac ttc gac ctg ccg cag cag gag gag cgg gag cgc ctg gtg aga ctg				1708
His Phe Asp Leu Pro Gln Gln Glu Glu Arg Glu Arg Leu Val Arg Leu				
426	431	436	441	
cat ttt gac aac tgt gtt ctt aag ccg gcc aca gaa gga aaa cgg cgc				1756
His Phe Asp Asn Cys Val Leu Lys Pro Ala Thr Glu Gly Lys Arg Arg				
442	447	452	457	
ctg aag ctg gcc cag ttt gac tac ggg agg aag tgc tgc gag gtc gct				1804
Leu Lys Leu Ala Gln Phe Asp Tyr Gly Arg Lys Cys Ser Glu Val Ala				
458	463	468	473	
cgg ctg acg gag ggc atg tgc ggc cgg gag atc gct cag ctg gcc gtg				1852
Arg Leu Thr Glu Gly Met Ser Gly Arg Glu Ile Ala Gln Leu Ala Val				
474	479	484	489	
tcc tgg cag gcc acg gca tat gcc tcc aag gac ggg gtc ctc act gag				1900
Ser Trp Gln Ala Thr Ala Tyr Ala Ser Lys Asp Gly Val Leu Thr Glu				
490	495	500	505	
gcc atg atg gac gcc tgt gtg caa gat gct gtc cag cag tac cga cag				1948
Ala Met Met Asp Ala Cys Val Gln Asp Ala Val Gln Gln Tyr Arg Gln				
506	511	516	521	
aag atg cgc tgg ctg aag gcg gag ggg cct ggg cgc cgg gtc gag cac				1996
Lys Met Arg Trp Leu Lys Ala Glu Gly Pro Gly Arg Arg Val Glu His				
522	527	532	537	
ccc cta tcc gga gtc caa ggc gag acc ctc acc tca tgg agc ctg gcc				2044
Pro Leu Ser Gly Val Gln Gly Glu Thr Leu Thr Ser Trp Ser Leu Ala				
538	543	548	553	
acg gac ccc tcc tac ccc tgc ctt gcc ggc ccc tgc aca ttt agg ata				2092
Thr Asp Pro Ser Tyr Pro Cys Leu Ala Gly Pro Cys Thr Phe Arg Ile				
554	559	564	569	
tgc tcc tgg atg ggg act ggg ctg tgc cca ggg cct ctg tcc ccc agg				2140
Cys Ser Trp Met Gly Thr Gly Leu Cys Pro Gly Pro Leu Ser Pro Arg				
570	575	580	585	
atg tct tgt ggt ggc ggt cgg ccg ttc tgc ccc cca ggg cac ccc ctg				2188
Met Ser Cys Gly Gly Gly Arg Pro Phe Cys Pro Pro Gly His Pro Leu				
586	591	596	601	

ttg tag gcactggcta gggaggggca ggcctccttc ctgcccctcg agacactctt 2244
 Leu *
 602

gggagatgca ttttccgtct ggctcacagg gggaggggtga ggctttgtac cccagcccct 2304

gcccaggcca ctgtgagggt ggggtgctggc tgagcccctg gggcagaagg agtggggcag 2364

gcgggggtctt tgttctcggc tcccacagca gagccagggtg aggggggggcc tgccaggact 2424

agacagaagt ggggcgggcct gaacctgtct tccagccatg gccagggggcc acggaacccg 2484

gcaggggtgt ctgaagccgc cctgtcagct ggccgggtcca agcctgtggc tggagctggg 2544

gtgtgtttat ctaataaagt cccacagggtg cctcaaaaaa aaaaaa 2590

<210> 68
 <211> 1956
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (76)..(1665)

<220>
 <221> misc_feature
 <222> (1)...(1956)
 <223> n = a,t,c or g

<400> 68
 ggaattcccg ggacgaccca cgcgtccgcc cgcgcgtccg gcgcgcactg cgggtcctga 60

ttggttgtgc acgcc atg gtg aaa aac ttg agc ggc tac tcc gag tcc tgc 111
 Met Val Lys Asn Leu Ser Gly Tyr Ser Glu Ser Cys
 1 5 10

aag ctc cta gtg tct cct ctg ggt gga cgc cta ggc gca cgg ccg tta 159
 Lys Leu Leu Val Ser Pro Leu Gly Gly Arg Leu Gly Ala Arg Pro Leu
 13 18 23 28

ctt ctc ttt cac ctg tgg att cgt cag ttt ctc gtt cgt ttc agg agg 207
 Leu Leu Phe His Leu Trp Ile Arg Gln Phe Leu Val Arg Phe Arg Arg
 29 34 39 44

cga tcc cgc gcc ctg ggt gcg gtg agg ccg ctg gga cag cgg agg tgc 255
 Arg Ser Arg Ala Leu Gly Ala Val Arg Pro Leu Gly Gln Arg Arg Cys
 45 50 55 60

ctc ccg acg cga agc agc gag ctg agg cgg cgg cca gcg ggg aag atg 303
 Leu Pro Thr Arg Ser Ser Glu Leu Arg Arg Arg Pro Ala Gly Lys Met
 61 66 71 76

agc ggc agc agc gcc agg tcc agc cac ctg tct cag ccc gtc gtg aag	351
Ser Gly Ser Ser Ala Arg Ser Ser His Leu Ser Gln Pro Val Val Lys	
77 82 87 92	
agc gtg ctt gtg tac cgc aac ggg gac ccc ttc tac gcg ggg cgc cgc	399
Ser Val Leu Val Tyr Arg Asn Gly Asp Pro Phe Tyr Ala Gly Arg Arg	
93 98 103 108	
gtc gtc atc cat gag aag aag gtg tcc agc ttc gaa gtc ttc ctg aag	447
Val Val Ile His Glu Lys Lys Val Ser Ser Phe Glu Val Phe Leu Lys	
109 114 119 124	
gag gtg acc ggc ggc gtt cag gca ccc ttt ggg gcc gtc agg aac atc	495
Glu Val Thr Gly Gly Val Gln Ala Pro Phe Gly Ala Val Arg Asn Ile	
125 130 135 140	
tac acc ccg cgg act ggc cac cga atc cgg aag cta gac cag atc cag	543
Tyr Thr Pro Arg Thr Gly His Arg Ile Arg Lys Leu Asp Gln Ile Gln	
141 146 151 156	
agc ggg ggc aat tac gtg gct gga ggc cag gaa gcc ttc aag aaa ctc	591
Ser Gly Gly Asn Tyr Val Ala Gly Gly Gln Glu Ala Phe Lys Lys Leu	
157 162 167 172	
aat tac ttg gac ata gga gaa atc aag aaa aga cca atg gaa gtt gtt	639
Asn Tyr Leu Asp Ile Gly Glu Ile Lys Lys Arg Pro Met Glu Val Val	
173 178 183 188	
aat aca gag gta aaa cca gta atc cat agc agg atc aac gtg tca gct	687
Asn Thr Glu Val Lys Pro Val Ile His Ser Arg Ile Asn Val Ser Ala	
189 194 199 204	
cgc ttt aga aaa ccg ctt cag gag ccg tgc act atc ttc ttg att gca	735
Arg Phe Arg Lys Pro Leu Gln Glu Pro Cys Thr Ile Phe Leu Ile Ala	
205 210 215 220	
aat gga gac ctc ata aac cca gct tct cgc ctc ctt atc ccc aga aaa	783
Asn Gly Asp Leu Ile Asn Pro Ala Ser Arg Leu Leu Ile Pro Arg Lys	
221 226 231 236	
acc ttg aat cag tgg gat cat gta cta caa atg gtc aca gaa aaa atc	831
Thr Leu Asn Gln Trp Asp His Val Leu Gln Met Val Thr Glu Lys Ile	
237 242 247 252	
act ctg agg agc ggg gct gtt cac agg ctt tat act tta gaa gga aaa	879
Thr Leu Arg Ser Gly Ala Val His Arg Leu Tyr Thr Leu Glu Gly Lys	
253 258 263 268	
ctt gtt gag agt gga gca gag ttg gag aat ggg cag ttt tat gtg gct	927
Leu Val Glu Ser Gly Ala Glu Leu Glu Asn Gly Gln Phe Tyr Val Ala	
269 274 279 284	
gtt ggc aga gat aag ttt aag aaa ctg cct tac ggt gag tta ctt ttt	975
Val Gly Arg Asp Lys Phe Lys Lys Leu Pro Tyr Gly Glu Leu Leu Phe	
285 290 295 300	
gac aag tca acg atg aga agg cct ttt ggt cag aaa gct tct tca cta	1023

Asp Lys Ser Thr Met Arg Arg Pro Phe Gly Gln Lys Ala Ser Ser Leu	
301 306 311 316	
cct cct att gta gga tcc aga aag tct aaa ggg agt gga aat gat cgc	1071
Pro Pro Ile Val Gly Ser Arg Lys Ser Lys Gly Ser Gly Asn Asp Arg	
317 322 327 332	
cac tct aag tca aca gtt gga tcc agt gac aac tca tct cct cag ccc	1119
His Ser Lys Ser Thr Val Gly Ser Ser Asp Asn Ser Ser Pro Gln Pro	
333 338 343 348	
ctg aag agg aaa ggg aaa aaa gaa gac gtg aat tca gaa aaa ctg acg	1167
Leu Lys Arg Lys Gly Lys Lys Glu Asp Val Asn Ser Glu Lys Leu Thr	
349 354 359 364	
aaa ttg aaa caa aat gta aaa tta aag aat tca caa gaa acc att cca	1215
Lys Leu Lys Gln Asn Val Lys Leu Lys Asn Ser Gln Glu Thr Ile Pro	
365 370 375 380	
aat agt gat gaa ggc att ttc aaa gct gga gca gag agg tct gaa aca	1263
Asn Ser Asp Glu Gly Ile Phe Lys Ala Gly Ala Glu Arg Ser Glu Thr	
381 386 391 396	
cgg ggg gca gca gaa gtc caa gaa gat gaa gat act cag gtt gag gtt	1311
Arg Gly Ala Ala Glu Val Gln Glu Asp Glu Asp Thr Gln Val Glu Val	
397 402 407 412	
cca gtc gat cag agg cca gca gaa ata gta gac gag gaa gaa gat gga	1359
Pro Val Asp Gln Arg Pro Ala Glu Ile Val Asp Glu Glu Glu Asp Gly	
413 418 423 428	
gag aag gca aac aag gat gca gaa cag aaa gaa gac ttt tca gga atg	1407
Glu Lys Ala Asn Lys Asp Ala Glu Gln Lys Glu Asp Phe Ser Gly Met	
429 434 439 444	
aat ggt gac ctt gaa gag gaa gga ggt agg gag gct aca gat gcc cct	1455
Asn Gly Asp Leu Glu Glu Glu Gly Gly Arg Glu Ala Thr Asp Ala Pro	
445 450 455 460	
gag caa gtc gag gag att ctg gat cac agt gag cag cag gca cgc cct	1503
Glu Gln Val Glu Glu Ile Leu Asp His Ser Glu Gln Gln Ala Arg Pro	
461 466 471 476	
gct cgt gta aat gga ggc acc gat gag gag aat ggt gag gag ctg cag	1551
Ala Arg Val Asn Gly Gly Thr Asp Glu Glu Asn Gly Glu Glu Leu Gln	
477 482 487 492	
cag gtt aat aat gag ctt caa ctg gtc cta gac aag gaa aga aag tct	1599
Gln Val Asn Asn Glu Leu Gln Leu Val Leu Asp Lys Glu Arg Lys Ser	
493 498 503 508	
caa gga gct ggc agt gga caa gat gag gta ttt cta ttg ctt ttg ctt	1647
Gln Gly Ala Gly Ser Gly Gln Asp Glu Val Phe Leu Leu Leu Leu Leu	
509 514 519 524	
gct tat gtg aat gca tga atatgt gtgtgtgtac atgcgtgcat tcagagaatt	1701
Ala Tyr Val Asn Ala *	

525

530

aatcaagtgt ttaggacttg tattgaaacc acttggtggtt gagtaggaaa gatccaatac 1761
 catttaatcc ctttacttac tagttatttc aaccatttaa caatactgcc attgacctga 1821
 cagtttgtgt ctgccctttt gcgtcgacgc ggccgcgaat tcggatcctc gagagatctc 1881
 tttttttggg tttggtgggg tatcttcac atcgaataga tagttatata atcgaccccc 1941
 aatnnnnncc ccacg 1956

<210> 69
 <211> 1690
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (128) .. (1522)

<400> 69
 ccggaattcc cgggtcgagc cgttgcagga gcgcgcgcgc ttgctgctgg cttccaagga 60
 gttgcaccag gtggcgcacg acctggacga cgagctggca tgggttcagg agcggctgcc 120
 actggcc atg cag aca gag cga ggc aac ggt ttg cag gcg gtc cag cag 169
 Met Gln Thr Glu Arg Gly Asn Gly Leu Gln Ala Val Gln Gln
 1 5 10
 cac atc aaa aag aac cag ggc ctg cgg cgg gag atc cag gcg cat ggg 217
 His Ile Lys Lys Asn Gln Gly Leu Arg Arg Glu Ile Gln Ala His Gly
 15 20 25 30
 ccg cgc ctg gag gag gtg ctg gag cgc gcg ggc gcg ctg gcg tcg ctg 265
 Pro Arg Leu Glu Glu Val Leu Glu Arg Ala Gly Ala Leu Ala Ser Leu
 31 36 41 46
 cgc agc ccg gag gca gag gca gtg cgc cgg ggc ctg gag cag ctg cag 313
 Arg Ser Pro Glu Ala Glu Ala Val Arg Arg Gly Leu Glu Gln Leu Gln
 47 52 57 62
 agc gcc tgg gcc gga ctg cgg gag gct gcc gag cga cgg cag cag gtg 361
 Ser Ala Trp Ala Gly Leu Arg Glu Ala Ala Glu Arg Arg Gln Gln Val
 63 68 73 78
 ctg gac gcc gcc ttc cag gtg gag cag tac tac ttc gac gtg gct gag 409
 Leu Asp Ala Ala Phe Gln Val Glu Gln Tyr Tyr Phe Asp Val Ala Glu
 79 84 89 94
 gtg gag gcg tgg ctg ggc gag cag gag ctg ctc atg atg agt gag gag 457
 Val Glu Ala Trp Leu Gly Glu Gln Glu Leu Leu Met Met Ser Glu Asp
 95 100 105 110

aag ggc aag gac gaa cag agc acc ctg cag ctg ctc aag aaa cac ctg	505
Lys Gly Lys Asp Glu Gln Ser Thr Leu Gln Leu Leu Lys Lys His Leu	
111 116 121 126	
cag ctg gag caa ggc gtg gag aac tac gag gaa agc atc gcg cag ctg	553
Gln Leu Glu Gln Gly Val Glu Asn Tyr Glu Glu Ser Ile Ala Gln Leu	
127 132 137 142	
tcg cgc cag tgc cgg gcg ctg ctg gag atg ggg cac ccg gac agc gag	601
Ser Arg Gln Cys Arg Ala Leu Leu Glu Met Gly His Pro Asp Ser Glu	
143 148 153 158	
cag atc agc cgg cgg cag tct cag gtg gac cgc ctg tac gtg gcg ctc	649
Gln Ile Ser Arg Arg Gln Ser Gln Val Asp Arg Leu Tyr Val Ala Leu	
159 164 169 174	
aag gag ctg ggt gag gag cgc cgg gtg gct ctg gaa cag cag tac tgg	697
Lys Glu Leu Gly Glu Glu Arg Arg Val Ala Leu Glu Gln Gln Tyr Trp	
175 180 185 190	
ctg tac cag ctc agc cgc cag gtg agc gag ctt gag cac tgg att gcc	745
Leu Tyr Gln Leu Ser Arg Gln Val Ser Glu Leu Glu His Trp Ile Ala	
191 196 201 206	
gag aag gag gtg gtg gct ggc tca ccc gag ctc ggc cag gac ttt gag	793
Glu Lys Glu Val Val Ala Gly Ser Pro Glu Leu Gly Gln Asp Phe Glu	
207 212 217 222	
cat gtc tcg gtg ctg cag gag aaa ttc tca gag ttt gcc agc gag aca	841
His Val Ser Val Leu Gln Glu Lys Phe Ser Glu Phe Ala Ser Glu Thr	
223 228 233 238	
ggt atg gca ggg cgg gaa cgg ctg gca gct gtg aac cag atg gtg gat	889
Gly Met Ala Gly Arg Glu Arg Leu Ala Ala Val Asn Gln Met Val Asp	
239 244 249 254	
gag ctg atc gag tgt ggc cat aca gca gcg gcc acc atg gcc gag tgg	937
Glu Leu Ile Glu Cys Gly His Thr Ala Ala Ala Thr Met Ala Glu Trp	
255 260 265 270	
aag gac gga ctg aac gag gcc tgg gct gag ctg ctg gag ctc atg ggc	985
Lys Asp Gly Leu Asn Glu Ala Trp Ala Glu Leu Leu Glu Leu Met Gly	
271 276 281 286	
aca cgg gcc cag ctg ctg gcc gcc tct cgg gag ctt cat aag ttc ttc	1033
Thr Arg Ala Gln Leu Leu Ala Ala Ser Arg Glu Leu His Lys Phe Phe	
287 292 297 302	
agt gac gcc cga gag ctt cag gga cag att gag gag aag cgg agg cgg	1081
Ser Asp Ala Arg Glu Leu Gln Gly Gln Ile Glu Glu Lys Arg Arg Arg	
303 308 313 318	
ctg ccc cgc ctg acc acc ccg cct gag ccg aga ccc agt gcc agt tcc	1129
Leu Pro Arg Leu Thr Thr Pro Pro Glu Pro Arg Pro Ser Ala Ser Ser	
319 324 329 334	
atg cag cgg acc ctg aga gcc ttt gag cat gac ctg cag ctc ctc gtg	1177

Met	Gln	Arg	Thr	Leu	Arg	Ala	Phe	Glu	His	Asp	Leu	Gln	Leu	Leu	Val	
335					340					345					350	
tcc	cag	gta	cgg	cag	ctg	cag	gag	ggg	gcg	gcc	cag	ctg	cgg	acg	gtg	1225
Ser	Gln	Val	Arg	Gln	Leu	Gln	Glu	Gly	Ala	Ala	Gln	Leu	Arg	Thr	Val	
351					356					361					366	
tat	gcg	ggt	gaa	cat	gcc	gag	gcc	atc	gct	agc	cgg	gag	cag	gag	gtg	1273
Tyr	Ala	Gly	Glu	His	Ala	Glu	Ala	Ile	Ala	Ser	Arg	Glu	Gln	Glu	Val	
367					372					377					382	
ctg	cag	ggt	tgg	aaa	gag	ctg	ctg	tca	gcc	tgt	gag	gat	gcc	cgc	ctg	1321
Leu	Gln	Gly	Trp	Lys	Glu	Leu	Leu	Ser	Ala	Cys	Glu	Asp	Ala	Arg	Leu	
383					388					393					398	
cat	gtc	agc	tcc	aca	gcc	gac	gcc	ctg	cgc	ttc	cac	agc	caa	gtc	cgc	1369
His	Val	Ser	Ser	Thr	Ala	Asp	Ala	Leu	Arg	Phe	His	Ser	Gln	Val	Arg	
399					404					409					414	
gac	ctg	ctc	tcc	tgg	atg	gat	ggc	atc	gcc	agc	cag	att	ggg	gca	gcc	1417
Asp	Leu	Leu	Ser	Trp	Met	Asp	Gly	Ile	Ala	Ser	Gln	Ile	Gly	Ala	Ala	
415					420					425					430	
gac	aag	ccc	agg	tgc	ccc	tca	tcc	ctc	ctc	ggg	ctt	cct	gcc	tcc	ccc	1465
Asp	Lys	Pro	Arg	Cys	Pro	Ser	Ser	Leu	Leu	Gly	Leu	Pro	Ala	Ser	Pro	
431					436					441					446	
tgg	tgg	cct	acc	cca	gcc	acc	ccc	agc	cca	ttg	aca	gcc	ccc	ttc	tca	1513
Trp	Trp	Pro	Thr	Pro	Ala	Thr	Pro	Ser	Pro	Leu	Thr	Ala	Pro	Phe	Ser	
447					452					457					462	
atg	gaa	tga	caacagc	caatatctgt	gtggcgccctc	tgtgtgctag	gcactgttct									1569
Met	Glu	*														
463																
agg	tgcttcg	tgtgtattca	gacccctttt	ttaggcctgt	cattggggct	cagaacaacg										1629
acagcggccg	ctctagagga	tccaagctta	cgtacgcgtg	catgcgacgt	catagctctt											1689
c																1690

<210> 70
 <211> 1911
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (162)..(1067)

<400> 70	
ctgtcattca caacccctg aaagcgctcg gggaccagtt ctacaaggaa gccattgagc	60
actgccggag ttacaactca cggctgtgtg cagagcgcag cgtgcgtctt cccttctctg	120

actcacagac tggggtggcc cagaacaact gctacatctg g	atg gag aag agg	173
	Met Glu Lys Arg	
	1	
cac cga ggc cca ggc ctt gcc ccg ggc cag ctg tat aca tac cct gcc		221
His Arg Gly Pro Gly Leu Ala Pro Gly Gln Leu Tyr Thr Tyr Pro Ala		
5 10 15 20		
cgc tgc tgg cgc aag aag aga cga ttg cac cca cct gaa gat cca aaa		269
Arg Cys Trp Arg Lys Lys Arg Arg Leu His Pro Pro Glu Asp Pro Lys		
21 26 31 36		
ctg cgg ctg ctg gag ata aaa cct gaa gtg gag ctt ccc ctg aag aag		317
Leu Arg Leu Leu Glu Ile Lys Pro Glu Val Glu Leu Pro Leu Lys Lys		
37 42 47 52		
gat ggg ttc acc tca gag agc acc acg ctg gaa gcc ttg ctc cgt ggc		365
Asp Gly Phe Thr Ser Glu Ser Thr Thr Leu Glu Ala Leu Leu Arg Gly		
53 58 63 68		
gag ggg gtt gag aag aag gtg gat gcc agg gag gag gaa agc atc cag		413
Glu Gly Val Glu Lys Lys Val Asp Ala Arg Glu Glu Glu Ser Ile Gln		
69 74 79 84		
gaa ata cag agg gtt ttg gaa aat gat gaa aat gta gaa gaa ggg aat		461
Glu Ile Gln Arg Val Leu Glu Asn Asp Glu Asn Val Glu Glu Gly Asn		
85 90 95 100		
gaa gaa gag gat ttg gaa gag gat att ccc aag cga aag aac agg act		509
Glu Glu Glu Asp Leu Glu Glu Asp Ile Pro Lys Arg Lys Asn Arg Thr		
101 106 111 116		
aga gga cgg gct cgc ggc tct gca ggg ggc agg agg agg cac gac gcc		557
Arg Gly Arg Ala Arg Gly Ser Ala Gly Gly Arg Arg Arg His Asp Ala		
117 122 127 132		
gcc tct cag gaa gac cac gac aaa cct tac gtc tgt gac atc tgt ggc		605
Ala Ser Gln Glu Asp His Asp Lys Pro Tyr Val Cys Asp Ile Cys Gly		
133 138 143 148		
aag cgc tac aag aac cga ccg ggg ctc agc tac cac tat gct cac act		653
Lys Arg Tyr Lys Asn Arg Pro Gly Leu Ser Tyr His Tyr Ala His Thr		
149 154 159 164		
cac ctg gcc agc gag gag ggg gat gaa gct caa gac cag gag act cgg		701
His Leu Ala Ser Glu Glu Gly Asp Glu Ala Gln Asp Gln Glu Thr Arg		
165 170 175 180		
tcc cca ccc aac cac aga aat gag aac cac agg ccc cag aaa gga ccg		749
Ser Pro Pro Asn His Arg Asn Glu Asn His Arg Pro Gln Lys Gly Pro		
181 186 191 196		
gat gga aca gtc att ccc aat aac tac tgt gac ttc tgc ttg ggg ggc		797
Asp Gly Thr Val Ile Pro Asn Asn Tyr Cys Asp Phe Cys Leu Gly Gly		
197 202 207 212		

tcc aac atg aac aag aag agt ggg cgg cct gaa gag ctg gtg tcc tgc	845
Ser Asn Met Asn Lys Lys Ser Gly Arg Pro Glu Glu Leu Val Ser Cys	
213 218 223 228	
gca gac tgt gga cgc tct gct cat ttg gga gga gaa ggc agg aag gag	893
Ala Asp Cys Gly Arg Ser Ala His Leu Gly Gly Glu Gly Arg Lys Glu	
229 234 239 244	
aag gag gca gcg gcc gca gca cgt acc acg gag gac tta ttc ggt tcc	941
Lys Glu Ala Ala Ala Ala Arg Thr Thr Glu Asp Leu Phe Gly Ser	
245 250 255 260	
acg tca gaa agt gac acg tca act ttc cac ggc ttt gat gag gac gat	989
Thr Ser Glu Ser Asp Thr Ser Thr Phe His Gly Phe Asp Glu Asp Asp	
261 266 271 276	
ttg gaa gag cct cgc tcc tgt cga gga cgc cgc agt ggc cgg ggt tcg	1037
Leu Glu Glu Pro Arg Ser Cys Arg Gly Arg Arg Ser Gly Arg Gly Ser	
277 282 287 292	
ccc aca gca gat aaa aag ggc agt tgc taa a cccacggaac agactctctg	1088
Pro Thr Ala Asp Lys Lys Gly Ser Cys *	
293 298	
ggcaattagc catccccctc tgactttggt cattgtgctg gttctgatat atattttttt	1148
taatgaaagg caactttaga ttttcctct atccttgctt tttttccctt cacctcccac	1208
gtgtccctcc atccctcccc ccacctctt gttttgggta tgtacaacag aagcacaaac	1268
tactgaaaca aaacaaaaca gcagaatgag cgttcttccg agagatggca tcgtgatgcg	1328
ctattttattt tccatagaaa taggaagtta gacggattgt ctcttttctg aggggagggg	1388
gtctttttga caggagcaga gttgatgtcc tcaattttca tatttattgg caaaaggaag	1448
agaagaggaa ctttggggtg gaaacaaaga accaataaca ttaaaacatt attatttata	1508
tattctagct gttattagaa tcagactttt tttgcgagag agagagagag agagagagaa	1568
gggaaatcaa agaaatcgaa gcaatatcct gtttagaggc aagccgcccg ggggggagaa	1628
ttttctcaat gggagacggt tgcactttct gtgccccacg gagtttgtgg ctccccgcgg	1688
cagaccctc cctcattctc ctccctgacc tttccatctt cctctctgct tgcgagaaaa	1748
tgtcagtagt tcccagagaa gtccggggta cccatacccg ggcttacctc cacaccttgg	1808
ggcctaaaac agccgtctcc tggggttatt actaatcga caagaggaga ttccagtttt	1868
ggttatagaa tgggttttcc agaaacattc ctccggggga atg	1911

<210> 71
<211> 1823

<212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (247)..(1458)

```

<400> 71
gacgggcgaa ctctgtgac cccgccacga tcgtgcacaa cttttcccga accgagcccc      60
ggactgttcc tgtttggcgg cagccacagc gggtcgagct ccaagttgca ggccctcttc      120
gcccaccgcg tgtacaacgt cccggaggag ccgcctctcc tgggagccga ggactcgctc      180
ctggccagcc aggaggcgct gcggtattac cggaggaagg tggcccgcgtg gaacaggcga      240

cacaag  atg tac aga gag cag atg aac ctt acc tcc ctg gac ccc cca      288
Met Tyr Arg Glu Gln Met Asn Leu Thr Ser Leu Asp Pro Pro
      1             5             10

ctg cag ctc cga ctc gag gcc agc tgg gtc cag ttc cac ctg ggt att      336
Leu Gln Leu Arg Leu Glu Ala Ser Trp Val Gln Phe His Leu Gly Ile
      15             20             25             30

aac cgc cat ggg ctc tac tcc cgg tcc agc cct gtt gtc agc aaa ctt      384
Asn Arg His Gly Leu Tyr Ser Arg Ser Ser Pro Val Val Ser Lys Leu
      31             36             41             46

ctg caa gac atg agg cac ttt ccc acc atc agt gct gat tac agt caa      432
Leu Gln Asp Met Arg His Phe Pro Thr Ile Ser Ala Asp Tyr Ser Gln
      47             52             57             62

gat gag aaa gcc ttg ctg ggg gca tgt gac tgc acc cag att gtg aaa      480
Asp Glu Lys Ala Leu Leu Gly Ala Cys Asp Cys Thr Gln Ile Val Lys
      63             68             73             78

ccc agt ggg gtc cac ctc aag ctg gtg ctg agg ttc tcg gat ttc ggg      528
Pro Ser Gly Val His Leu Lys Leu Val Leu Arg Phe Ser Asp Phe Gly
      79             84             89             94

aag gcc atg ttc aaa ccc atg aga cag cag cga gat gag gag aca cca      576
Lys Ala Met Phe Lys Pro Met Arg Gln Gln Arg Asp Glu Glu Thr Pro
      95             100             105             110

gtg gac ttc ttc tac ttc att gac ttt cag aga cac aat gct gag atc      624
Val Asp Phe Phe Tyr Phe Ile Asp Phe Gln Arg His Asn Ala Glu Ile
      111             116             121             126

gca gct ttc cat ctg gac agg att ctg gac ttc cga cgg gtg ccg cca      672
Ala Ala Phe His Leu Asp Arg Ile Leu Asp Phe Arg Arg Val Pro Pro
      127             132             137             142

aca gtg ggg agg ata gta aat gtc acc aag gaa atc cta gag gtc acc      720
Thr Val Gly Arg Ile Val Asn Val Thr Lys Glu Ile Leu Glu Val Thr
      143             148             153             158

aag aat gaa atc ctg cag agt gtt ttc ttt gtc tct cca gcg agc aac      768

```

Lys Asn Glu Ile Leu Gln Ser Val Phe Phe Val Ser Pro Ala Ser Asn
159 164 169 174

gtg tgc ttc ttc gcc aag tgt cca tac atg tgc aag acg gag tat gct 816
Val Cys Phe Phe Ala Lys Cys Pro Tyr Met Cys Lys Thr Glu Tyr Ala
175 180 185 190

gtc tgt ggc aaa cca cac ctg ctg gag ggt tcc ctc tct gcc ttc ctg 864
Val Cys Gly Lys Pro His Leu Leu Glu Gly Ser Leu Ser Ala Phe Leu
191 196 201 206

ccg tcc ctc aac ctg gcc ccc agg ctg tct gtg ccc aac ccc tgg atc 912
Pro Ser Leu Asn Leu Ala Pro Arg Leu Ser Val Pro Asn Pro Trp Ile
207 212 217 222

cgc tcc tac aca ctg gca gga aaa gag gag tgg gag gtc aat ccc ctt 960
Arg Ser Tyr Thr Leu Ala Gly Lys Glu Glu Trp Glu Val Asn Pro Leu
223 228 233 238

tac tgt gac aca gtg aaa cag atc tac ccg tac aac aac agc cag cgg 1008
Tyr Cys Asp Thr Val Lys Gln Ile Tyr Pro Tyr Asn Asn Ser Gln Arg
239 244 249 254

ctc ctc aat gtc atc gac atg gcc atc ttc gac ttc ttg ata ggg aat 1056
Leu Leu Asn Val Ile Asp Met Ala Ile Phe Asp Phe Leu Ile Gly Asn
255 260 265 270

atg gac cgg cac cat tat gag atg ttc acc aag ttc ggg gat gat ggg 1104
Met Asp Arg His His Tyr Glu Met Phe Thr Lys Phe Gly Asp Asp Gly
271 276 281 286

ttc ctt att cac ctt gac aac gcc aga ggg ttc gga cga cac tcc cat 1152
Phe Leu Ile His Leu Asp Asn Ala Arg Gly Phe Gly Arg His Ser His
287 292 297 302

gat gaa atc tcc atc ctc tcg cct ctc tcc cag tgc tgc atg ata aaa 1200
Asp Glu Ile Ser Ile Leu Ser Pro Leu Ser Gln Cys Cys Met Ile Lys
303 308 313 318

aag aaa aca ctt ttg cac ctg cag ctg ctg gcc caa gct gac tac aga 1248
Lys Lys Thr Leu Leu His Leu Gln Leu Leu Ala Gln Ala Asp Tyr Arg
319 324 329 334

ctc agc gat gtg atg cga gaa tca ctg ctg gaa gac cag ctc agc cct 1296
Leu Ser Asp Val Met Arg Glu Ser Leu Leu Glu Asp Gln Leu Ser Pro
335 340 345 350

gtc ctc act gaa ccc cac ctc ctt gcc ctg gat cga agg ctc caa acc 1344
Val Leu Thr Glu Pro His Leu Leu Ala Leu Asp Arg Arg Leu Gln Thr
351 356 361 366

atc cta agg aca gtg gag ggg tgc ata gtg gcc cat gga cag cag agt 1392
Ile Leu Arg Thr Val Glu Gly Cys Ile Val Ala His Gly Gln Gln Ser
367 372 377 382

gtc ata gtc gac ggc cca gtg gaa cag tcg gcc cca gac tct ggc cag 1440
Val Ile Val Asp Gly Pro Val Glu Gln Ser Ala Pro Asp Ser Gly Gln

383	388	393	398	
gct aac ttg aca agc taa gggctg gcagagtcca gtttcagaaa atacgcctgg				1494
Ala Asn Leu Thr Ser *				
399	404			
agccagagca gtcgactcga gtgccgaccc tgcgtcctca ctcccacctg ttactgctgg				1554
gagtcaagtc agctaggaag gaagcaggac attttctcaa acagcaagtg gggcccatgg				1614
aactgaatct ttactccttg gtgcaccgct tctgtcgtgc gttgccttgc tccgtttttc				1674
ccaaaaagca ctggcttcat caaggccacc gacgatctcc tgagtgcact gggaaatctg				1734
ggatataggtc aggccttgga gcccttgatcc caggagagta ctaatggtaa caagtcaa				1794
aaaaggacat caagtggaaa aaaaaaaaaa				1823

<210> 72
 <211> 5824
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (590)..(5824)

<400> 72				
ttcgagatcc	ctagtcagtg	tggtggaatt	cotttacacc	agacaggcct cattttaaat 60
cctgtctcta	cggtttacta	gctgtgtgat	cttgggcaag	atacttaacc tctctgagtt 120
tctgtttcct	catctatcaa	tgaagatgat	actatgaacc	caataaggct gttaaaacag 180
gttttttatt	acctaccacg	gcgggctgta	catctctgac	gtacagaagg aggaagcct 240
ctccacctat	cgtgtcatca	ccaagcacia	gtatagcggg	gagaccgagc agagcaatgg 300
ggcagcctc	tctgtgacag	accctgctga	gtgatcccc	accatcctgg atggcttcca 360
ctcccaggaa	gtgtgggccc	gccacaccgt	ggagctgccc	tgaccgcct cgggctaccc 420
tatccccgcc	atccgctggc	tcaaggatgg	ccggcccctc	cgggctgaca gccgctggac 480
caagcgcac	acagggctga	ccatcagcga	cttgcggaac	gaggacagcg gcacctacat 540
ttgtgaggtc	accaacacct	tcgggtcggc	agaggccaca	ggcatcctc atg gtc 595
				Met Val
				1
att gat ccc ctt cat gtg acc ctg aca cca aag aag ctg aag acc ggc				643
Ile Asp Pro Leu His Val Thr Leu Thr Pro Lys Lys Leu Lys Thr Gly				
3	8	13	18	

att ggc agc acg gtc atc ctc tcc tgt gcc ctg acg ggc tcc cca gag	691
Ile Gly Ser Thr Val Ile Leu Ser Cys Ala Leu Thr Gly Ser Pro Glu	
19 24 29 34	
ttc acc atc cgc tgg tat cgc aac acg gag ctg gtg ctg cct gac gag	739
Phe Thr Ile Arg Trp Tyr Arg Asn Thr Glu Leu Val Leu Pro Asp Glu	
35 40 45 50	
gcc atc tcc atc cgc ggg ctc agc aac gag acg ctg ctc atc acc tcg	787
Ala Ile Ser Ile Arg Gly Leu Ser Asn Glu Thr Leu Leu Ile Thr Ser	
51 56 61 66	
gcc cag aag agc cat tcc ggg gcc tac cag tgc ttc gct acc cgc aag	835
Ala Gln Lys Ser His Ser Gly Ala Tyr Gln Cys Phe Ala Thr Arg Lys	
67 72 77 82	
gcc cag acc gcc cag gac ttt gcc atc att gca ctt gag gat ggc acg	883
Ala Gln Thr Ala Gln Asp Phe Ala Ile Ile Ala Leu Glu Asp Gly Thr	
83 88 93 98	
ccc cgc atc gtc tcg tcc ttc agc gag aag gtg gtc aac ccc ggg gag	931
Pro Arg Ile Val Ser Ser Phe Ser Glu Lys Val Val Asn Pro Gly Glu	
99 104 109 114	
cag ttc tca ctg atg tgt gcg gcc aag ggc gcc ccg ccc ccc acg gtc	979
Gln Phe Ser Leu Met Cys Ala Ala Lys Gly Ala Pro Pro Pro Thr Val	
115 120 125 130	
acc tgg gcc ctc gac gat gag ccc atc gtg cgg gat ggc agc cac cgc	1027
Thr Trp Ala Leu Asp Asp Glu Pro Ile Val Arg Asp Gly Ser His Arg	
131 136 141 146	
acc aac cag tac acc atg tcg gac ggc acc acc atc agc cac atg aac	1075
Thr Asn Gln Tyr Thr Met Ser Asp Gly Thr Thr Ile Ser His Met Asn	
147 152 157 162	
gtc aca ggc ccc cag atc cgc gac ggg ggc gtg tac cgg tgc aca gcg	1123
Val Thr Gly Pro Gln Ile Arg Asp Gly Gly Val Tyr Arg Cys Thr Ala	
163 168 173 178	
cgg aac ttg gtg ggc agt gct gaa tat cag gcg cga ata aac gta aga	1171
Arg Asn Leu Val Gly Ser Ala Glu Tyr Gln Ala Arg Ile Asn Val Arg	
179 184 189 194	
ggc cca ccc agc atc cgg gct atg cgg aac atc aca gca gtc gcc ggg	1219
Gly Pro Pro Ser Ile Arg Ala Met Arg Asn Ile Thr Ala Val Ala Gly	
195 200 205 210	
cgg gac acc ctt atc aac tgc agg gtc atc ggc tat ccc tac tac tcc	1267
Arg Asp Thr Leu Ile Asn Cys Arg Val Ile Gly Tyr Pro Tyr Tyr Ser	
211 216 221 226	
atc aag tgg tac aag gat gcc ctg ctg ctg cca gac aac cac cgc cag	1315
Ile Lys Trp Tyr Lys Asp Ala Leu Leu Leu Pro Asp Asn His Arg Gln	
227 232 237 242	
gtg gtg ttt gag aat ggg acc ctc aag ctg act gac gtg cag aag ggc	1363

Val Val Phe Glu Asn Gly Thr Leu Lys Leu Thr Asp Val Gln Lys Gly	
243 248 253 258	
atg gat gag ggg gag tac ctg tgc agt gtc ctc atc cag ccc cag ctc	1411
Met Asp Glu Gly Glu Tyr Leu Cys Ser Val Leu Ile Gln Pro Gln Leu	
259 264 269 274	
tcc atc agc cag agc gtt cac gta gcc gtc aaa gtg ccc cct ctg atc	1459
Ser Ile Ser Gln Ser Val His Val Ala Val Lys Val Pro Pro Leu Ile	
275 280 285 290	
cag ccc ttc gaa ttc cca ccc gcc tcc atc ggc cag ctg ctc tac att	1507
Gln Pro Phe Glu Phe Pro Pro Ala Ser Ile Gly Gln Leu Leu Tyr Ile	
291 296 301 306	
ccc tgt gtg gtg tcc tcg ggg gac atg ccc atc cgt atc acc tgg agg	1555
Pro Cys Val Val Ser Ser Gly Asp Met Pro Ile Arg Ile Thr Trp Arg	
307 312 317 322	
aag gac gga cag gtg atc atc tca ggc tcg ggc gtg acc atc gag agc	1603
Lys Asp Gly Gln Val Ile Ile Ser Gly Ser Gly Val Thr Ile Glu Ser	
323 328 333 338	
aag gaa ttc atg agc tcc ctg cag atc tct agc gtc tcc ctc aag cac	1651
Lys Glu Phe Met Ser Ser Leu Gln Ile Ser Ser Val Ser Leu Lys His	
339 344 349 354	
aac ggc aac tat aca tgc atc gcc agc aac gca gcc gcc acc gtg agc	1699
Asn Gly Asn Tyr Thr Cys Ile Ala Ser Asn Ala Ala Ala Thr Val Ser	
355 360 365 370	
cgg gag cgc cag ctc atc gtg cgt gtg ccc cct cga ttt gtg gtg caa	1747
Arg Glu Arg Gln Leu Ile Val Arg Val Pro Pro Arg Phe Val Val Gln	
371 376 381 386	
ccc aac aac cag gat ggc atc tac ggc aaa gct ggt gtg ctc aac tgc	1795
Pro Asn Asn Gln Asp Gly Ile Tyr Gly Lys Ala Gly Val Leu Asn Cys	
387 392 397 402	
tcg gtg gac ggc tac ccc cca ccc aag gtc atg tgg aag cat gcc aag	1843
Ser Val Asp Gly Tyr Pro Pro Pro Lys Val Met Trp Lys His Ala Lys	
403 408 413 418	
ggg agc ggg aac ccc cag cag tac cac cct gtg ccc ctc act ggc cgc	1891
Gly Ser Gly Asn Pro Gln Gln Tyr His Pro Val Pro Leu Thr Gly Arg	
419 424 429 434	
atc cag atc ctg ccc aac agc tcg ctg ctg atc cgc cac gtc cta gaa	1939
Ile Gln Ile Leu Pro Asn Ser Ser Leu Leu Ile Arg His Val Leu Glu	
435 440 445 450	
gag gac atc ggc tac tac ctc tgc cag gcc agc aac ggc gta ggc acc	1987
Glu Asp Ile Gly Tyr Tyr Leu Cys Gln Ala Ser Asn Gly Val Gly Thr	
451 456 461 466	
gac atc agc aag tcc atg ttc ctc aca gtc aag atc ccg gcc atg atc	2035
Asp Ile Ser Lys Ser Met Phe Leu Thr Val Lys Ile Pro Ala Met Ile	

467	472	477	482	
act tcc cac ccc aac acc acc atc gcc atc aag ggc cat gcg aag gag				2083
Thr Ser His Pro Asn Thr Thr Ile Ala Ile Lys Gly His Ala Lys Glu				
483	488	493	498	
cta aac tgc acg gca cgg ggt gag cgg ccc atc atc atc cgc tgg gag				2131
Leu Asn Cys Thr Ala Arg Gly Glu Arg Pro Ile Ile Ile Arg Trp Glu				
499	504	509	514	
aag ggg gac aca gtc atc gac cct gac cgc gtc atg cgg tat gcc atc				2179
Lys Gly Asp Thr Val Ile Asp Pro Asp Arg Val Met Arg Tyr Ala Ile				
515	520	525	530	
gcc acc aag gac aac ggc gac gag gtc gtc tcc aca ctg aag ctc aag				2227
Ala Thr Lys Asp Asn Gly Asp Glu Val Val Ser Thr Leu Lys Leu Lys				
531	536	541	546	
ccc gct gac cgt ggg gac tct gtg ttc ttc agc tgc cat gcc atc aac				2275
Pro Ala Asp Arg Gly Asp Ser Val Phe Phe Ser Cys His Ala Ile Asn				
547	552	557	562	
tcg tat ggg gag gac cgg ggc ttg atc caa ctc act gtg caa gag ccc				2323
Ser Tyr Gly Glu Asp Arg Gly Leu Ile Gln Leu Thr Val Gln Glu Pro				
563	568	573	578	
ccc gac ccc cca gag ctg gag atc cgg gag gtg aag gcc cgg agc atg				2371
Pro Asp Pro Pro Glu Leu Glu Ile Arg Glu Val Lys Ala Arg Ser Met				
579	584	589	594	
aac ctg cgc tgg acc cag cga ttc gac ggg aac agc atc atc acg ggc				2419
Asn Leu Arg Trp Thr Gln Arg Phe Asp Gly Asn Ser Ile Ile Thr Gly				
595	600	605	610	
ttc gac att gaa tac aag aac aaa tca gat tcc tgg gac ttc aag cag				2467
Phe Asp Ile Glu Tyr Lys Asn Lys Ser Asp Ser Trp Asp Phe Lys Gln				
611	616	621	626	
tcc aca cgc aac atc tcc ccc acc atc aac cag gcc aac att gtg gac				2515
Ser Thr Arg Asn Ile Ser Pro Thr Ile Asn Gln Ala Asn Ile Val Asp				
627	632	637	642	
ttg cac ccg gca tct gtg tac agc atc cgc atg tac tct ttc aac aag				2563
Leu His Pro Ala Ser Val Tyr Ser Ile Arg Met Tyr Ser Phe Asn Lys				
643	648	653	658	
att ggc cgc agt gaa cca agc aag gag ctc acc atc agc act gag gag				2611
Ile Gly Arg Ser Glu Pro Ser Lys Glu Leu Thr Ile Ser Thr Glu Glu				
659	664	669	674	
gcc gct ccc gat ggg ccc ccc atg gat gtt acc ttg cag cca gtg acc				2659
Ala Ala Pro Asp Gly Pro Pro Met Asp Val Thr Leu Gln Pro Val Thr				
675	680	685	690	
tca cag agc atc cag gtg acc tgg aag gca ccc aag aag gag ctg cag				2707
Ser Gln Ser Ile Gln Val Thr Trp Lys Ala Pro Lys Lys Glu Leu Gln				
691	696	701	706	

aac ggt gtc atc cgg ggc tac cag att ggc tac aga gag aac agc ccc Asn Gly Val Ile Arg Gly Tyr Gln Ile Gly Tyr Arg Glu Asn Ser Pro 707 712 717 722	2755
ggc agc aac ggg cag tac agc atc gtg gag atg aag gcc acg ggg gac Gly Ser Asn Gly Gln Tyr Ser Ile Val Glu Met Lys Ala Thr Gly Asp 723 728 733 738	2803
agc gag gtc tac acc ctg gac aac ctc aag aag ttc gcc cag tat ggg Ser Glu Val Tyr Thr Leu Asp Asn Leu Lys Lys Phe Ala Gln Tyr Gly 739 744 749 754	2851
gtg gtg gtc caa gcc ttc aat cgg gct ggc acg ggg ccc tct tcc agc Val Val Val Gln Ala Phe Asn Arg Ala Gly Thr Gly Pro Ser Ser Ser 755 760 765 770	2899
gag atc aat gcc acc act ctg gag gat gtg ccc agc cag ccc cct gag Glu Ile Asn Ala Thr Thr Leu Glu Asp Val Pro Ser Gln Pro Pro Glu 771 776 781 786	2947
aac gtc cgg gcc ctg tcc atc act tct gac gtg gcc gtc atc tcc tgg Asn Val Arg Ala Leu Ser Ile Thr Ser Asp Val Ala Val Ile Ser Trp 787 792 797 802	2995
tca gag ccc ccg cgc agc acc ctc aat ggc gtc ctc aaa ggc tat cgg Ser Glu Pro Pro Arg Ser Thr Leu Asn Gly Val Leu Lys Gly Tyr Arg 803 808 813 818	3043
gtc atc ttc tgg tcc ctc tat gtt gat ggg gag tgg ggc gag atg cag Val Ile Phe Trp Ser Leu Tyr Val Asp Gly Glu Trp Gly Glu Met Gln 819 824 829 834	3091
aac atc acc acc acg cgg gag cgg gtg gag ctg cgg ggc atg gag aag Asn Ile Thr Thr Thr Arg Glu Arg Val Glu Leu Arg Gly Met Glu Lys 835 840 845 850	3139
ttc acc aac tac agc gtc cag gtg ctg gcc tac acc cag gct ggg gac Phe Thr Asn Tyr Ser Val Gln Val Leu Ala Tyr Thr Gln Ala Gly Asp 851 856 861 866	3187
ggc gta cgc agc agt gtg ctc tac atc cag acc aag gag gac gtt cca Gly Val Arg Ser Ser Val Leu Tyr Ile Gln Thr Lys Glu Asp Val Pro 867 872 877 882	3235
ggt ccc cct gct ggc atc aaa gct gtc cct tca tca gct agc agt gtg Gly Pro Pro Ala Gly Ile Lys Ala Val Pro Ser Ser Ala Ser Ser Val 883 888 893 898	3283
gtt gtg tct tgg ctc ccc cct acc aag ccc aac ggg gtg atc cgc aag Val Val Ser Trp Leu Pro Pro Thr Lys Pro Asn Gly Val Ile Arg Lys 899 904 909 914	3331
tac acc atc ttc tgt tcc agc ccc ggg tct ggc cag ccg gct ccc agc Tyr Thr Ile Phe Cys Ser Ser Pro Gly Ser Gly Gln Pro Ala Pro Ser 915 920 925 930	3379

gag tac gag acg agt cca gag cag ctc ttc tac cgg atc gcc cac cta	3427
Glu Tyr Glu Thr Ser Pro Glu Gln Leu Phe Tyr Arg Ile Ala His Leu	
931 936 941 946	
aac cgc ggt cag cag tat ctg ctg tgg gtg gcc gcc gtc acc tct gcc	3475
Asn Arg Gly Gln Gln Tyr Leu Leu Trp Val Ala Ala Val Thr Ser Ala	
947 952 957 962	
ggc cgg ggc aac agc agc gag aag gtg acc atc gag cct gct ggc aag	3523
Gly Arg Gly Asn Ser Ser Glu Lys Val Thr Ile Glu Pro Ala Gly Lys	
963 968 973 978	
gcc cca gca aag atc atc tcc ttt ggg ggc acc gtg aca aca cct tgg	3571
Ala Pro Ala Lys Ile Ile Ser Phe Gly Gly Thr Val Thr Thr Pro Trp	
979 984 989 994	
atg aaa gat gtt cgg ctg cct tgc aat tca gtg gga gat cca gcc cct	3619
Met Lys Asp Val Arg Leu Pro Cys Asn Ser Val Gly Asp Pro Ala Pro	
995 1000 1005 1010	
gct gtg aag tgg acc aag gac agt gaa gac tcg gcc att cca gtg tcc	3667
Ala Val Lys Trp Thr Lys Asp Ser Glu Asp Ser Ala Ile Pro Val Ser	
1011 1016 1021 1026	
atg gat ggg cac cgg ctc atc cac acc aat ggc aca ctg ctg ctg cgt	3715
Met Asp Gly His Arg Leu Ile His Thr Asn Gly Thr Leu Leu Leu Arg	
1027 1032 1037 1042	
gca gtg aag gct gag gac tct ggc tac tac acg tgc acg gcc acc aac	3763
Ala Val Lys Ala Glu Asp Ser Gly Tyr Tyr Thr Cys Thr Ala Thr Asn	
1043 1048 1053 1058	
act ggt ggc ttt gac acc atc atc gtc aac ctt ctg gtg caa gtt ccc	3811
Thr Gly Gly Phe Asp Thr Ile Ile Val Asn Leu Leu Val Gln Val Pro	
1059 1064 1069 1074	
ccg gac cag ccc cgc ctc act gtc tcc aaa acc tca gct tcg tcc atc	3859
Pro Asp Gln Pro Arg Leu Thr Val Ser Lys Thr Ser Ala Ser Ser Ile	
1075 1080 1085 1090	
acc ctg acc tgg att cca ggt gac aat ggg ggc agc tcc atc cga ggc	3907
Thr Leu Thr Trp Ile Pro Gly Asp Asn Gly Gly Ser Ser Ile Arg Gly	
1091 1096 1101 1106	
ttc gtg cta cag tac tcg gtg gac aac agc gag gag tgg aag gat gtg	3955
Phe Val Leu Gln Tyr Ser Val Asp Asn Ser Glu Glu Trp Lys Asp Val	
1107 1112 1117 1122	
ttc atc agc tcc agc gag cgc tcc ttc aag ctg gac agc ctc aag tgt	4003
Phe Ile Ser Ser Ser Glu Arg Ser Phe Lys Leu Asp Ser Leu Lys Cys	
1123 1128 1133 1138	
ggc acg tgg tac aag gtg aag ctg gca gcc aag aac agc gtg ggc tct	4051
Gly Thr Trp Tyr Lys Val Lys Leu Ala Ala Lys Asn Ser Val Gly Ser	
1139 1144 1149 1154	
ggg cgc atc agc gag atc atc gag gcc aag acc cac ggg cgg gag ccc	4099

Gly Arg Ile Ser Glu Ile Ile Glu Ala Lys Thr His Gly Arg Glu Pro	
1155 1160 1165 1170	
toc ttc agc aaa gac caa cac ctc ttc acc cac atc aac tcc acg cat	4147
Ser Phe Ser Lys Asp Gln His Leu Phe Thr His Ile Asn Ser Thr His	
1171 1176 1181 1186	
gct cgg ctt aac ctg cag ggc tgg aac aat ggg ggc tgc cct atc aca	4195
Ala Arg Leu Asn Leu Gln Gly Trp Asn Asn Gly Gly Cys Pro Ile Thr	
1187 1192 1197 1202	
gcc atc gtt ctg gag tac cgg ccc aag ggg acc tgg gcc tgg cag ggc	4243
Ala Ile Val Leu Glu Tyr Arg Pro Lys Gly Thr Trp Ala Trp Gln Gly	
1203 1208 1213 1218	
ctc cgg gcc aac agc tcc ggg gag gtg ttt ctg acg gaa ctg cga gag	4291
Leu Arg Ala Asn Ser Ser Gly Glu Val Phe Leu Thr Glu Leu Arg Glu	
1219 1224 1229 1234	
gcc acg tgg tac gag ctg cgc atg agg gct tgc aac agt gcg ggc tgc	4339
Ala Thr Trp Tyr Glu Leu Arg Met Arg Ala Cys Asn Ser Ala Gly Cys	
1235 1240 1245 1250	
ggc aat gaa aca gcc cag ttc gcc acc ctg gac tac gat ggc agc acc	4387
Gly Asn Glu Thr Ala Gln Phe Ala Thr Leu Asp Tyr Asp Gly Ser Thr	
1251 1256 1261 1266	
att cca ccc atc aag tct gct caa ggt gaa ggg gat gat gtg aag aag	4435
Ile Pro Pro Ile Lys Ser Ala Gln Gly Glu Gly Asp Asp Val Lys Lys	
1267 1272 1277 1282	
ctg ttc acc atc ggc tgc cct gtc atc ctg gcc aca ctg ggg gtg gca	4483
Leu Phe Thr Ile Gly Cys Pro Val Ile Leu Ala Thr Leu Gly Val Ala	
1283 1288 1293 1298	
ctg ctc ttc atc gta cgc aag aag agg aag gag aaa cgg ctg aag cga	4531
Leu Leu Phe Ile Val Arg Lys Lys Arg Lys Glu Lys Arg Leu Lys Arg	
1299 1304 1309 1314	
ctc cga gat gca aag agt ttg gca gaa atg ttg ata agc aag aac aat	4579
Leu Arg Asp Ala Lys Ser Leu Ala Glu Met Leu Ile Ser Lys Asn Asn	
1315 1320 1325 1330	
aga agc ttt gac acc cct gtg aaa ggg cca ccc cag ggc cca cgg cta	4627
Arg Ser Phe Asp Thr Pro Val Lys Gly Pro Pro Gln Gly Pro Arg Leu	
1331 1336 1341 1346	
cac att gac atc ccc agg gtc cag ctg ctc atc gag gac aaa gaa ggc	4675
His Ile Asp Ile Pro Arg Val Gln Leu Leu Ile Glu Asp Lys Glu Gly	
1347 1352 1357 1362	
atc aag caa ctg gga gat gac aag gcc acc atc cct gtg aca gat gct	4723
Ile Lys Gln Leu Gly Asp Asp Lys Ala Thr Ile Pro Val Thr Asp Ala	
1363 1368 1373 1378	
gag ttc agc caa gct gtc aac cca cag agc ttc tgt act ggc gtc tcc	4771
Glu Phe Ser Gln Ala Val Asn Pro Gln Ser Phe Cys Thr Gly Val Ser	

1379	1384	1389	1394	
ttg cac cac cca acc ctc atc cag agc aca gga ccc ctc atc gac atg				4819
Leu His His Pro Thr Leu Ile Gln Ser Thr Gly Pro Leu Ile Asp Met				
1395	1400	1405	1410	
tct gac atc cgg cca gga acc aat cca gtg tcc agg aag aat gtg aag				4867
Ser Asp Ile Arg Pro Gly Thr Asn Pro Val Ser Arg Lys Asn Val Lys				
1411	1416	1421	1426	
tca gcc cac agc acc cgg aac cgg tac tca agc cag tgg acc ctg acc				4915
Ser Ala His Ser Thr Arg Asn Arg Tyr Ser Ser Gln Trp Thr Leu Thr				
1427	1432	1437	1442	
aag tgc cag gcc tcc aca cct gcc cgc acc ctc acc tcc gac tgg cgc				4963
Lys Cys Gln Ala Ser Thr Pro Ala Arg Thr Leu Thr Ser Asp Trp Arg				
1443	1448	1453	1458	
acc gtg ggc tcc cag cat ggt gtc acg gtc act gag agt gac agc tac				5011
Thr Val Gly Ser Gln His Gly Val Thr Val Thr Glu Ser Asp Ser Tyr				
1459	1464	1469	1474	
agt gcc agc ctg tcc cag gac aca gac aaa gga agg aac agc atg gtg				5059
Ser Ala Ser Leu Ser Gln Asp Thr Asp Lys Gly Arg Asn Ser Met Val				
1475	1480	1485	1490	
tcc act gag agt gcc tct tcc acc tac gag gag ctg gcc cgg gcc tat				5107
Ser Thr Glu Ser Ala Ser Ser Thr Tyr Glu Glu Leu Ala Arg Ala Tyr				
1491	1496	1501	1506	
gag cat gcc aag ctg gag gag cag ctg cag cac gcc aag ttt gag atc				5155
Glu His Ala Lys Leu Glu Glu Gln Leu Gln His Ala Lys Phe Glu Ile				
1507	1512	1517	1522	
acc gag tgc ttc atc tct gac agt tcc tct gac cag atg acc aca ggc				5203
Thr Glu Cys Phe Ile Ser Asp Ser Ser Ser Asp Gln Met Thr Thr Gly				
1523	1528	1533	1538	
acc aac gag aac gcc gac agc atg aca tcc atg agc aca ccc tca gag				5251
Thr Asn Glu Asn Ala Asp Ser Met Thr Ser Met Ser Thr Pro Ser Glu				
1539	1544	1549	1554	
cct ggc atc tgc cgc ttt acc gcc tca cca ccc aag ccc cag gat gcg				5299
Pro Gly Ile Cys Arg Phe Thr Ala Ser Pro Pro Lys Pro Gln Asp Ala				
1555	1560	1565	1570	
gac cgg ggc aaa aac gtg gct gtg ccc atc cct cac cgg gcc aac aag				5347
Asp Arg Gly Lys Asn Val Ala Val Pro Ile Pro His Arg Ala Asn Lys				
1571	1576	1581	1586	
agt gac tac tgc aac ctg ccc ctg tat gcc aag tca gag gcc ttc ttt				5395
Ser Asp Tyr Cys Asn Leu Pro Leu Tyr Ala Lys Ser Glu Ala Phe Phe				
1587	1592	1597	1602	
cga aag gca gat gga cgt gag ccc tgc ccc gtg gtc cca ccc cgt gag				5443
Arg Lys Ala Asp Gly Arg Glu Pro Cys Pro Val Val Pro Pro Arg Glu				
1603	1608	1613	1618	

ataag	atg att gtg gac agg cag tat atg ggc gtg tct aag cgg aag	227
	Met Ile Val Asp Arg Gln Tyr Met Gly Val Ser Lys Arg Lys	
	1 5 10	
tgC atC gtg tgg ggt gtc gcc ttc ttg tcc gat ggc act atC ata agt	275	
Cys Ile Val Trp Gly Val Ala Phe Leu Ser Asp Gly Thr Ile Ile Ser		
15 20 25 30		
gtg gac tct gct ggg aag gtg cag ttc tgg gac tca gcc act ggg acg	323	
Val Asp Ser Ala Gly Lys Val Gln Phe Trp Asp Ser Ala Thr Gly Thr		
31 36 41 46		
ctt gtg aag agC cat ctC atC gct aat gct gac gtg cag tcc att gct	371	
Leu Val Lys Ser His Leu Ile Ala Asn Ala Asp Val Gln Ser Ile Ala		
47 52 57 62		
gta gct gac ttt ttc cca ggt cat gag tct cgg gct aca gaa gct ttg	419	
Val Ala Asp Phe Phe Pro Gly His Glu Ser Arg Ala Thr Glu Ala Leu		
63 68 73 78		
tgC tgg gca gaa gga cag cga ctC ttt agt gct ggg ctC aat ggc gag	467	
Cys Trp Ala Glu Gly Gln Arg Leu Phe Ser Ala Gly Leu Asn Gly Glu		
79 84 89 94		
att atg gag tat gat tta cag gcg tta aac atC aag tat gct atg gat	515	
Ile Met Glu Tyr Asp Leu Gln Ala Leu Asn Ile Lys Tyr Ala Met Asp		
95 100 105 110		
gcc ttt gga gga cct att tgg agC atg gct gcc agC ccc agt ggc tct	563	
Ala Phe Gly Gly Pro Ile Trp Ser Met Ala Ala Ser Pro Ser Gly Ser		
111 116 121 126		
caa ctt ttg gtt ggt tgt gaa gat gga tct gtg aaa ctA ttt caa att	611	
Gln Leu Leu Val Gly Cys Glu Asp Gly Ser Val Lys Leu Phe Gln Ile		
127 132 137 142		
acc cca gac aaa atC cag ttt gaa aga aat ttt gat cgg cag aaa agt	659	
Thr Pro Asp Lys Ile Gln Phe Glu Arg Asn Phe Asp Arg Gln Lys Ser		
143 148 153 158		
cgc atC ctg agt ctC agC tgg cat ccc tct ggt acc cac att gca gct	707	
Arg Ile Leu Ser Leu Ser Trp His Pro Ser Gly Thr His Ile Ala Ala		
159 164 169 174		
ggt tcc ata gac tac att agt gtg ttt gat gtc aaa tca ggc agC gct	755	
Gly Ser Ile Asp Tyr Ile Ser Val Phe Asp Val Lys Ser Gly Ser Ala		
175 180 185 190		
gtt cat aag atg att gtg gac agg cag tat atg ggc gtg tct aag cgg	803	
Val His Lys Met Ile Val Asp Arg Gln Tyr Met Gly Val Ser Lys Arg		
191 196 201 206		
aag tgC atC gtg tgg ggt gtc gcc ttc ttg tcc gat ggc act atC ata	851	
Lys Cys Ile Val Trp Gly Val Ala Phe Leu Ser Asp Gly Thr Ile Ile		
207 212 217 222		

agt gtg gac tct gct ggg aag gtg cag ttc tgg gac tca gcc act ggg	899
Ser Val Asp Ser Ala Gly Lys Val Gln Phe Trp Asp Ser Ala Thr Gly	
223 228 233 238	
acg ctt gtg aag agc cat ctc atc gct aat gct gac gtg cag tcc att	947
Thr Leu Val Lys Ser His Leu Ile Ala Asn Ala Asp Val Gln Ser Ile	
239 244 249 254	
gct gta gct gac caa gaa gac agt ttc gtg gtg ggc aca gcc gag gga	995
Ala Val Ala Asp Gln Glu Asp Ser Phe Val Val Gly Thr Ala Glu Gly	
255 260 265 270	
aca gtc ttc cat ttt cag ctg gtc cct gtg aca tct aac agc agt gag	1043
Thr Val Phe His Phe Gln Leu Val Pro Val Thr Ser Asn Ser Ser Glu	
271 276 281 286	
aag cag tgg gtg cgg aca aaa ccg ttc cag cat cac act cat gac gtg	1091
Lys Gln Trp Val Arg Thr Lys Pro Phe Gln His His Thr His Asp Val	
287 292 297 302	
cgc act gtg gcc cac agc cca aca gcg ctg ata tct gga ggc act gac	1139
Arg Thr Val Ala His Ser Pro Thr Ala Leu Ile Ser Gly Gly Thr Asp	
303 308 313 318	
acc cac tta gtc ttt cgt cct ctc atg gag aag gtg gaa gta aag aat	1187
Thr His Leu Val Phe Arg Pro Leu Met Glu Lys Val Glu Val Lys Asn	
319 324 329 334	
tac gat gcc gct ctc cga aaa atc acc ttt cac cac cga tgt ctc atc	1235
Tyr Asp Ala Ala Leu Arg Lys Ile Thr Phe His His Arg Cys Leu Ile	
335 340 345 350	
tcc tgt tct aaa aag agg cag ctt ctc ctc ttc cag ttt gct cat cac	1283
Ser Cys Ser Lys Lys Arg Gln Leu Leu Leu Phe Gln Phe Ala His His	
351 356 361 366	
tta gaa ctt tgg cga ctg gga tcc aca gtt gca aca ggc aag aat ggg	1331
Leu Glu Leu Trp Arg Leu Gly Ser Thr Val Ala Thr Gly Lys Asn Gly	
367 372 377 382	
gat act ctt cca ctc tct aaa aat gca gat cat tta ctg cac cta aag	1379
Asp Thr Leu Pro Leu Ser Lys Asn Ala Asp His Leu Leu His Leu Lys	
383 388 393 398	
aca aag ggt cct gag aac att atc tgt agc tgt atc tcc cca tgt gga	1427
Thr Lys Gly Pro Glu Asn Ile Ile Cys Ser Cys Ile Ser Pro Cys Gly	
399 404 409 414	
agt tgg ata gcc tat tct aca gtt tct cgg ttt ttt ctc tat cgg ctg	1475
Ser Trp Ile Ala Tyr Ser Thr Val Ser Arg Phe Phe Leu Tyr Arg Leu	
415 420 425 430	
aat tat gaa cat gac aac ata agc ctc aaa agg gtt tcc aaa atg cca	1523
Asn Tyr Glu His Asp Asn Ile Ser Leu Lys Arg Val Ser Lys Met Pro	
431 436 441 446	
gca ttc ctt cgc tct gcc ctt cag att ttg ttt tct gaa gat tca aca	1571

Ala Phe Leu Arg Ser Ala Leu Gln Ile Leu Phe Ser Glu Asp Ser Thr	
447	452 457 462
aag ctc ttt gta gca tca aat caa gga gct ctg cat att gtt cag ctg	1619
Lys Leu Phe Val Ala Ser Asn Gln Gly Ala Leu His Ile Val Gln Leu	
463	468 473 478
tca gga gga agc ttc aag cac ctg cat gct ttc cag cct cag tca gga	1667
Ser Gly Gly Ser Phe Lys His Leu His Ala Phe Gln Pro Gln Ser Gly	
479	484 489 494
aca gtg gag gcc atg tgt ctt ttg gca gtc agt cca gat ggg aat tgg	1715
Thr Val Glu Ala Met Cys Leu Leu Ala Val Ser Pro Asp Gly Asn Trp	
495	500 505 510
cta gct gca tca ggt acc agt gct gga gtc cat gtc tac aac gta aaa	1763
Leu Ala Ala Ser Gly Thr Ser Ala Gly Val His Val Tyr Asn Val Lys	
511	516 521 526
cag cta aag ctt cac tgc acg gtg cct gct tac aat ttc cca gtg act	1811
Gln Leu Lys Leu His Cys Thr Val Pro Ala Tyr Asn Phe Pro Val Thr	
527	532 537 542
gct atg gct att gcc ccc aat acc aac aac ctt gtc atc gct cat tcg	1859
Ala Met Ala Ile Ala Pro Asn Thr Asn Asn Leu Val Ile Ala His Ser	
543	548 553 558
gac cag cag gta ttt gag tac agc atc cca gac aaa cag tat aca gat	1907
Asp Gln Gln Val Phe Glu Tyr Ser Ile Pro Asp Lys Gln Tyr Thr Asp	
559	564 569 574
tgg agc cgg act gtc cag aag cag ggc ttt cac cac ctt tgg ctc caa	1955
Trp Ser Arg Thr Val Gln Lys Gln Gly Phe His His Leu Trp Leu Gln	
575	580 585 590
agg gat act cct atc aca cac atc agt ttt cat ccc aag aga ccg atg	2003
Arg Asp Thr Pro Ile Thr His Ile Ser Phe His Pro Lys Arg Pro Met	
591	596 601 606
cac atc ctt ctc cat gat gcc tac atg ttc tgc atc att gac aag tca	2051
His Ile Leu Leu His Asp Ala Tyr Met Phe Cys Ile Ile Asp Lys Ser	
607	612 617 622
ttg ccc ctt cca aat gac aaa acc tta ctc tac aat cca ttt cct ccc	2099
Leu Pro Leu Pro Asn Asp Lys Thr Leu Leu Tyr Asn Pro Phe Pro Pro	
623	628 633 638
acg aat gac atc att gct cag ctc cca cca ccc att aaa aag aag aaa	2147
Thr Asn Asp Ile Ile Ala Gln Leu Pro Pro Pro Ile Lys Lys Lys Lys	
639	644 649 654
ttt gga acc taa aac agggcactgt ctgtgtcctt ccttgaactg tctaccctgt	2202
Phe Gly Thr *	
655	
tgctttttcac aaatcatggt aataaaacaa gttattcttg aaaaaaaaaa aa	2254

<210> 74
 <211> 3718
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (90)..(3122)

<400> 74
 caccgggtccg gaattcccgg gtgcagcatt tcgtcctgac ctgcagcctc cggacctcgc 60
 tgcagcgcgg acccggccccg cccgcccga atg agt cag ctg agg ctg ctg ccg 113
 Met Ser Gln Leu Arg Leu Leu Pro
 1 5
 tcc cgt ctt ggg gta cag gct gcg agg ctc ctg gct gca cat gac gtc 161
 Ser Arg Leu Gly Val Gln Ala Ala Arg Leu Leu Ala Ala His Asp Val
 9 14 19 24
 ccg gtg ttt ggc tgg cgc agc agg tcc tcc ggg cca ccg gcc acc ttc 209
 Pro Val Phe Gly Trp Arg Ser Arg Ser Ser Gly Pro Pro Ala Thr Phe
 25 30 35 40
 cca agc agc aaa ggt gga ggc ggc tcc agt tac atg gag gag atg tac 257
 Pro Ser Ser Lys Gly Gly Gly Gly Ser Ser Tyr Met Glu Glu Met Tyr
 41 46 51 56
 ttc gcc tgg ttg gaa aac ccc cag agt gtc cac aag tcc tgg gac agc 305
 Phe Ala Trp Leu Glu Asn Pro Gln Ser Val His Lys Ser Trp Asp Ser
 57 62 67 72
 ttc ttc agg gaa gcc agc gag gaa gcc ttt tct ggc tct gct cag cca 353
 Phe Phe Arg Glu Ala Ser Glu Glu Ala Phe Ser Gly Ser Ala Gln Pro
 73 78 83 88
 cgg ccc cct tct gtt gtc cat gag agc agg tct gca gtc tca agt cgg 401
 Arg Pro Pro Ser Val Val His Glu Ser Arg Ser Ala Val Ser Ser Arg
 89 94 99 104
 acc aag acc agc aaa ttg gtg gag gac cac ctg gct gtg cag tcc ctg 449
 Thr Lys Thr Ser Lys Leu Val Glu Asp His Leu Ala Val Gln Ser Leu
 105 110 115 120
 atc cgg gcc tac cag atc cgg ggt cac cat gtg gcc cag ctg gac ccc 497
 Ile Arg Ala Tyr Gln Ile Arg Gly His His Val Ala Gln Leu Asp Pro
 121 126 131 136
 ctg ggc att ctg gat gca gac ctg gac tcc ttt gtg ccc tca gac ttg 545
 Leu Gly Ile Leu Asp Ala Asp Leu Asp Ser Phe Val Pro Ser Asp Leu
 137 142 147 152
 atc aca acc att gat aaa ctg gcc ttc tat gac ctt cag gag gct gac 593
 Ile Thr Thr Ile Asp Lys Leu Ala Phe Tyr Asp Leu Gln Glu Ala Asp

153	158	163	168	
ctt gat aag gag ttc cag ctg ccg aca acc acc ttc att ggg ggc tct				641
Leu Asp Lys Glu Phe Gln Leu Pro Thr Thr Thr Phe Ile Gly Gly Ser				
169	174	179	184	
gaa aac acc ctt tct ctg cgg gag atc att cgg cgc ctg gag aac acc				689
Glu Asn Thr Leu Ser Leu Arg Glu Ile Ile Arg Arg Leu Glu Asn Thr				
185	190	195	200	
tac tgc cag cac att ggc ctg gag ttc atg ttc atc aac gat gtg gag				737
Tyr Cys Gln His Ile Gly Leu Glu Phe Met Phe Ile Asn Asp Val Glu				
201	206	211	216	
cag tgc cag tgg atc cgg cag aag ttt gag acc cct ggt gtg atg cag				785
Gln Cys Gln Trp Ile Arg Gln Lys Phe Glu Thr Pro Gly Val Met Gln				
217	222	227	232	
ttc tcc agc gag gag aag cgg acc ctg ctg gcc cgg cta gtg cgc tcc				833
Phe Ser Ser Glu Glu Lys Arg Thr Leu Leu Ala Arg Leu Val Arg Ser				
233	238	243	248	
atg agg ttt gaa gac ttc ctg gcc cgg aaa tgg tcc tca gag aag cgg				881
Met Arg Phe Glu Asp Phe Leu Ala Arg Lys Trp Ser Ser Glu Lys Arg				
249	254	259	264	
ttt ggc ctg gag ggc tgt gaa gtg atg att cct gcc ctc aag acc atc				929
Phe Gly Leu Glu Gly Cys Glu Val Met Ile Pro Ala Leu Lys Thr Ile				
265	270	275	280	
atc gac aaa tcc agc gag atg ggg att gag aat gtc atc ttg ggg atg				977
Ile Asp Lys Ser Ser Glu Met Gly Ile Glu Asn Val Ile Leu Gly Met				
281	286	291	296	
cca cac agg gga agg ctg aac gtg ctg gcc aac gtg atc cgc aag gac				1025
Pro His Arg Gly Arg Leu Asn Val Leu Ala Asn Val Ile Arg Lys Asp				
297	302	307	312	
ctg gag cag atc ttc tgc cgg ttt gac ccc aag ctg gag gcg gcg gac				1073
Leu Glu Gln Ile Phe Cys Arg Phe Asp Pro Lys Leu Glu Ala Ala Asp				
313	318	323	328	
gag ggc tcc ggg gat gtc aag tac cac ctg ggc atg tac cat gag agg				1121
Glu Gly Ser Gly Asp Val Lys Tyr His Leu Gly Met Tyr His Glu Arg				
329	334	339	344	
atc aac cgc gtc acc aac cgg aac atc act ctg tcg ctg gtt gcc aac				1169
Ile Asn Arg Val Thr Asn Arg Asn Ile Thr Leu Ser Leu Val Ala Asn				
345	350	355	360	
ccc tcc cac ctg gag gca gtg gac cct gtg gtg cag ggg aag aca aag				1217
Pro Ser His Leu Glu Ala Val Asp Pro Val Val Gln Gly Lys Thr Lys				
361	366	371	376	
gca gag cag ttc tac cgt gga gat gcc cag ggc aag aag gtc atg tcc				1265
Ala Glu Gln Phe Tyr Arg Gly Asp Ala Gln Gly Lys Lys Val Met Ser				
377	382	387	392	

atc ctg gtt cat ggg gac gcc gcc ttt gct ggc cag ggc gtg gta tat	1313
Ile Leu Val His Gly Asp Ala Ala Phe Ala Gly Gln Gly Val Val Tyr	
393 398 403 408	
gag acc ttc cac ctg agc gac ctg ccc tcc tac acg acc aat ggt acc	1361
Glu Thr Phe His Leu Ser Asp Leu Pro Ser Tyr Thr Thr Asn Gly Thr	
409 414 419 424	
gtg cac gtc gtc gtc aac aac cag att gga ttc acc aca gac ccc cga	1409
Val His Val Val Val Asn Asn Gln Ile Gly Phe Thr Thr Asp Pro Arg	
425 430 435 440	
atg gcc cgc tcc tca cca tac ccg acc gac gtg gcc cgg gtg gtc aat	1457
Met Ala Arg Ser Ser Pro Tyr Pro Thr Asp Val Ala Arg Val Val Asn	
441 446 451 456	
gcg cct atc ttc cat gtg aat gcc gat gac cca gag gct gtg ata tat	1505
Ala Pro Ile Phe His Val Asn Ala Asp Asp Pro Glu Ala Val Ile Tyr	
457 462 467 472	
gtg tgc agt gtg gca gcc gaa tgg aga aac act ttc aac aaa gat gtt	1553
Val Cys Ser Val Ala Ala Glu Trp Arg Asn Thr Phe Asn Lys Asp Val	
473 478 483 488	
gtc gtg gac ctg gtc tgt tac cgc cgg cgt ggc cac aat gag atg gac	1601
Val Val Asp Leu Val Cys Tyr Arg Arg Arg Gly His Asn Glu Met Asp	
489 494 499 504	
gag ccc atg ttc acc cag ccg ctc atg tac aag cag atc cac aga cag	1649
Glu Pro Met Phe Thr Gln Pro Leu Met Tyr Lys Gln Ile His Arg Gln	
505 510 515 520	
gtg cct gtg ctg aag aag tac gca gac aag ctg att gcc gag ggc aca	1697
Val Pro Val Leu Lys Lys Tyr Ala Asp Lys Leu Ile Ala Glu Gly Thr	
521 526 531 536	
gtc acc ctg cag gag ttt gag gaa gaa att gcc aaa tac gac cgg atc	1745
Val Thr Leu Gln Glu Phe Glu Glu Glu Ile Ala Lys Tyr Asp Arg Ile	
537 542 547 552	
tgt gag gag gct tat ggc agg tcc aag gat aaa aag att ctg cat ata	1793
Cys Glu Glu Ala Tyr Gly Arg Ser Lys Asp Lys Lys Ile Leu His Ile	
553 558 563 568	
aag cac tgg ttg gac tcc ccc tgg cct ggc ttc ttc aac gta gat ggg	1841
Lys His Trp Leu Asp Ser Pro Trp Pro Gly Phe Phe Asn Val Asp Gly	
569 574 579 584	
gag ccc aag agc atg aca tgc cca gcc acg ggg atc cct gag gac atg	1889
Glu Pro Lys Ser Met Thr Cys Pro Ala Thr Gly Ile Pro Glu Asp Met	
585 590 595 600	
ctc acc cac atc ggc agt gtg gcc agc tct gtg ccc ctg gag gac ttt	1937
Leu Thr His Ile Gly Ser Val Ala Ser Ser Val Pro Leu Glu Asp Phe	
601 606 611 616	

aag atc cac act ggc ctc tct cgc att ctg cgg ggc cgt gcg gac atg	1985
Lys Ile His Thr Gly Leu Ser Arg Ile Leu Arg Gly Arg Ala Asp Met	
617 622 627 632	
acc aag aac cgg acg gtg gac tgg gcg ttg gca gag tac atg gcc ttt	2033
Thr Lys Asn Arg Thr Val Asp Trp Ala Leu Ala Glu Tyr Met Ala Phe	
633 638 643 648	
ggc tcc ctg ctg aag gaa ggc atc cac gtg cgg ctc agc ggg cag gat	2081
Gly Ser Leu Leu Lys Glu Gly Ile His Val Arg Leu Ser Gly Gln Asp	
649 654 659 664	
gtg gag agg ggc aca ttc agt cac cgg cac cat gtt ctc cat gac cag	2129
Val Glu Arg Gly Thr Phe Ser His Arg His His Val Leu His Asp Gln	
665 670 675 680	
gag gtt gac cgc agg acg tgt gtg cct atg aat cat ctc tgg cct gac	2177
Glu Val Asp Arg Arg Thr Cys Val Pro Met Asn His Leu Trp Pro Asp	
681 686 691 696	
cag gcc ccg tac acc gtg tgc aac agc tcc ctc tcg gag tac gga gtc	2225
Gln Ala Pro Tyr Thr Val Cys Asn Ser Ser Leu Ser Glu Tyr Gly Val	
697 702 707 712	
ctg ggc ttt gag ctg ggc tat gcc atg gcc agc ccc aat gcc ctg gtc	2273
Leu Gly Phe Glu Leu Gly Tyr Ala Met Ala Ser Pro Asn Ala Leu Val	
713 718 723 728	
ctc tgg gag gcc cag ttt ggg gac ttc cac aac acg gcc cag tgc atc	2321
Leu Trp Glu Ala Gln Phe Gly Asp Phe His Asn Thr Ala Gln Cys Ile	
729 734 739 744	
atc gac cag ttc atc agc acc ggc cag gcc aag tgg gtg cgg cat aat	2369
Ile Asp Gln Phe Ile Ser Thr Gly Gln Ala Lys Trp Val Arg His Asn	
745 750 755 760	
ggc att gtg ctg ctg ctg ccc cat ggc atg gaa ggc atg ggc cca gag	2417
Gly Ile Val Leu Leu Leu Pro His Gly Met Glu Gly Met Gly Pro Glu	
761 766 771 776	
cac tcg tca gcg agg ccc gaa agg ttc ctg cag atg agc aat gat gac	2465
His Ser Ser Ala Arg Pro Glu Arg Phe Leu Gln Met Ser Asn Asp Asp	
777 782 787 792	
tcg gat gcc tac cct gca ttc acc aag gac ttc gag gtg agc cag ctc	2513
Ser Asp Ala Tyr Pro Ala Phe Thr Lys Asp Phe Glu Val Ser Gln Leu	
793 798 803 808	
tat gac tgc aac tgg atc gtg gtc aac tgc tcc aca ccg gcc aac tac	2561
Tyr Asp Cys Asn Trp Ile Val Val Asn Cys Ser Thr Pro Ala Asn Tyr	
809 814 819 824	
ttc cac gtg ctg cgc cgg cag atc ctg ctg ccc ttc cgc aag ccg ctg	2609
Phe His Val Leu Arg Arg Gln Ile Leu Leu Pro Phe Arg Lys Pro Leu	
825 830 835 840	
att atc ttc aca cct aaa tct ctg ctg agg cac cca gag gcc aag tcc	2657

Ile Ile Phe Thr Pro Lys Ser Leu Leu Arg His Pro Glu Ala Lys Ser	
841 846 851 856	
agc ttt gac caa atg gta tcc ggg acc agc ttc cag cgg gtg att cct	2705
Ser Phe Asp Gln Met Val Ser Gly Thr Ser Phe Gln Arg Val Ile Pro	
857 862 867 872	
gaa gat ggg gcc gca gca cgg gcc cct gag cag gtg cag cgg ctc atc	2753
Glu Asp Gly Ala Ala Ala Arg Ala Pro Glu Gln Val Gln Arg Leu Ile	
873 878 883 888	
ttc tgc acg gga aag gtg tac tat gac ctg gtg aag gag cgg agc agc	2801
Phe Cys Thr Gly Lys Val Tyr Tyr Asp Leu Val Lys Glu Arg Ser Ser	
889 894 899 904	
cag gac ctg gag gag aaa gtg gcc atc acg cgc ctg gag cag atc tct	2849
Gln Asp Leu Glu Glu Lys Val Ala Ile Thr Arg Leu Glu Gln Ile Ser	
905 910 915 920	
cca ttc ccc ttc gac ctg atc aag cag gag gca gag aag tac cca ggt	2897
Pro Phe Pro Phe Asp Leu Ile Lys Gln Glu Ala Glu Lys Tyr Pro Gly	
921 926 931 936	
gcg gag ctg gcc tgg tgt cag gag gag cac aag aac atg ggc tac tat	2945
Ala Glu Leu Ala Trp Cys Gln Glu Glu His Lys Asn Met Gly Tyr Tyr	
937 942 947 952	
gac tac atc agc cca cgc ttc atg acc atc ctg agg cgc gca cgg ccc	2993
Asp Tyr Ile Ser Pro Arg Phe Met Thr Ile Leu Arg Arg Ala Arg Pro	
953 958 963 968	
ata tgg tat gtt ggc cgg gac cca gcg gct gca cca gcc aca gga aac	3041
Ile Trp Tyr Val Gly Arg Asp Pro Ala Ala Ala Pro Ala Thr Gly Asn	
969 974 979 984	
agg aac act cac ctg gtg tca ctg aag aag ttt ctg gat act gcc ttc	3089
Arg Asn Thr His Leu Val Ser Leu Lys Lys Phe Leu Asp Thr Ala Phe	
985 990 995 1000	
aat ctc cag gcc ttt gag ggc aag aca ttt tag agctgggc aaaacctgtg	3140
Asn Leu Gln Ala Phe Glu Gly Lys Thr Phe *	
1001 1006 1011	
taggtctcgc tgtgggtttg ctggggacca aggggggtgat gaaaagggga ggggcggagc	3200
tcctgccccaa gagagggggct gtggggcccc aggataaaac agacacagtg acagggccaa	3260
gagccagcac tgctggcctt ggtgtcatgc cagaatctac caggactgag ggagccagag	3320
gagtccataa ggcaggctac tgtgtctggag catccccag ctgctcccat cttgtctggaa	3380
tttcttgggc ggcttctcca cctgtatctc aagacagaca cccggggggcc tgtgtctgtg	3440
gccgctccca tcccggcagc cctggctgct gctcgcccca ccctcgctta tdtgtagatt	3500
caaagcgatg ttctcttctg tgctcttaga agtagggagt tcagcagtaa cagccaggtg	3560

aagcgaacct gctgggtgat ttgtttgcgc tctgttttat ggggcattcc tgcgagatgt 3620
gtcagcttct gtgtgaaatg cagccacagc tcatgtgtac caaagtagaa aaccaaata 3680
cagagaaata aaaacatgct tcagagaaaa aaaaaaaa 3718

<210> 75
<211> 13857
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(13857)

<400> 75

atg cca gcc cag tat gct cta acc tcc agc ctg gtt ctc ctg gtg ctg 48
Met Pro Ala Gln Tyr Ala Leu Thr Ser Ser Leu Val Leu Leu Val Leu
1 5 10

ctg agc aca gcc aga gca ggc ccc ttc tct tca cgg tcc aat gtg aca 96
Leu Ser Thr Ala Arg Ala Gly Pro Phe Ser Ser Arg Ser Asn Val Thr
17 22 27 32

ctg cca gcc ccc cgg ccc cct ccc cag cca ggg ggc cac aca gtg ggg 144
Leu Pro Ala Pro Arg Pro Pro Pro Gln Pro Gly Gly His Thr Val Gly
33 38 43 48

gct gga gtg gga agc ccc tct tct cag ctt tac gag cac aca gtg gaa 192
Ala Gly Val Gly Ser Pro Ser Ser Gln Leu Tyr Glu His Thr Val Glu
49 54 59 64

gga ggg gag aag cag gtg gta ttc acc cac cgc att aac ctg ccc cct 240
Gly Gly Glu Lys Gln Val Val Phe Thr His Arg Ile Asn Leu Pro Pro
65 70 75 80

tcc act ggc tgt ggc tgt ccc cca ggc acc gag ccc cca gtc ctt gct 288
Ser Thr Gly Cys Gly Cys Pro Pro Gly Thr Glu Pro Pro Val Leu Ala
81 86 91 96

tca gag gta cag gcc ctg agg gtc cgt cta gag atc ctg gag gag ttg 336
Ser Glu Val Gln Ala Leu Arg Val Arg Leu Glu Ile Leu Glu Glu Leu
97 102 107 112

gtg aag ggg ctc aag gaa cag tgc act ggg gga tgt tgt cct gcc tct 384
Val Lys Gly Leu Lys Glu Gln Cys Thr Gly Gly Cys Cys Pro Ala Ser
113 118 123 128

gcc caa gct ggc aca ggt cag aca gat gtg cgg acc ctc tgc agt ctc 432
Ala Gln Ala Gly Thr Gly Gln Thr Asp Val Arg Thr Leu Cys Ser Leu
129 134 139 144

cat ggt gtg ttt gat ctg agc cgc tgc acc tgt tcc tgt gag cca ggc 480
His Gly Val Phe Asp Leu Ser Arg Cys Thr Cys Ser Cys Glu Pro Gly

145		150		155		160	
tgg ggt ggg ccc acc tgc tca gac ccc aca gat gct gag atc cct ccc	528						
Trp Gly Gly Pro Thr Cys Ser Asp Pro Thr Asp Ala Glu Ile Pro Pro							
161		166		171		176	
tct tcc cca ccc tca gcc tcg ggg tcc tgc cca gat gac tgc aat gat	576						
Ser Ser Pro Pro Ser Ala Ser Gly Ser Cys Pro Asp Asp Cys Asn Asp							
177		182		187		192	
cag ggt cgc tgt gtc cgt ggt cgt tgc gtg tgc ttt ccc ggc tac act	624						
Gln Gly Arg Cys Val Arg Gly Arg Cys Val Cys Phe Pro Gly Tyr Thr							
193		198		203		208	
ggc ccc agc tgt ggc tgg cca tcc tgt ccc ggg gac tgc caa ggc cgt	672						
Gly Pro Ser Cys Gly Trp Pro Ser Cys Pro Gly Asp Cys Gln Gly Arg							
209		214		219		224	
ggg cgc tgc gtg cag ggc gtg tgt gtg tgc cgg gca ggc ttc tca ggc	720						
Gly Arg Cys Val Gln Gly Val Cys Val Cys Arg Ala Gly Phe Ser Gly							
225		230		235		240	
ccc gac tgc agc cag cgc tcc tgc cct cga ggt tgc agc cag agg gga	768						
Pro Asp Cys Ser Gln Arg Ser Cys Pro Arg Gly Cys Ser Gln Arg Gly							
241		246		251		256	
cgc tgt gag ggt ggg cgc tgc gtg tgt gac cca ggc tac act ggt gac	816						
Arg Cys Glu Gly Gly Arg Cys Val Cys Asp Pro Gly Tyr Thr Gly Asp							
257		262		267		272	
gac tgt ggc atg agg agc tgc cct cgc ggt tgc agt cag agg ggg cgc	864						
Asp Cys Gly Met Arg Ser Cys Pro Arg Gly Cys Ser Gln Arg Gly Arg							
273		278		283		288	
tgt gag aat ggg cgc tgc gtg tgt aac ccc ggc tac act ggc gag gac	912						
Cys Glu Asn Gly Arg Cys Val Cys Asn Pro Gly Tyr Thr Gly Glu Asp							
289		294		299		304	
tgt ggg gtg agg agc tgc cct cgg ggc tgc agc cag cgg gga cgc tgc	960						
Cys Gly Val Arg Ser Cys Pro Arg Gly Cys Ser Gln Arg Gly Arg Cys							
305		310		315		320	
aag gac ggg cgc tgc gtg tgt gac ccc ggc tac act ggc gag gac tgt	1008						
Lys Asp Gly Arg Cys Val Cys Asp Pro Gly Tyr Thr Gly Glu Asp Cys							
321		326		331		336	
ggg acg cgg agc tgc ccc tgg gac tgt ggc gag ggc ggg cgc tgc gtg	1056						
Gly Thr Arg Ser Cys Pro Trp Asp Cys Gly Glu Gly Gly Arg Cys Val							
337		342		347		352	
gac ggc cgc tgc gtg tgc tgg ccc ggg tac aca ggc gag gac tgc agc	1104						
Asp Gly Arg Cys Val Cys Trp Pro Gly Tyr Thr Gly Glu Asp Cys Ser							
353		358		363		368	
acg cgg aca tgt ccg agg gac tgc cgg ggc cgc ggg cgc tgc gag gac	1152						
Thr Arg Thr Cys Pro Arg Asp Cys Arg Gly Arg Gly Arg Cys Glu Asp							
369		374		379		384	

ggc gaa tgc att tgc gac acg ggc tac agc ggg gac gac tgc ggc gtg	1200
Gly Glu Cys Ile Cys Asp Thr Gly Tyr Ser Gly Asp Asp Cys Gly Val	
385 390 395 400	
cgc agc tgc cct ggc gac tgc aac caa agg ggc cgc tgc gag gac ggc	1248
Arg Ser Cys Pro Gly Asp Cys Asn Gln Arg Gly Arg Cys Glu Asp Gly	
401 406 411 416	
cgc tgc gtg tgc tgg ccg ggg tac act gga acc gat tgc ggc tcg cgc	1296
Arg Cys Val Cys Trp Pro Gly Tyr Thr Gly Thr Asp Cys Gly Ser Arg	
417 422 427 432	
gcc tgc cca cgc gac tgt aga ggt cgc ggg cgc tgc gag aac ggc gtg	1344
Ala Cys Pro Arg Asp Cys Arg Gly Arg Gly Arg Cys Glu Asn Gly Val	
433 438 443 448	
tgt gtt tgc aat gcg ggc tac agc ggc gag gac tgc ggt gtg cgc agc	1392
Cys Val Cys Asn Ala Gly Tyr Ser Gly Glu Asp Cys Gly Val Arg Ser	
449 454 459 464	
tgt cct ggg gac tgt cgt ggc cgg ggc cgc tgt gag agt ggc cgc tgc	1440
Cys Pro Gly Asp Cys Arg Gly Arg Gly Arg Cys Glu Ser Gly Arg Cys	
465 470 475 480	
atg tgt tgg ccg ggg tac aca ggc cgg gac tgc ggc acg cgc gcc tgt	1488
Met Cys Trp Pro Gly Tyr Thr Gly Arg Asp Cys Gly Thr Arg Ala Cys	
481 486 491 496	
cct ggc gac tgt cgc ggg cgc ggg cgc tgc gtg gat ggc cgc tgc gtg	1536
Pro Gly Asp Cys Arg Gly Arg Gly Arg Cys Val Asp Gly Arg Cys Val	
497 502 507 512	
tgc aac ccg ggc ttc acc ggt gag gac tgt ggg agc cgt cgc tgt ccc	1584
Cys Asn Pro Gly Phe Thr Gly Glu Asp Cys Gly Ser Arg Arg Cys Pro	
513 518 523 528	
ggg gac tgc cgt ggg cac ggc ctt tgc gag gat ggc gtg tgc gtg tgt	1632
Gly Asp Cys Arg Gly His Gly Leu Cys Glu Asp Gly Val Cys Val Cys	
529 534 539 544	
gac gca ggc tac tca ggg gaa gac tgc agc acg cgc agc tgc ccc ggg	1680
Asp Ala Gly Tyr Ser Gly Glu Asp Cys Ser Thr Arg Ser Cys Pro Gly	
545 550 555 560	
ggc tgc cga ggc cgc ggc cag tgc cta gat ggg cgg tgt gtg tgc gag	1728
Gly Cys Arg Gly Arg Gly Gln Cys Leu Asp Gly Arg Cys Val Cys Glu	
561 566 571 576	
gac ggc tac tct ggc gag gat tgc ggt gtg agg cag tgc ccg aat gac	1776
Asp Gly Tyr Ser Gly Glu Asp Cys Gly Val Arg Gln Cys Pro Asn Asp	
577 582 587 592	
tgc agc cag cac ggc gtg tgc cag gac ggt gtg tgc atc tgt tgg gaa	1824
Cys Ser Gln His Gly Val Cys Gln Asp Gly Val Cys Ile Cys Trp Glu	
593 598 603 608	

ggc tac gtg agt gag gac tgc agc atc cgc acc tgc ccc tcc aac tgc	1872
Gly Tyr Val Ser Glu Asp Cys Ser Ile Arg Thr Cys Pro Ser Asn Cys	
609 614 619 624	
cac ggg agg ggc cgc tgt gag gaa ggg cgc tgc ctg tgc gac cca ggc	1920
His Gly Arg Gly Arg Cys Glu Glu Gly Arg Cys Leu Cys Asp Pro Gly	
625 630 635 640	
tac acc ggc cct acc tgt gcc acc cgc atg tgc ccg gct gac tgc cgg	1968
Tyr Thr Gly Pro Thr Cys Ala Thr Arg Met Cys Pro Ala Asp Cys Arg	
641 646 651 656	
gga cgt ggg cgg tgt gtg caa gga gtg tgc ctg tgc cac gtg ggc tat	2016
Gly Arg Gly Arg Cys Val Gln Gly Val Cys Leu Cys His Val Gly Tyr	
657 662 667 672	
ggc ggt gag gac tgc ggg cag gaa gag cct cca gcc agc gcc tgc cct	2064
Gly Gly Glu Asp Cys Gly Gln Glu Glu Pro Pro Ala Ser Ala Cys Pro	
673 678 683 688	
gga ggc tgc ggg ccc cgg gaa ctg tgc cgg gca ggc cag tgt gtg tgt	2112
Gly Gly Cys Gly Pro Arg Glu Leu Cys Arg Ala Gly Gln Cys Val Cys	
689 694 699 704	
gta gag ggc ttc cga ggc cct gac tgt gcc atc cag aca tgc cca ggg	2160
Val Glu Gly Phe Arg Gly Pro Asp Cys Ala Ile Gln Thr Cys Pro Gly	
705 710 715 720	
gac tgc cgt ggc cga gga gag tgt cac gat ggc agc tgt gtc tgc aaa	2208
Asp Cys Arg Gly Arg Gly Glu Cys His Asp Gly Ser Cys Val Cys Lys	
721 726 731 736	
gat ggg tat gct ggc gaa gac tgc gga gaa gag gtg cca acc att gag	2256
Asp Gly Tyr Ala Gly Glu Asp Cys Gly Glu Glu Val Pro Thr Ile Glu	
737 742 747 752	
ggc atg agg atg cat ctc ttg gag gag aca aca gtt cgg aca gag tgg	2304
Gly Met Arg Met His Leu Leu Glu Glu Thr Thr Val Arg Thr Glu Trp	
753 758 763 768	
acc ccg gct cct ggc ccc gtg gat gcc tat gaa att cag ttc atc ccc	2352
Thr Pro Ala Pro Gly Pro Val Asp Ala Tyr Glu Ile Gln Phe Ile Pro	
769 774 779 784	
acg aca gag ggg gcg agc ccc cca ttc aca gca cgg gtt cca agc tct	2400
Thr Thr Glu Gly Ala Ser Pro Pro Phe Thr Ala Arg Val Pro Ser Ser	
785 790 795 800	
gcc tca gcc tat gac cag aga gga ctg gcc cct gga cag gag tac cag	2448
Ala Ser Ala Tyr Asp Gln Arg Gly Leu Ala Pro Gly Gln Glu Tyr Gln	
801 806 811 816	
gtc act gtc cga gcc ctt cga ggg acc agc tgg ggc ctt cct gcc tcc	2496
Val Thr Val Arg Ala Leu Arg Gly Thr Ser Trp Gly Leu Pro Ala Ser	
817 822 827 832	
aag acc atc acc acc atg atc gat ggg ccc cag gac ctc cga gtg gtg	2544

Lys Thr Ile Thr Thr	Met Ile Asp Gly Pro Gln Asp Leu Arg Val Val	
833	838	843 848
gct gtg aca ccg aca	aca ctg gag ctt ggc tgg ctg cgt ccc cag gct	2592
Ala Val Thr Pro Thr	Thr Leu Glu Leu Gly Trp Leu Arg Pro Gln Ala	
849	854 859	864
gag gtg gac cga ttt	gtg gtg tcc tac gtc agt gcc ggc aac cag agg	2640
Glu Val Asp Arg Phe	Val Val Ser Tyr Val Ser Ala Gly Asn Gln Arg	
865	870 875	880
gtg agg ctg gaa gtg	ccc cct gaa gca gac ggg acg ctg ctg act gac	2688
Val Arg Leu Glu Val	Pro Pro Glu Ala Asp Gly Thr Leu Leu Thr Asp	
881	886 891	896
ctg atg cca ggc gta	gaa tat gtg gtg act gtc aca gcg gag cgg ggc	2736
Leu Met Pro Gly Val	Glu Tyr Val Val Thr Val Thr Ala Glu Arg Gly	
897	902 907	912
cgg gca gtc agc tac	cca gct tct gtc agg gcc aac aca ggg cac caa	2784
Arg Ala Val Ser Tyr	Pro Ala Ser Val Arg Ala Asn Thr Gly His Gln	
913	918 923	928
cag tgg tgg gct tgg	agg gga atg ggg ggg ctg cgg gac act gac cga	2832
Gln Trp Trp Ala Trp	Arg Gly Met Gly Gly Leu Arg Asp Thr Asp Arg	
929	934 939	944
ttt ccc tcc gtt ctc	ttt cca gca cca ggc cac tac agt tac ccg gag	2880
Phe Pro Ser Val Leu	Phe Pro Ala Pro Gly His Tyr Ser Tyr Pro Glu	
945	950 955	960
gtg cgc ccc cca gcc	ccg ccc ccc aag tcc cgg ccc cgg cca gcc cca	2928
Val Arg Pro Pro Ala	Pro Pro Pro Lys Ser Arg Pro Arg Pro Ala Pro	
961	966 971	976
gcc ccg cgg ccc cca	cgg ccc cct tgg ccc tcg agg cca gca gag gaa	2976
Ala Pro Arg Pro Pro	Arg Pro Pro Trp Pro Ser Arg Pro Ala Glu Glu	
977	982 987	992
agg gag gag gag tcc	ccg ccc agg cca agc ctg tcc cag ccc cca cgg	3024
Arg Glu Glu Glu Ser	Pro Pro Arg Pro Ser Leu Ser Gln Pro Pro Arg	
993	998 1003	1008
cgg cct tgg ggc aac	ctg acg gcc gag ctg agc cgt ttc cgc ggc acg	3072
Arg Pro Trp Gly Asn	Leu Thr Ala Glu Leu Ser Arg Phe Arg Gly Thr	
1009	1014 1019	1024
gtg cag gac ctg gag	cgc cac ctg cgg gct cac ggc tac cca ctg cgg	3120
Val Gln Asp Leu Glu	Arg His Leu Arg Ala His Gly Tyr Pro Leu Arg	
1025	1030 1035	1040
gcc aac cag act tac	acg tcg gtg gcg cgc cac atc cat gaa tac ttg	3168
Ala Asn Gln Thr Tyr	Thr Ser Val Ala Arg His Ile His Glu Tyr Leu	
1041	1046 1051	1056
cag cgg cgt ctg ttg	gcc gcc gcc cca gcc ggc tcc ccc gca ccc ccg	3216
Gln Arg Arg Leu Leu	Ala Ala Ala Pro Ala Gly Ser Pro Ala Pro Pro	

1057	1062	1067	1072	
ccc cgc cac ccc cgc ccc acc gcc agc cct gat ccc ggc acc agg aaa				3264
Pro Arg His Pro Arg Pro Thr Ala Ser Pro Asp Pro Gly Thr Arg Lys				
1073	1078	1083	1088	
cgg gac tcc aac cag gga atc tac ggc ctc tcg cct gaa ggc gtc gac				3312
Arg Asp Ser Asn Gln Gly Ile Tyr Gly Leu Ser Pro Glu Gly Val Asp				
1089	1094	1099	1104	
cgg gtg gct gcg tcc cgc cac ccc aag cca gag gtg ctg ggc agt tcc				3360
Arg Val Ala Ala Ser Arg His Pro Lys Pro Glu Val Leu Gly Ser Ser				
1105	1110	1115	1120	
gcc gat ggc gcg ctt ctc gtg tct ctc gac ggg ctc cgc ggc cag ttc				3408
Ala Asp Gly Ala Leu Leu Val Ser Leu Asp Gly Leu Arg Gly Gln Phe				
1121	1126	1131	1136	
gag cgc gtg gtg ctg cgc tgg cgg cct cag ccg cct gca gag ggc ccc				3456
Glu Arg Val Val Leu Arg Trp Arg Pro Gln Pro Pro Ala Glu Gly Pro				
1137	1142	1147	1152	
ggc ggt gag ctg act gtg ccg ggc acc acg cgc acc gtc agc ctg ccc				3504
Gly Gly Glu Leu Thr Val Pro Gly Thr Thr Arg Thr Val Ser Leu Pro				
1153	1158	1163	1168	
gac ctc agg ccc ggc acc acc tac cac gtg gag gtc cac ggg gtg cgg				3552
Asp Leu Arg Pro Gly Thr Thr Tyr His Val Glu Val His Gly Val Arg				
1169	1174	1179	1184	
gcg ggg cag acc tcc aag tcc tac gcc ttc atc acc acc aca ggg tcc				3600
Ala Gly Gln Thr Ser Lys Ser Tyr Ala Phe Ile Thr Thr Thr Gly Ser				
1185	1190	1195	1200	
tca ccc ttg ggc ctc ttg ggg act acc gat gag cct cct ccc tca ggc				3648
Ser Pro Leu Gly Leu Leu Gly Thr Thr Asp Glu Pro Pro Pro Ser Gly				
1201	1206	1211	1216	
ccc tcg acg acg caa ggg gcc cag gct cct ctc ctg cag cag cgc ccc				3696
Pro Ser Thr Thr Gln Gly Ala Gln Ala Pro Leu Leu Gln Gln Arg Pro				
1217	1222	1227	1232	
cag gag ctg gga gag ttg agg gtg ctg ggc aga gat gag aca ggg cgc				3744
Gln Glu Leu Gly Glu Leu Arg Val Leu Gly Arg Asp Glu Thr Gly Arg				
1233	1238	1243	1248	
ctc cgt gtg gtc tgg acc gcc cag cct gac acc ttt gcc tac ttc caa				3792
Leu Arg Val Val Trp Thr Ala Gln Pro Asp Thr Phe Ala Tyr Phe Gln				
1249	1254	1259	1264	
ctg cgc atg cgg gtg ccc gag ggg ccg ggg gca cat gag gaa gtg ctg				3840
Leu Arg Met Arg Val Pro Glu Gly Pro Gly Ala His Glu Glu Val Leu				
1265	1270	1275	1280	
cca ggg gac gtc cgc cag gct ctg gtg cct cca ccc cct cct gga acc				3888
Pro Gly Asp Val Arg Gln Ala Leu Val Pro Pro Pro Pro Gly Thr				
1281	1286	1291	1296	

ccg tat gag ctg tca ctt cat ggg gtc cct cct ggg ggc aag ccc tct	3936
Pro Tyr Glu Leu Ser Leu His Gly Val Pro Pro Gly Gly Lys Pro Ser	
1297 1302 1307 1312	
gac ccc atc atc tac caa ggc att atg gac aag gat gag gag aag cct	3984
Asp Pro Ile Ile Tyr Gln Gly Ile Met Asp Lys Asp Glu Glu Lys Pro	
1313 1318 1323 1328	
ggg aag tcc tca ggc cca cca cgc ctg ggt gag ctg acg gtg aca gac	4032
Gly Lys Ser Ser Gly Pro Pro Arg Leu Gly Glu Leu Thr Val Thr Asp	
1329 1334 1339 1344	
agg acc tcc gac tcc ttg ctc ctg cgc tgg acg gtc ccc gag ggc gag	4080
Arg Thr Ser Asp Ser Leu Leu Leu Arg Trp Thr Val Pro Glu Gly Glu	
1345 1350 1355 1360	
ttt gac tcc ttc gtg atc cag tac aaa gac agg gac ggg cag ccc cag	4128
Phe Asp Ser Phe Val Ile Gln Tyr Lys Asp Arg Asp Gly Gln Pro Gln	
1361 1366 1371 1376	
gtg gtg ccc gtg gaa gga ccc cag cgc tcg gcc gtc atc acc tcc ctg	4176
Val Val Pro Val Glu Gly Pro Gln Arg Ser Ala Val Ile Thr Ser Leu	
1377 1382 1387 1392	
gat cct ggc cgc aag tac aaa ttt gtc ctg tat ggg ttt gtt ggc aag	4224
Asp Pro Gly Arg Lys Tyr Lys Phe Val Leu Tyr Gly Phe Val Gly Lys	
1393 1398 1403 1408	
aag agg cat ggt ccg ctg gtg gct gaa gcc aag atc ttg cct cag agt	4272
Lys Arg His Gly Pro Leu Val Ala Glu Ala Lys Ile Leu Pro Gln Ser	
1409 1414 1419 1424	
gac cca agt cca ggg act cca ccc cac ctg gga aac ctg tgg gtg aca	4320
Asp Pro Ser Pro Gly Thr Pro Pro His Leu Gly Asn Leu Trp Val Thr	
1425 1430 1435 1440	
gac cct acc cca gat tca ctg cac ctc tcc tgg act gtc cct gag ggc	4368
Asp Pro Thr Pro Asp Ser Leu His Leu Ser Trp Thr Val Pro Glu Gly	
1441 1446 1451 1456	
cag ttt gac acc ttc atg gtc cag tac agg gac agg gat gga cgg ccc	4416
Gln Phe Asp Thr Phe Met Val Gln Tyr Arg Asp Arg Asp Gly Arg Pro	
1457 1462 1467 1472	
cag gtg gta cct gtg gaa ggg ccc gag cgt tca ttt gtt gtc tcc tca	4464
Gln Val Val Pro Val Glu Gly Pro Glu Arg Ser Phe Val Val Ser Ser	
1473 1478 1483 1488	
ctg gac cct gac cac aag tac aga ttc act ctg ttt gga att gcg aac	4512
Leu Asp Pro Asp His Lys Tyr Arg Phe Thr Leu Phe Gly Ile Ala Asn	
1489 1494 1499 1504	
aag aag cgg tat ggc ccc ctc acg gcc gat ggc acc act ggt gtg aca	4560
Lys Lys Arg Tyr Gly Pro Leu Thr Ala Asp Gly Thr Thr Gly Val Thr	
1505 1510 1515 1520	

tcc cgt cga aac ccc aag ccc cag tcc cag gct gcc agt tca gca cct	4608
Ser Arg Arg Asn Pro Lys Pro Gln Ser Gln Ala Ala Ser Ser Ala Pro	
1521 1526 1531 1536	
ggc tgg atc tcc ttg ttt aca gct cca gag agg aaa gag gag ccc ccc	4656
Gly Trp Ile Ser Leu Phe Thr Ala Pro Glu Arg Lys Glu Glu Pro Pro	
1537 1542 1547 1552	
cgc cct gag ttc ctg gag cag ccc ctc ctg ggg gaa ctg aca gtg acc	4704
Arg Pro Glu Phe Leu Glu Gln Pro Leu Leu Gly Glu Leu Thr Val Thr	
1553 1558 1563 1568	
ggc gtg acc cca gac tcc ttg cgt ctc tca tgg aca gtg gcc cag ggc	4752
Gly Val Thr Pro Asp Ser Leu Arg Leu Ser Trp Thr Val Ala Gln Gly	
1569 1574 1579 1584	
ccc ttc gac tca ttc atg gtc cag tac aag gat gca cag ggg cag ccc	4800
Pro Phe Asp Ser Phe Met Val Gln Tyr Lys Asp Ala Gln Gly Gln Pro	
1585 1590 1595 1600	
cag gca gtg cct gtt gcg ggg gat gag aat gag gtt act gtc ccc ggc	4848
Gln Ala Val Pro Val Ala Gly Asp Glu Asn Glu Val Thr Val Pro Gly	
1601 1606 1611 1616	
ctg gat ccc gac cgg aag tat aag atg aac ctc tac ggg ctt cgt ggc	4896
Leu Asp Pro Asp Arg Lys Tyr Lys Met Asn Leu Tyr Gly Leu Arg Gly	
1617 1622 1627 1632	
agg cag cgt gtg ggg ccc gag tct gtg gtg gcc aag act gct cct cag	4944
Arg Gln Arg Val Gly Pro Glu Ser Val Val Ala Lys Thr Ala Pro Gln	
1633 1638 1643 1648	
gag gat gtg gac gag acc ccc agc ccc aca gaa ctg ggc acg gag gcc	4992
Glu Asp Val Asp Glu Thr Pro Ser Pro Thr Glu Leu Gly Thr Glu Ala	
1649 1654 1659 1664	
ccg gag tcc ccc gag gag ccg ctc ctg ggg gag ctg aca gtg aca gga	5040
Pro Glu Ser Pro Glu Glu Pro Leu Leu Gly Glu Leu Thr Val Thr Gly	
1665 1670 1675 1680	
tcc tcc cct gat tcc ctg agc ctc ttc tgg acc gtc ccc cag ggc agc	5088
Ser Ser Pro Asp Ser Leu Ser Leu Phe Trp Thr Val Pro Gln Gly Ser	
1681 1686 1691 1696	
ttc gac tct ttc acc gtg cag tac aag gac agg gat ggg cgg ccc cgg	5136
Phe Asp Ser Phe Thr Val Gln Tyr Lys Asp Arg Asp Gly Arg Pro Arg	
1697 1702 1707 1712	
gcg gtg cgt gtt ggg ggc aag gag agt gag gtc acc gtg gga ggc cta	5184
Ala Val Arg Val Gly Gly Lys Glu Ser Glu Val Thr Val Gly Gly Leu	
1713 1718 1723 1728	
gag ccc ggg cac aag tac aag atg cac ctg tac ggc ctc cac gag ggg	5232
Glu Pro Gly His Lys Tyr Lys Met His Leu Tyr Gly Leu His Glu Gly	
1729 1734 1739 1744	
cag cgc gtg ggc ccg gtg tcc gcc gtg ggc gtg aca ggg acc cac act	5280

Gln Arg Val Gly Pro Val Ser Ala Val Gly Val Thr Gly Thr His Thr	
1745	1750 1755 1760
ggg ctc tgt gag gcc ctg tgc ctg gtc cct ggg atg agg ccc ttt agg	5328
Gly Leu Cys Glu Ala Leu Cys Leu Val Pro Gly Met Arg Pro Phe Arg	
1761	1766 1771 1776
aaa gaa atg ggc atc agt gcg cat tat cag agc agc aaa agg acg aag	5376
Lys Glu Met Gly Ile Ser Ala His Tyr Gln Ser Ser Lys Arg Thr Lys	
1777	1782 1787 1792
cag ctg gag tcc gcc aag ctg ggg gct gtg tct ggc agc aca cac agt	5424
Gln Leu Glu Ser Ala Lys Leu Gly Ala Val Ser Gly Ser Thr His Ser	
1793	1798 1803 1808
gca gtt gcc agg ggg aga gcc tca gac acc gag cag gga cct agt gaa	5472
Ala Val Ala Arg Gly Arg Ala Ser Asp Thr Glu Gln Gly Pro Ser Glu	
1809	1814 1819 1824
gga ctg ttg acc aga cag atg ttc aga tca atg cgc ttt tac atc aaa	5520
Gly Leu Leu Thr Arg Gln Met Phe Arg Ser Met Arg Phe Tyr Ile Lys	
1825	1830 1835 1840
acc atc atg cgg gtt cca caa atg caa cag aca tcg ctg gcc cca caa	5568
Thr Ile Met Arg Val Pro Gln Met Gln Gln Thr Ser Leu Ala Pro Gln	
1841	1846 1851 1856
caa gaa gag acc cct cca gcc act gag tcc ccg ctg gag cca cgc cta	5616
Gln Glu Glu Thr Pro Pro Ala Thr Glu Ser Pro Leu Glu Pro Arg Leu	
1857	1862 1867 1872
gga gag ctg aca gtg aca gat gtg acc ccc aac tct gtg ggc ctc tcc	5664
Gly Glu Leu Thr Val Thr Asp Val Thr Pro Asn Ser Val Gly Leu Ser	
1873	1878 1883 1888
tgg aca gtc ccc gag ggc cag ttt gac tcc ttc ata gtc cag tac aag	5712
Trp Thr Val Pro Glu Gly Gln Phe Asp Ser Phe Ile Val Gln Tyr Lys	
1889	1894 1899 1904
gac aag gac ggg cag ccc cag gtg gtg ccg gtg gcg gca gac cag cga	5760
Asp Lys Asp Gly Gln Pro Gln Val Val Pro Val Ala Ala Asp Gln Arg	
1905	1910 1915 1920
gag gtc aca gtc tac aac ctg gag cct gag aga aaa tat aag atg aac	5808
Glu Val Thr Val Tyr Asn Leu Glu Pro Glu Arg Lys Tyr Lys Met Asn	
1921	1926 1931 1936
atg tat gga cta cat gat ggg caa cgc atg ggc ccc ctg tct gtg gtc	5856
Met Tyr Gly Leu His Asp Gly Gln Arg Met Gly Pro Leu Ser Val Val	
1937	1942 1947 1952
atc gtg acg gcc cca gcc aca gag gcc tcc aag cct ccc ctg gag cca	5904
Ile Val Thr Ala Pro Ala Thr Glu Ala Ser Lys Pro Pro Leu Glu Pro	
1953	1958 1963 1968
cgc cta ggg gag ctg aca gtg acg gat ata acc cct gac tct gtg ggc	5952
Arg Leu Gly Glu Leu Thr Val Thr Asp Ile Thr Pro Asp Ser Val Gly	

1969	1974	1979	1984	
ctc tca tgg aca gtc cct gag ggt gaa ttc gac tcc ttt gtg gtt cag				6000
Leu Ser Trp Thr Val Pro Glu Gly Glu Phe Asp Ser Phe Val Val Gln				
1985	1990	1995	2000	
tac aag gac agg gac ggg cag ccc cag gtg gtg ccc gtg gct gca gat				6048
Tyr Lys Asp Arg Asp Gly Gln Pro Gln Val Val Pro Val Ala Ala Asp				
2001	2006	2011	2016	
cag cgg gag gtc act atc cct gac ctg gaa ccc tcc cgc aag tac aag				6096
Gln Arg Glu Val Thr Ile Pro Asp Leu Glu Pro Ser Arg Lys Tyr Lys				
2017	2022	2027	2032	
ttc ctg ctc ttt ggg atc cag gat ggg aaa cga cgc agc cca gtc tct				6144
Phe Leu Leu Phe Gly Ile Gln Asp Gly Lys Arg Arg Ser Pro Val Ser				
2033	2038	2043	2048	
gtg gag gca aag acg gtt gcc cga ggt gac gcc agc cca ggg gcc cca				6192
Val Glu Ala Lys Thr Val Ala Arg Gly Asp Ala Ser Pro Gly Ala Pro				
2049	2054	2059	2064	
ccc cgc ott ggg gag ctg tgg gtg aca gac ccc acc cca gac tca ctg				6240
Pro Arg Leu Gly Glu Leu Trp Val Thr Asp Pro Thr Pro Asp Ser Leu				
2065	2070	2075	2080	
cgc ctc tcc tgg acg gtt cct gag ggc cag ttc gac tct ttt gtg gtc				6288
Arg Leu Ser Trp Thr Val Pro Glu Gly Gln Phe Asp Ser Phe Val Val				
2081	2086	2091	2096	
cag ttc aag gac aaa gac ggg ccc cag gtg gtg ccc gtg gag ggc cat				6336
Gln Phe Lys Asp Lys Asp Gly Pro Gln Val Val Pro Val Glu Gly His				
2097	2102	2107	2112	
gag cgc tct gtc act gtc acc cct ctg gat gcc ggc cgc aag tac aga				6384
Glu Arg Ser Val Thr Val Thr Pro Leu Asp Ala Gly Arg Lys Tyr Arg				
2113	2118	2123	2128	
ttc ctc ctc tat ggc ctc ctg ggc aag aag cgc cat ggc cct ctc act				6432
Phe Leu Leu Tyr Gly Leu Leu Gly Lys Lys Arg His Gly Pro Leu Thr				
2129	2134	2139	2144	
gcc gac ggc acc acg gaa gcc cgg agt gct atg gat gat act gga aca				6480
Ala Asp Gly Thr Thr Glu Ala Arg Ser Ala Met Asp Asp Thr Gly Thr				
2145	2150	2155	2160	
aag cgt ccc cca aaa ccc cgt ctg ggg gag gag ctg cag gtg acc acc				6528
Lys Arg Pro Pro Lys Pro Arg Leu Gly Glu Glu Leu Gln Val Thr Thr				
2161	2166	2171	2176	
gtg acc cag aac tcc gtg ggc ctc tcc tgg aca gtc cct gag ggc cag				6576
Val Thr Gln Asn Ser Val Gly Leu Ser Trp Thr Val Pro Glu Gly Gln				
2177	2182	2187	2192	
ttt gac tcc ttt gtg gtc cag tac aaa gac agg gac ggg cag ccc cag				6624
Phe Asp Ser Phe Val Val Gln Tyr Lys Asp Arg Asp Gly Gln Pro Gln				
2193	2198	2203	2208	

cac ggt ggc cag cgc atg ggc cct gtg tct gtc gtc ggg gtg aca gct	7344
His Gly Gly Gln Arg Met Gly Pro Val Ser Val Val Gly Val Thr Ala	
2433 2438 2443 2448	
gca gag gaa gag acc ccc agc ccc aca gaa ccc agc atg gag gcc ccg	7392
Ala Glu Glu Glu Thr Pro Ser Pro Thr Glu Pro Ser Met Glu Ala Pro	
2449 2454 2459 2464	
gag ccc gct gag gag ccg ctc ctg ggg gag cta aca gtg aca gga tcc	7440
Glu Pro Ala Glu Glu Pro Leu Leu Gly Glu Leu Thr Val Thr Gly Ser	
2465 2470 2475 2480	
tcc cct gac tcg ctg agc ctc tcc tgg acc gtc ccc cag ggc cgc ttc	7488
Ser Pro Asp Ser Leu Ser Leu Ser Trp Thr Val Pro Gln Gly Arg Phe	
2481 2486 2491 2496	
gac tcc ttc acc gtg cag tac aag gac agg gac ggg cgg ccc cag gtg	7536
Asp Ser Phe Thr Val Gln Tyr Lys Asp Arg Asp Gly Arg Pro Gln Val	
2497 2502 2507 2512	
gtg cgt gtt ggg ggc gag gag agt gaa gtc acc gtg ggg ggc ctg gag	7584
Val Arg Val Gly Gly Glu Glu Ser Glu Val Thr Val Gly Gly Leu Glu	
2513 2518 2523 2528	
cct ggg cgc aag tac aag atg cac ctg tac ggc ctc cac gag ggg cgg	7632
Pro Gly Arg Lys Tyr Lys Met His Leu Tyr Gly Leu His Glu Gly Arg	
2529 2534 2539 2544	
cgc gtg ggc cca gtg tct gct gtg ggc gtc acg gcc ccc gaa gag gag	7680
Arg Val Gly Pro Val Ser Ala Val Gly Val Thr Ala Pro Glu Glu Glu	
2545 2550 2555 2560	
tcc cct gat gct cct ctt gca aag ctg cgc cta ggg cag atg aca gtg	7728
Ser Pro Asp Ala Pro Leu Ala Lys Leu Arg Leu Gly Gln Met Thr Val	
2561 2566 2571 2576	
aga gac atc acc tcc gac tcc ctc agc ctc tcc tgg aca gtc ccc gag	7776
Arg Asp Ile Thr Ser Asp Ser Leu Ser Leu Ser Trp Thr Val Pro Glu	
2577 2582 2587 2592	
ggc cag ttt gac cat ttc ttg gtc cag ttt aag aat ggg gac ggg cag	7824
Gly Gln Phe Asp His Phe Leu Val Gln Phe Lys Asn Gly Asp Gly Gln	
2593 2598 2603 2608	
ccc aag gcg gtg cgg gtg ccg gga cac gag gat ggg gtc acc atc tcg	7872
Pro Lys Ala Val Arg Val Pro Gly His Glu Asp Gly Val Thr Ile Ser	
2609 2614 2619 2624	
ggc ctg gag cca gac cac aag tac aag atg aac ctg tac ggc ttc cac	7920
Gly Leu Glu Pro Asp His Lys Tyr Lys Met Asn Leu Tyr Gly Phe His	
2625 2630 2635 2640	
ggt ggc cag cgc gtg ggc ccc gtg tct gct gtt ggt tta act gcc cca	7968
Gly Gly Gln Arg Val Gly Pro Val Ser Ala Val Gly Leu Thr Ala Pro	
2641 2646 2651 2656	
gga aag gat gaa gaa atg gcc cca gcc tcg aca gaa cct ccc acc cct	8016

2881	2886	2891	2896	
cct ctc ctg ggg gag ctg aca gtg aca gga tcc tcc cct gac tcg ctg				8736
Pro Leu Leu Gly Glu Leu Thr Val Thr Gly Ser Ser Pro Asp Ser Leu				
2897	2902	2907	2912	
agc ctt tcc tgg acc gtc ccc cag ggc cgc ttt gac tcc ttc acc gtg				8784
Ser Leu Ser Trp Thr Val Pro Gln Gly Arg Phe Asp Ser Phe Thr Val				
2913	2918	2923	2928	
cag tac aag gac agg gac ggg cgg ccc cag gcg gtg cgt gtt ggg ggc				8832
Gln Tyr Lys Asp Arg Asp Gly Arg Pro Gln Ala Val Arg Val Gly Gly				
2929	2934	2939	2944	
cag gag agc aag gtc act gtg agg ggc ctg gag cct ggg cgc aag tac				8880
Gln Glu Ser Lys Val Thr Val Arg Gly Leu Glu Pro Gly Arg Lys Tyr				
2945	2950	2955	2960	
aag atg cac ctg tac ggc ctc cac gag ggg cgg cgc ctg ggc ccg gtg				8928
Lys Met His Leu Tyr Gly Leu His Glu Gly Arg Arg Leu Gly Pro Val				
2961	2966	2971	2976	
tct gcc gtg ggc gtc aca gag gat gaa gcc gag acc acc caa gca gtg				8976
Ser Ala Val Gly Val Thr Glu Asp Glu Ala Glu Thr Thr Gln Ala Val				
2977	2982	2987	2992	
cct acc atg acc cct gag ccc ccc atc aag cct cgc ctg ggg gag ctg				9024
Pro Thr Met Thr Pro Glu Pro Pro Ile Lys Pro Arg Leu Gly Glu Leu				
2993	2998	3003	3008	
acc atg aca gat gcc acc cct gac tcc ctc agc ctg tcc tgg acg gtt				9072
Thr Met Thr Asp Ala Thr Pro Asp Ser Leu Ser Leu Ser Trp Thr Val				
3009	3014	3019	3024	
ccc gag ggc cag ttt gac cac ttc ctg gtc cag tac agg aat ggg gat				9120
Pro Glu Gly Gln Phe Asp His Phe Leu Val Gln Tyr Arg Asn Gly Asp				
3025	3030	3035	3040	
ggg cag ccc aag gcg gtg cgg gtg ccg ggg cac gag gac ggg gtc acc				9168
Gly Gln Pro Lys Ala Val Arg Val Pro Gly His Glu Asp Gly Val Thr				
3041	3046	3051	3056	
atc tca ggc ctg gag cca gac cat aaa tac aag atg aac ctg tac ggc				9216
Ile Ser Gly Leu Glu Pro Asp His Lys Tyr Lys Met Asn Leu Tyr Gly				
3057	3062	3067	3072	
ttc cac ggt ggc cag cgc gtg ggc ccc atc tct gtc att ggg gtg acg				9264
Phe His Gly Gly Gln Arg Val Gly Pro Ile Ser Val Ile Gly Val Thr				
3073	3078	3083	3088	
gct gca gag gaa gag acc ccc agc ccc acg gaa ctc agc act gag gcc				9312
Ala Ala Glu Glu Glu Thr Pro Ser Pro Thr Glu Leu Ser Thr Glu Ala				
3089	3094	3099	3104	
cgg gag ccc cct gag gag ccg ctc ctg ggg gag ctg aca gtg aca gga				9360
Arg Glu Pro Pro Glu Glu Pro Leu Leu Gly Glu Leu Thr Val Thr Gly				
3105	3110	3115	3120	

tcc tcc cct gac tgg ctg agc ctc tcc tgg acc atc ccc cag ggc cac	9408
Ser Ser Pro Asp Ser Leu Ser Leu Ser Trp Thr Ile Pro Gln Gly His	
3121 3126 3131 3136	
ttc gac tcc ttc acc gtg cag tac aag gac agg gac ggg cgg ccc cag	9456
Phe Asp Ser Phe Thr Val Gln Tyr Lys Asp Arg Asp Gly Arg Pro Gln	
3137 3142 3147 3152	
gtg atg cgt gtc agg ggc gag gag agc gag gtc acc gtg ggg ggc ctg	9504
Val Met Arg Val Arg Gly Glu Glu Ser Glu Val Thr Val Gly Gly Leu	
3153 3158 3163 3168	
gag ccc ggg cgc aaa tac aag atg cac ctg tac ggc ctc cac gag ggg	9552
Glu Pro Gly Arg Lys Tyr Lys Met His Leu Tyr Gly Leu His Glu Gly	
3169 3174 3179 3184	
cgg cgt gtg ggc ccg gtg tcc acc gtg ggt gtg aca gct cca gag gat	9600
Arg Arg Val Gly Pro Val Ser Thr Val Gly Val Thr Ala Pro Glu Asp	
3185 3190 3195 3200	
gaa gca gag acc acc caa gca gtg ccc acc aca acc cct gag ccc ccc	9648
Glu Ala Glu Thr Thr Gln Ala Val Pro Thr Thr Thr Pro Glu Pro Pro	
3201 3206 3211 3216	
aac aag cct cgc ctc ggg gag ctg acc gtg aca gat gcc acc cct gac	9696
Asn Lys Pro Arg Leu Gly Glu Leu Thr Val Thr Asp Ala Thr Pro Asp	
3217 3222 3227 3232	
tcc ctc agc ctg tcc tgg atg gtc ccc gag ggc cag ttt gac cac ttc	9744
Ser Leu Ser Leu Ser Trp Met Val Pro Glu Gly Gln Phe Asp His Phe	
3233 3238 3243 3248	
ctg gtc cag tac agg aat ggg gat ggg cag ccc aag gtg gtg cgg gtg	9792
Leu Val Gln Tyr Arg Asn Gly Asp Gly Gln Pro Lys Val Val Arg Val	
3249 3254 3259 3264	
ccg ggg cac gag gac ggg gtc acc atc tca ggc ctg gag cca gac cac	9840
Pro Gly His Glu Asp Gly Val Thr Ile Ser Gly Leu Glu Pro Asp His	
3265 3270 3275 3280	
aag tac aag atg aac ctg tac ggc ttc cac ggt ggc cag cgc gtg ggc	9888
Lys Tyr Lys Met Asn Leu Tyr Gly Phe His Gly Gly Gln Arg Val Gly	
3281 3286 3291 3296	
ccc atc tct gtc att ggg gtg aca gct gca gag gaa gaa act ccc gcc	9936
Pro Ile Ser Val Ile Gly Val Thr Ala Ala Glu Glu Glu Thr Pro Ala	
3297 3302 3307 3312	
ccc aca gaa ccc agc acg gag gcc ccg gag ccc cct gag gag ccg ctc	9984
Pro Thr Glu Pro Ser Thr Glu Ala Pro Glu Pro Pro Glu Glu Pro Leu	
3313 3318 3323 3328	
ctg ggg gag ctg aca gtg aca gga tcc tcc cct gac tgg ctg agc ctc	10032
Leu Gly Glu Leu Thr Val Thr Gly Ser Ser Pro Asp Ser Leu Ser Leu	
3329 3334 3339 3344	

tcc tgg acc atc ccc cag ggc cgc ttc gac tcc ttc act gtg cag tac	10080
Ser Trp Thr Ile Pro Gln Gly Arg Phe Asp Ser Phe Thr Val Gln Tyr	
3345 3350 3355 3360	
aag gac agg gac ggg cgg ccc cag gtg gtg cgt gtc agg ggc gag gag	10128
Lys Asp Arg Asp Gly Arg Pro Gln Val Val Arg Val Arg Gly Glu Glu	
3361 3366 3371 3376	
agc gag gtc acc gtg ggg ggc ctg gag ccc ggg tgc aaa tac aag atg	10176
Ser Glu Val Thr Val Gly Gly Leu Glu Pro Gly Cys Lys Tyr Lys Met	
3377 3382 3387 3392	
cac ctg tac ggc ctc cac gag ggg cag cgc gtg ggc cca gtg tcc gct	10224
His Leu Tyr Gly Leu His Glu Gly Gln Arg Val Gly Pro Val Ser Ala	
3393 3398 3403 3408	
gtg ggt gtg aca gct cca aag gat gaa gcc gag acc acc caa gca gtg	10272
Val Gly Val Thr Ala Pro Lys Asp Glu Ala Glu Thr Thr Gln Ala Val	
3409 3414 3419 3424	
cct acc atg acc cct gag ccc ccc atc aag cct cgc ctg ggg gag ctg	10320
Pro Thr Met Thr Pro Glu Pro Pro Ile Lys Pro Arg Leu Gly Glu Leu	
3425 3430 3435 3440	
acc gtg aca gat gcc acc ccc gac tcc ctc agc ctg tcc tgg atg gtt	10368
Thr Val Thr Asp Ala Thr Pro Asp Ser Leu Ser Leu Ser Trp Met Val	
3441 3446 3451 3456	
ccc gag ggc cag ttt gac cac ttc ctg gtc cag tac agg aat ggg gat	10416
Pro Glu Gly Gln Phe Asp His Phe Leu Val Gln Tyr Arg Asn Gly Asp	
3457 3462 3467 3472	
ggg cag ccc aag gcg gtg cgg gtg ccg ggg cac gag gac ggg gtc acc	10464
Gly Gln Pro Lys Ala Val Arg Val Pro Gly His Glu Asp Gly Val Thr	
3473 3478 3483 3488	
atc tca ggc ctg gag cca gac cat aaa tac aag atg aac ctg tac ggc	10512
Ile Ser Gly Leu Glu Pro Asp His Lys Tyr Lys Met Asn Leu Tyr Gly	
3489 3494 3499 3504	
ttc cac ggt ggc cag cgc gta ggc cct gtg tct gcc att ggg gtg acg	10560
Phe His Gly Gly Gln Arg Val Gly Pro Val Ser Ala Ile Gly Val Thr	
3505 3510 3515 3520	
gag gaa gag acc ccc agc ccc aca gaa ccc agc act gag gcc ccg gag	10608
Glu Glu Glu Thr Pro Ser Pro Thr Glu Pro Ser Thr Glu Ala Pro Glu	
3521 3526 3531 3536	
gcc cct gag gag ccg ctc ctg ggg gag ttg aca gtg aca gga tcc tcc	10656
Ala Pro Glu Glu Pro Leu Leu Gly Glu Leu Thr Val Thr Gly Ser Ser	
3537 3542 3547 3552	
cct gac tcg ctg agc ctc tcc tgg acc gtc ccc cag ggc cgc ttc gac	10704
Pro Asp Ser Leu Ser Leu Ser Trp Thr Val Pro Gln Gly Arg Phe Asp	
3553 3558 3563 3568	
tcc ttc acc gtg cag tac aag gac agg gac ggg cag ccc cag gtg gtg	10752

Ser Phe Thr Val Gln Tyr Lys Asp Arg Asp Gly Gln Pro Gln Val Val	
3569 3574 3579 3584	
cgt gtc agg ggc gag gag agc gag gtc acc gtg ggg ggc ctg gag ccc	10800
Arg Val Arg Gly Glu Glu Ser Glu Val Thr Val Gly Gly Leu Glu Pro	
3585 3590 3595 3600	
ggg cgc aaa tac aag atg cat ctg tac ggc ctc cac gag ggg cag cgc	10848
Gly Arg Lys Tyr Lys Met His Leu Tyr Gly Leu His Glu Gly Gln Arg	
3601 3606 3611 3616	
gtg ggc cca gtg tcc acc gtg ggc atc acg gcg ccc ctg ccc aca cca	10896
Val Gly Pro Val Ser Thr Val Gly Ile Thr Ala Pro Leu Pro Thr Pro	
3617 3622 3627 3632	
ctg ccg gtg gag ccc cgc ctg ggg gag ctg gcg gtg gcg gcc gtg acc	10944
Leu Pro Val Glu Pro Arg Leu Gly Glu Leu Ala Val Ala Ala Val Thr	
3633 3638 3643 3648	
tcg gac tca gtg ggc ctc tca tgg acg gtg gcc cag ggc ccc ttt gac	10992
Ser Asp Ser Val Gly Leu Ser Trp Thr Val Ala Gln Gly Pro Phe Asp	
3649 3654 3659 3664	
tcc ttc ctg gta cag tac agg gac gcg cag ggg cag ccc cag gca gtg	11040
Ser Phe Leu Val Gln Tyr Arg Asp Ala Gln Gly Gln Pro Gln Ala Val	
3665 3670 3675 3680	
cct gtg agc gga gac ctc cga gcg gtc gcc gtc tcg ggg ctg gac ccg	11088
Pro Val Ser Gly Asp Leu Arg Ala Val Ala Val Ser Gly Leu Asp Pro	
3681 3686 3691 3696	
gcc cgc aag tac aag ttc ctg ctc ttt gga ctc cag aat ggg aaa cgc	11136
Ala Arg Lys Tyr Lys Phe Leu Leu Phe Gly Leu Gln Asn Gly Lys Arg	
3697 3702 3707 3712	
cac ggc cca gtc cct gtg gag gcc agg acc gcc cca gac acc aaa ccg	11184
His Gly Pro Val Pro Val Glu Ala Arg Thr Ala Pro Asp Thr Lys Pro	
3713 3718 3723 3728	
tct ccc cgc ctg ggg gag ctg act gtg aca gat gcg acc cct gac tcc	11232
Ser Pro Arg Leu Gly Glu Leu Thr Val Thr Asp Ala Thr Pro Asp Ser	
3729 3734 3739 3744	
gtg ggc ctc tcg tgg acg gtc cct gag ggc gaa ttc gac tcc ttc gtg	11280
Val Gly Leu Ser Trp Thr Val Pro Glu Gly Glu Phe Asp Ser Phe Val	
3745 3750 3755 3760	
gtc cag tac aag gat aag gat ggt cgg ctc cag gtg gtg ccg gtg gca	11328
Val Gln Tyr Lys Asp Lys Asp Gly Arg Leu Gln Val Val Pro Val Ala	
3761 3766 3771 3776	
gcc aac cag cgg gag gtc aca gtc cag ggc ctg gag ccc agt agg aaa	11376
Ala Asn Gln Arg Glu Val Thr Val Gln Gly Leu Glu Pro Ser Arg Lys	
3777 3782 3787 3792	
tac agg ttc ctg ctc tat ggt ctg tca ggc agg aaa cga ctg ggc ccc	11424
Tyr Arg Phe Leu Leu Tyr Gly Leu Ser Gly Arg Lys Arg Leu Gly Pro	

3793	3798	3803	3808	
atc tct gct gac agc acc	aca gct ccc ctg gag	aag gag cta cct ccc	11472	
Ile Ser Ala Asp Ser Thr	Thr Ala Pro Leu Glu Lys	Glu Leu Pro Pro		
3809	3814	3819	3824	
cac ctg ggg gaa ctg acc	gtg gct gag gag acc	tcc agc tct ctg cgc	11520	
His Leu Gly Glu Leu Thr	Val Ala Glu Glu Thr	Ser Ser Ser Leu Arg		
3825	3830	3835	3840	
ctg tcc tgg acg gta gcc	cag ggc ccc ttt gac	tcc ttc gtg gtc cag	11568	
Leu Ser Trp Thr Val Ala	Gln Gly Pro Phe Asp	Ser Phe Val Val Gln		
3841	3846	3851	3856	
tac agg gac acg gac ggg	cag ccc agg gca gtg	cct gtg gcc gca gac	11616	
Tyr Arg Asp Thr Asp Gly	Gln Pro Arg Ala Val	Pro Val Ala Ala Asp		
3857	3862	3867	3872	
cag cgc aca gtc acc gta	gag gac ctg gag cct	ggc aag aaa tac aag	11664	
Gln Arg Thr Val Thr Val	Glu Asp Leu Glu Pro	Gly Lys Lys Tyr Lys		
3873	3878	3883	3888	
ttt ctg ctc tac ggg ctc	ctt ggg gga aag cgc	ctg ggc ccg gtc tct	11712	
Phe Leu Leu Tyr Gly Leu	Leu Gly Gly Lys Arg	Leu Gly Pro Val Ser		
3889	3894	3899	3904	
gcc ctg gga atg aca gcc	cca gaa gag gac aca	cca gcc cca gag tta	11760	
Ala Leu Gly Met Thr Ala	Pro Glu Glu Asp Thr	Pro Ala Pro Glu Leu		
3905	3910	3915	3920	
gcc cca gag gcc cct gag	cct cct gaa gag ccc	cgc cta gga gtg ctg	11808	
Ala Pro Glu Ala Pro Glu	Pro Pro Glu Glu Pro	Arg Leu Gly Val Leu		
3921	3926	3931	3936	
acc gtg acc gac aca acc	cca gac tcc atg cgc	ctc tcg tgg agc gtg	11856	
Thr Val Thr Asp Thr Thr	Pro Asp Ser Met Arg	Leu Ser Trp Ser Val		
3937	3942	3947	3952	
gcc cag ggc ccc ttt gat	tcc ttc gtg gtc cag	tat gag gac acg aac	11904	
Ala Gln Gly Pro Phe Asp	Ser Phe Val Val Gln	Tyr Glu Asp Thr Asn		
3953	3958	3963	3968	
ggg cag ccc cag gcc ttg	ctc gtg gac ggc gac	cag agc aag atc ctc	11952	
Gly Gln Pro Gln Ala Leu	Leu Val Asp Gly Asp	Gln Ser Lys Ile Leu		
3969	3974	3979	3984	
atc tca ggc ctg gag ccc	agc acc ccc tac agg	ttc ctc ctc tat ggc	12000	
Ile Ser Gly Leu Glu Pro	Ser Thr Pro Tyr Arg	Phe Leu Leu Tyr Gly		
3985	3990	3995	4000	
ctc cat gaa ggg aag cgc	ctg ggg ccc ctc tca	gct gag ggc acc aca	12048	
Leu His Glu Gly Lys Arg	Leu Gly Pro Leu Ser	Ala Glu Gly Thr Thr		
4001	4006	4011	4016	
ggg ctg gct cct gct ggt	cag acc tca gag gag	tca agg ccc cgc ctg	12096	
Gly Leu Ala Pro Ala Gly	Gln Thr Ser Glu Glu	Ser Arg Pro Arg Leu		
4017	4022	4027	4032	

tcc cag ctg tct gtg act gac gtg acc acc agt tca ctg agg ctc aac	12144
Ser Gln Leu Ser Val Thr Asp Val Thr Thr Ser Ser Leu Arg Leu Asn	
4033 4038 4043 4048	
tgg gag gcc cca ccg ggg gcc ttc gac tcc ttc ctg ctc cgc ttt ggg	12192
Trp Glu Ala Pro Pro Gly Ala Phe Asp Ser Phe Leu Leu Arg Phe Gly	
4049 4054 4059 4064	
gtt cca tca cca agc act ctg gag ccg cat ccg cgt cca ctg ctg cag	12240
Val Pro Ser Pro Ser Thr Leu Glu Pro His Pro Arg Pro Leu Leu Gln	
4065 4070 4075 4080	
cgc gag ctg atg gtg ccg ggg aca cgg cac tcg gcc gtg ctc cgg gac	12288
Arg Glu Leu Met Val Pro Gly Thr Arg His Ser Ala Val Leu Arg Asp	
4081 4086 4091 4096	
ctg cgt tcc ggg act ctg tac agc ctg aca ctg tat ggg ctg cga gga	12336
Leu Arg Ser Gly Thr Leu Tyr Ser Leu Thr Leu Tyr Gly Leu Arg Gly	
4097 4102 4107 4112	
ccc cac aag gcc gac agc atc cag gga acc gcc cgc acc ctc agc cca	12384
Pro His Lys Ala Asp Ser Ile Gln Gly Thr Ala Arg Thr Leu Ser Pro	
4113 4118 4123 4128	
gtt ctg gag agc ccc cgt gac ctc caa ttc agt gaa atc agg gag acc	12432
Val Leu Glu Ser Pro Arg Asp Leu Gln Phe Ser Glu Ile Arg Glu Thr	
4129 4134 4139 4144	
tca gcc aag gtc aac tgg atg ccc cca cca tcc cgg gcg gac agc ttc	12480
Ser Ala Lys Val Asn Trp Met Pro Pro Pro Ser Arg Ala Asp Ser Phe	
4145 4150 4155 4160	
aaa gtc tcc tac cag ctg gcg gac gga ggg gag cct cag agt gtg cag	12528
Lys Val Ser Tyr Gln Leu Ala Asp Gly Gly Glu Pro Gln Ser Val Gln	
4161 4166 4171 4176	
gtg gat ggc cag gcc ccg acc cag aaa ctc cag ggg ctg atc cca gcc	12576
Val Asp Gly Gln Ala Arg Thr Gln Lys Leu Gln Gly Leu Ile Pro Gly	
4177 4182 4187 4192	
gct cgc tat gag gtg acc gtg gtc tcg gtc cga ggc ttt gag gag agt	12624
Ala Arg Tyr Glu Val Thr Val Val Ser Val Arg Gly Phe Glu Glu Ser	
4193 4198 4203 4208	
gag cct ctc aca ggc ttc ctc acc acg gtt cct gac ggt ccc aca cag	12672
Glu Pro Leu Thr Gly Phe Leu Thr Thr Val Pro Asp Gly Pro Thr Gln	
4209 4214 4219 4224	
ttg cgt gca ctg aac ttg acc gag gga ttc gcc gtg ctg cac tgg aag	12720
Leu Arg Ala Leu Asn Leu Thr Glu Gly Phe Ala Val Leu His Trp Lys	
4225 4230 4235 4240	
ccc ccc cag aat cct gtg gac acc tat gac gtc cag gtc aca gcc cct	12768
Pro Pro Gln Asn Pro Val Asp Thr Tyr Asp Val Gln Val Thr Ala Pro	
4241 4246 4251 4256	

ggg gcc ccg cct ctg cag gcg gag acc cca ggc agc gcg gtg gac tac	12816
Gly Ala Pro Pro Leu Gln Ala Glu Thr Pro Gly Ser Ala Val Asp Tyr	
4257 4262 4267 4272	
ccc ctg cat gac ctt gtc ctc cac acc aac tac acc gcc aca gtg cgt	12864
Pro Leu His Asp Leu Val Leu His Thr Asn Tyr Thr Ala Thr Val Arg	
4273 4278 4283 4288	
ggc ctg cgg ggc ccc aac ctc act tcc cca gcc agc atc acc ttc acc	12912
Gly Leu Arg Gly Pro Asn Leu Thr Ser Pro Ala Ser Ile Thr Phe Thr	
4289 4294 4299 4304	
aca ggg cta gag gcc cct cgg gac ttg gag gcc aag gaa gtg acc ccc	12960
Thr Gly Leu Glu Ala Pro Arg Asp Leu Glu Ala Lys Glu Val Thr Pro	
4305 4310 4315 4320	
cgc acc gcc ctg ctc act tgg act gag ccc cca gtc cgg ccc gca ggc	13008
Arg Thr Ala Leu Leu Thr Trp Thr Glu Pro Pro Val Arg Pro Ala Gly	
4321 4326 4331 4336	
tac ctg ctc agc ttc cac acc cct ggt gga cag aac cag gag atc ctg	13056
Tyr Leu Leu Ser Phe His Thr Pro Gly Gly Gln Asn Gln Glu Ile Leu	
4337 4342 4347 4352	
ctc cca gga ggg atc aca tct cac cag ctc qtt ggc ctc ttt ccc tcc	13104
Leu Pro Gly Gly Ile Thr Ser His Gln Leu Leu Gly Leu Phe Pro Ser	
4353 4358 4363 4368	
acc tcc tac aat gca cgg ctc cag gcc atg tgg ggc cag agc ctc ctg	13152
Thr Ser Tyr Asn Ala Arg Leu Gln Ala Met Trp Gly Gln Ser Leu Leu	
4369 4374 4379 4384	
ccg ccc gtg tcc acc tct ttc acc acg ggt ggg ctg cgg atc ccc ttc	13200
Pro Pro Val Ser Thr Ser Phe Thr Thr Gly Gly Leu Arg Ile Pro Phe	
4385 4390 4395 4400	
ccc agg gac tgc ggg gag gag atg cag aac gga gcc ggt gcc tcc agg	13248
Pro Arg Asp Cys Gly Glu Glu Met Gln Asn Gly Ala Gly Ala Ser Arg	
4401 4406 4411 4416	
acc agc acc atc ttc ctc aac ggc aac cgc gag cgg ccc ctg aac gtg	13296
Thr Ser Thr Ile Phe Leu Asn Gly Asn Arg Glu Arg Pro Leu Asn Val	
4417 4422 4427 4432	
ttt tgc gac atg gag act gat ggg ggc ggc tgg ctg gtg ttc cag cgc	13344
Phe Cys Asp Met Glu Thr Asp Gly Gly Gly Trp Leu Val Phe Gln Arg	
4433 4438 4443 4448	
cgc atg gat gga cag aca gac ttc tgg agg gac tgg gag gac tat gcc	13392
Arg Met Asp Gly Gln Thr Asp Phe Trp Arg Asp Trp Glu Asp Tyr Ala	
4449 4454 4459 4464	
cat ggt ttt ggg aac atc tct gga gag ttc tgg ctg ggc aat gag gcc	13440
His Gly Phe Gly Asn Ile Ser Gly Glu Phe Trp Leu Gly Asn Glu Ala	
4465 4470 4475 4480	
ctg cac agc ctg aca cag gca ggt gac tac tcc atg cgc gtg gac ctg	13488

[illegible]

```
<220>  
<221> CDS  
<222> (61)..(1335)
```

1

17	22	27	32	
atc cac cgg cac tgc caa gat cag aat gtt cca gtg gaa aac ttc ttt				204
Ile His Arg His Cys Gln Asp Gln Asn Val Pro Val Glu Asn Phe Phe				
33	38	43	48	
gtg aaa tgc aat gga gca ctc att aac acc agt gac aca gtg cag cat				252
Val Lys Cys Asn Gly Ala Leu Ile Asn Thr Ser Asp Thr Val Gln His				
49	54	59	64	
gga gct gtt tat agt ttg gaa ccc aga ctt tgc ggt gga aaa gga ggt				300
Gly Ala Val Tyr Ser Leu Glu Pro Arg Leu Cys Gly Gly Lys Gly Gly				
65	70	75	80	
ttt gga tct atg ctc cga gca ctt ggt gct cag att gag aag aca acc				348
Phe Gly Ser Met Leu Arg Ala Leu Gly Ala Gln Ile Glu Lys Thr Thr				
81	86	91	96	
aat cga gaa gct tgt cgg gat ctc agt gga agg aga cta cgc gat gtc				396
Asn Arg Glu Ala Cys Arg Asp Leu Ser Gly Arg Arg Leu Arg Asp Val				
97	102	107	112	
aat cat gaa aaa gca atg gct gaa tgg gta aaa caa caa gcc gag cga				444
Asn His Glu Lys Ala Met Ala Glu Trp Val Lys Gln Gln Ala Glu Arg				
113	118	123	128	
gag gct gaa aag gag cag aag cgg ctg gag cga ctg cag cgg aag ctt				492
Glu Ala Glu Lys Glu Gln Lys Arg Leu Glu Arg Leu Gln Arg Lys Leu				
129	134	139	144	
gta gaa ccc aag cac tgc ttc acc agc ccc gac tac cag cag cag tgc				540
Val Glu Pro Lys His Cys Phe Thr Ser Pro Asp Tyr Gln Gln Gln Cys				
145	150	155	160	
cat gag atg gct gag cgt ctg gag gat tcc gtc ctc aaa ggt atg cag				588
His Glu Met Ala Glu Arg Leu Glu Asp Ser Val Leu Lys Gly Met Gln				
161	166	171	176	
gct gcc tcc agc aag atg gtt tca gca gaa atc agt gag aat cgg aaa				636
Ala Ala Ser Ser Lys Met Val Ser Ala Glu Ile Ser Glu Asn Arg Lys				
177	182	187	192	
cgg caa tgg cct act aaa tct caa aca gac aga gga gcc agt gcg gga				684
Arg Gln Trp Pro Thr Lys Ser Gln Thr Asp Arg Gly Ala Ser Ala Gly				
193	198	203	208	
aag agg aga tgc ttc tgg ttg ggc atg gag gga cta gag act gca gaa				732
Lys Arg Arg Cys Phe Trp Leu Gly Met Glu Gly Leu Glu Thr Ala Glu				
209	214	219	224	
ggg tcc aac tct gag agt tca gat gat gac agt gaa gaa gca cca agc				780
Gly Ser Asn Ser Glu Ser Ser Asp Asp Asp Ser Glu Glu Ala Pro Ser				
225	230	235	240	
act tca gga atg ggt ttc cat gct cca aaa att ggt agc aat ggt gtc				828
Thr Ser Gly Met Gly Phe His Ala Pro Lys Ile Gly Ser Asn Gly Val				
241	246	251	256	

gag atg gca gcc aaa ttt ccc agt ggt tct cag agg gcg aga gta gtg	876
Glu Met Ala Ala Lys Phe Pro Ser Gly Ser Gln Arg Ala Arg Val Val	
257 262 267 272	
aat aca gac cat gga tca cca gaa caa ctg cag atc ccg gtg act gac	924
Asn Thr Asp His Gly Ser Pro Glu Gln Leu Gln Ile Pro Val Thr Asp	
273 278 283 288	
tct ggg agg cat att tta gaa gac tca tgt gct gag ctg ggg gag tcc	972
Ser Gly Arg His Ile Leu Glu Asp Ser Cys Ala Glu Leu Gly Glu Ser	
289 294 299 304	
aaa gag cac atg gaa agc agg atg gtt aca gaa aca gaa gag acc cag	1020
Lys Glu His Met Glu Ser Arg Met Val Thr Glu Thr Glu Glu Thr Gln	
305 310 315 320	
gag aag aag gca gag agt aaa gaa ccc ata gaa gag gag ccc act ggg	1068
Glu Lys Lys Ala Glu Ser Lys Glu Pro Ile Glu Glu Glu Pro Thr Gly	
321 326 331 336	
gct gga ctg aat aag gat aaa gag aca gaa gaa agg act gat ggg gaa	1116
Ala Gly Leu Asn Lys Asp Lys Glu Thr Glu Glu Arg Thr Asp Gly Glu	
337 342 347 352	
aga gtt gct gag gta gca cct gaa gaa agg gaa aac gtt gcc gtt gcc	1164
Arg Val Ala Glu Val Ala Pro Glu Glu Arg Glu Asn Val Ala Val Ala	
353 358 363 368	
aaa ctg cag gaa agc cag cca gga aac gca gtt att gat aag gaa act	1212
Lys Leu Gln Glu Ser Gln Pro Gly Asn Ala Val Ile Asp Lys Glu Thr	
369 374 379 384	
ata gat tta ttg gcg ttc acc tct gtt gca gaa ctg gag ttg ctg ggt	1260
Ile Asp Leu Leu Ala Phe Thr Ser Val Ala Glu Leu Glu Leu Leu Gly	
385 390 395 400	
ttg gag aag ctc aaa tgt gaa ctg atg gcc ctt gga ctg aaa tgt ggg	1308
Leu Glu Lys Leu Lys Cys Glu Leu Met Ala Leu Gly Leu Lys Cys Gly	
401 406 411 416	
ggc act ctg cag aag cgg ccg ctctag aggat ccaagcttac gtacgcgtgc	1360
Gly Thr Leu Gln Lys Arg Pro Leu *	
417 422	
atgcgacgtc gaccag	1376

<210> 77
 <211> 1923
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (112)..(1233)

<400> 77

ccccgccccca accttatctg atgctgtgca ttagacagca cactgctgac tgttttcagt	60
tgtttctgta acagcagaaa gtgcactcac taggagtagt cagaattcaa a atg ctg	117
Met Leu	1
aag aga aag cca tcc aat gtt tca gag aag gag aaa cat caa aaa cca	165
Lys Arg Lys Pro Ser Asn Val Ser Glu Lys Glu Lys His Gln Lys Pro	3 8 13 18
aag cga agc agc agt ttt ggg aat ttc gat cgt ttt cgg aat aat tct	213
Lys Arg Ser Ser Ser Phe Gly Asn Phe Asp Arg Phe Arg Asn Asn Ser	19 24 29 34
tta tca aaa cca gat gat tca act gag gca cat gaa gga gat ccc aca	261
Leu Ser Lys Pro Asp Asp Ser Thr Glu Ala His Glu Gly Asp Pro Thr	35 40 45 50
aat gga agt gga gaa caa agt aaa act tca aat aat gga ggc ggt ttg	309
Asn Gly Ser Gly Glu Gln Ser Lys Thr Ser Asn Asn Gly Gly Gly Leu	51 56 61 66
ggt aaa aaa atg aga gct att tca tgg aca atg aag aaa aaa gtg ggt	357
Gly Lys Lys Met Arg Ala Ile Ser Trp Thr Met Lys Lys Lys Val Gly	67 72 77 82
aaa aag tac atc aaa gcc ctt tct gag gaa aag gat gag gaa gat gga	405
Lys Lys Tyr Ile Lys Ala Leu Ser Glu Glu Lys Asp Glu Glu Asp Gly	83 88 93 98
gag aat gcc cac cca tat aga aac agt gac cct gtg att ggg acc cac	453
Glu Asn Ala His Pro Tyr Arg Asn Ser Asp Pro Val Ile Gly Thr His	99 104 109 114
aca gag aag gtg tcc ctc aaa gcc agt gac tcc atg gat agt ctc tac	501
Thr Glu Lys Val Ser Leu Lys Ala Ser Asp Ser Met Asp Ser Leu Tyr	115 120 125 130
agt gga cag agc tca tca agt ggc ata aca agc tgt tca gat ggt aca	549
Ser Gly Gln Ser Ser Ser Ser Gly Ile Thr Ser Cys Ser Asp Gly Thr	131 136 141 146
agt aac cgg gac agc ttt cga ctg gat gac gat ggc ccc tat tca gga	597
Ser Asn Arg Asp Ser Phe Arg Leu Asp Asp Asp Gly Pro Tyr Ser Gly	147 152 157 162
cca ttc tgt ggc cgt gcc aga gtg cat acg gat ttc acg cca agt ccc	645
Pro Phe Cys Gly Arg Ala Arg Val His Thr Asp Phe Thr Pro Ser Pro	163 168 173 178
tat gac act gac tcc ctc aaa atc aag aaa gga gac atc ata gac att	693
Tyr Asp Thr Asp Ser Leu Lys Ile Lys Lys Gly Asp Ile Ile Asp Ile	179 184 189 194

att tgc aaa aca cca atg ggg atg tgg aca gga atg ttg aac aat aaa	741
Ile Cys Lys Thr Pro Met Gly Met Trp Thr Gly Met Leu Asn Asn Lys	
195 200 205 210	
gtg gga aac ttc aaa ttc att tat gtg gat gtc atc tca gaa gag gaa	789
Val Gly Asn Phe Lys Phe Ile Tyr Val Asp Val Ile Ser Glu Glu Glu	
211 216 221 226	
gca gcc ccc aag aaa ata aag gca aac cga agg agt aac agc aaa aaa	837
Ala Ala Pro Lys Lys Ile Lys Ala Asn Arg Arg Ser Asn Ser Lys Lys	
227 232 237 242	
tcc aag act ctg cag gag ttc cta gag agg att cat ctg cag gaa tac	885
Ser Lys Thr Leu Gln Glu Phe Leu Glu Arg Ile His Leu Gln Glu Tyr	
243 248 253 258	
acc tca aca ctt ttg ctc aat ggt tat gag act cta gaa gat tta aaa	933
Thr Ser Thr Leu Leu Leu Asn Gly Tyr Glu Thr Leu Glu Asp Leu Lys	
259 264 269 274	
gat ata aaa gag agt cac ctc att gaa tta aat att gaa aac cca gat	981
Asp Ile Lys Glu Ser His Leu Ile Glu Leu Asn Ile Glu Asn Pro Asp	
275 280 285 290	
gac aga aga agg tta cta tca gct gct gaa aac ttc ctt gaa gaa gaa	1029
Asp Arg Arg Arg Leu Leu Ser Ala Ala Glu Asn Phe Leu Glu Glu Glu	
291 296 301 306	
att att caa gag caa gaa aat gaa cct gag ccc cta tcc ttg agc tca	1077
Ile Ile Gln Glu Gln Glu Asn Glu Pro Glu Pro Leu Ser Leu Ser Ser	
307 312 317 322	
gac atc tcc tta aat aag tca cag tta gat gac tgc cca agg gac tct	1125
Asp Ile Ser Leu Asn Lys Ser Gln Leu Asp Asp Cys Pro Arg Asp Ser	
323 328 333 338	
ggt tgc tat atc tca tca gga aat tca gat aat ggc aaa gag gat ctg	1173
Gly Cys Tyr Ile Ser Ser Gly Asn Ser Asp Asn Gly Lys Glu Asp Leu	
339 344 349 354	
gag tct gaa aat ctg tct gac atg gta cat aag att att atc aca gag	1221
Glu Ser Glu Asn Leu Ser Asp Met Val His Lys Ile Ile Ile Thr Glu	
355 360 365 370	
cca agt gac tga aca cgcattccca actatatatc tacagatgca ttccatttta	1276
Pro Ser Asp *	
371	
actcttcttg agctaaaacg tcaaataagga gaggaagata agataaatat ttgtaaataa	1336
aacctaaagt ttaaattgttt taatctgaat aattgtacat aaaattttgt atctctaaca	1396
ttccaaatta ctgtcaataa aatatatatt tattatttta aatgctatgt gttaatatatt	1456
cacttgcttg tattagaaag gcaaaatgta agactttggt atgtgtgaca tatgctttat	1516
ttggctttat tttaacaagta cagtatctgc aaaaaacaaa gtaacctttt ttcataacctg	1576

ccagttttga atttatatat gttattgaac aaatagtaat agaggattcg ctgttgaaac 1636
aagttgtcca agcaatgtta tattcatttt tataacttatt gggaaagtgt gagttaatat 1696
tggacacatt ttatcctgat ccacagtgga gtttttagtaa ttatatTTTtg ttgatttctt 1756
cattttgttt tctggtataa aagtagagat aatgtgtagt cacttctgat ttagtgaaac 1816
caattgtaat aattgtggaa atgttttgtc ttttaagtga aatattttta aatttgacat 1876
accctaattg taataataaa aagaactatt tgcataaaaa aaaaaaa 1923

<210> 78
<211> 2179
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (284)..(1957)

<400> 78
ccggaattcc cgggtcgacc cacgcgtccg cagcgactaa ggccggcagag gagcggcgggt 60
ggtggcggcg ctgcagcagc gggcgggact gggatggtgg ttccacaggg cagaccccg 120
tgcactcaca gggaggagga ggccggcagcg gcggaggaag gcggcgcacc ccgagaggtg 180
gattgtctca ttgttagtgc tgaatcttct tgcctacttg tatctgggaa ttttaactttg 240
aagaggaaga gagtgaatat gaataactga aaaataaaat ggc atg ccc aaa gaa 295
Met Pro Lys Glu
1
aaa tac gag ccc cct gac cct cgg agg atg tat aca att atg tct tct 343
Lys Tyr Glu Pro Pro Asp Pro Arg Arg Met Tyr Thr Ile Met Ser Ser
5 10 15 20
gag gaa gca gca aat gga aag aaa tcc cac tgg gca gag ctt gaa ata 391
Glu Glu Ala Ala Asn Gly Lys Lys Ser His Trp Ala Glu Leu Glu Ile
21 26 31 36
agt gga aaa gta aga agc tta agc gca tct ttg tgg tca cta act cac 439
Ser Gly Lys Val Arg Ser Leu Ser Ala Ser Leu Trp Ser Leu Thr His
37 42 47 52
ctg aca gct ttg cat ttg agt gac aat tcc ctg tcc cga att cct tca 487
Leu Thr Ala Leu His Leu Ser Asp Asn Ser Leu Ser Arg Ile Pro Ser
53 58 63 68
gac att gcc aag ctt cac aat ctg gtg tat ttg gac ctg tca tct aat 535
Asp Ile Ala Lys Leu His Asn Leu Val Tyr Leu Asp Leu Ser Ser Asn
69 74 79 84

aat tct gag ggg tct gaa gct atg ctg aac aga gtc atg aca aaa gat	1255
Asn Ser Glu Gly Ser Glu Ala Met Leu Asn Arg Val Met Thr Lys Asp	
309 314 319 324	
aac att ggg gtt gca gta ctg cta gaa ctt cgg aag gaa tcg att gaa	1303
Asn Ile Gly Val Ala Val Leu Leu Glu Leu Arg Lys Glu Ser Ile Glu	
325 330 335 340	
atg ccg tct gga aag cca cat ctt gga aca gaa aaa caa ctt att ctt	1351
Met Pro Ser Gly Lys Pro His Leu Gly Thr Glu Lys Gln Leu Ile Leu	
341 346 351 356	
gtg gct aac gcc cac atg cat tgg gac cct gaa tac tct gat gtg aag	1399
Val Ala Asn Ala His Met His Trp Asp Pro Glu Tyr Ser Asp Val Lys	
357 362 367 372	
ttg gta caa act atg atg ttc ctc tca gaa gtg aag aac att att gat	1447
Leu Val Gln Thr Met Met Phe Leu Ser Glu Val Lys Asn Ile Ile Asp	
373 378 383 388	
aaa gcc tct cgc aac ctc aaa tcc agt gtt ttg gga gaa ttt gga act	1495
Lys Ala Ser Arg Asn Leu Lys Ser Ser Val Leu Gly Glu Phe Gly Thr	
389 394 399 404	
att cca ctt gtg tta tgt gca gat ctt aat tct ttg cca gac tct ggt	1543
Ile Pro Leu Val Leu Cys Ala Asp Leu Asn Ser Leu Pro Asp Ser Gly	
405 410 415 420	
gtt gta gaa tat ttg agc aca ggt gga gta gaa aca aat cac aaa gac	1591
Val Val Glu Tyr Leu Ser Thr Gly Gly Val Glu Thr Asn His Lys Asp	
421 426 431 436	
ttt aag gag ttg agg tat aat gaa agt ctc aca aac ttc agc tgt cat	1639
Phe Lys Glu Leu Arg Tyr Asn Glu Ser Leu Thr Asn Phe Ser Cys His	
437 442 447 452	
ggg aag aat gga acc acc aat gga agg atc act cat ggt ttc aag tta	1687
Gly Lys Asn Gly Thr Thr Asn Gly Arg Ile Thr His Gly Phe Lys Leu	
453 458 463 468	
cag agt gcc tat gag agt ggc ctg atg cct tac acg aat tac aca ttt	1735
Gln Ser Ala Tyr Glu Ser Gly Leu Met Pro Tyr Thr Asn Tyr Thr Phe	
469 474 479 484	
gat ttc aag ggt ata ata gac tac att ttc tat tct aaa cct cag ctg	1783
Asp Phe Lys Gly Ile Ile Asp Tyr Ile Phe Tyr Ser Lys Pro Gln Leu	
485 490 495 500	
aac acc tta ggc atc ctg ggc cct ctg gac cac cac tgg ctg gtt gag	1831
Asn Thr Leu Gly Ile Leu Gly Pro Leu Asp His His Trp Leu Val Glu	
501 506 511 516	
aat aac atc agt ggc tgc ccg cac ccc ctc atc ccc tct gac cac ttc	1879
Asn Asn Ile Ser Gly Cys Pro His Pro Leu Ile Pro Ser Asp His Phe	
517 522 527 532	
tca ctt ttt gca caa ctg gag ctc tta ctg cct ttc ctg ccc caa gtc	1927

Ser Leu Phe Ala Gln Leu Glu Leu Leu Leu Pro Phe Leu Pro Gln Val
 533 538 543 548

aac ggc atc cac ctt cct ggc agg agg tag t caagcacctt cagaggacag 1978
 Asn Gly Ile His Leu Pro Gly Arg Arg *
 549 554

ccttgattca cttgtaaact tgtgaaaatc tgaacatagg ggagtggagt atggccactg 2038

aggatttttg cttgcttaag aatgatttgg actttcaatc tgattatttg ataaggatat 2098

agtatgagag ccaggtgcta gcaacagaca aattctgagc ccaatatgct ttatactgct 2158

agacagggat tgggtgtgtt g 2179

<210> 79
 <211> 2072
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (46)..(1686)

<400> 79

tgcgcgtaccg gtccggaatt cccgggtcga cgatttcgtc tcatc atg ctg att 54
 Met Leu Ile
 1

gcc agg ctg gac tat gag ctg atc cag cgc ttc acc ctg acg atc att 102
 Ala Arg Leu Asp Tyr Glu Leu Ile Gln Arg Phe Thr Leu Thr Ile Ile
 4 9 14 19

gcc cgg gac ggg ggc ggc gag gag acc aca ggc cgg gtc agg atc aat 150
 Ala Arg Asp Gly Gly Gly Glu Glu Thr Thr Gly Arg Val Arg Ile Asn
 20 25 30 35

gtg ttg gat gtc aac gac aac gtg ccc acc ttc cag aag gat gcc tac 198
 Val Leu Asp Val Asn Asp Asn Val Pro Thr Phe Gln Lys Asp Ala Tyr
 36 41 46 51

gtg ggt gct ctg cgg gag aac gag cct tct gtc aca cag ctg gtg cgg 246
 Val Gly Ala Leu Arg Glu Asn Glu Pro Ser Val Thr Gln Leu Val Arg
 52 57 62 67

ctc cgg gca aca gat gaa gac tcc cct ccc aac aac cag atc acc tac 294
 Leu Arg Ala Thr Asp Glu Asp Ser Pro Pro Asn Asn Gln Ile Thr Tyr
 68 73 78 83

agc att gtc agt gca tct gcc ttt ggc agc tac ttc gac atc agc ctg 342
 Ser Ile Val Ser Ala Ser Ala Phe Gly Ser Tyr Phe Asp Ile Ser Leu
 84 89 94 99

tac gag ggc tat gga gtg atc agc gtc agt cgc ccc ctg gat tat gaa 390

Tyr Glu Gly Tyr Gly Val Ile Ser Val Ser Arg Pro Leu Asp Tyr Glu	
100 105 110 115	
cag ata tcc aat ggg ctg att tat ctg acg gtc atg gcc atg gat gct	438
Gln Ile Ser Asn Gly Leu Ile Tyr Leu Thr Val Met Ala Met Asp Ala	
116 121 126 131	
ggc aac ccc cct ctc aac agc acc gtc cct gtc acc atc gag gtg ttt	486
Gly Asn Pro Pro Leu Asn Ser Thr Val Pro Val Thr Ile Glu Val Phe	
132 137 142 147	
gat gag aat gac gac cct ccc acc ttc agc aag ccc gcc tac ttc gtc	534
Asp Glu Asn Asp Asp Pro Pro Thr Phe Ser Lys Pro Ala Tyr Phe Val	
148 153 158 163	
tcc gtg gtg gag aac atc atg gca gga gcc acg gtg ctg ttc ctg aat	582
Ser Val Val Glu Asn Ile Met Ala Gly Ala Thr Val Leu Phe Leu Asn	
164 169 174 179	
gcc aca gac ctg gac cgc tcc cgg gag tac gcc cag gag tcc atc atc	630
Ala Thr Asp Leu Asp Arg Ser Arg Glu Tyr Gly Gln Glu Ser Ile Ile	
180 185 190 195	
tac tcc ttg gaa ggc tcc acc cag ttt cgg atc aat gcc cgc tca ggg	678
Tyr Ser Leu Glu Gly Ser Thr Gln Phe Arg Ile Asn Ala Arg Ser Gly	
196 201 206 211	
gaa atc acc acc acg tct ctg ctt gac cga gag acc aag tct gaa tac	726
Glu Ile Thr Thr Thr Ser Leu Leu Asp Arg Glu Thr Lys Ser Glu Tyr	
212 217 222 227	
atc ctc atc gtt cgc gca gtg gac ggg ggt gtg gcc cac aac cag aaa	774
Ile Leu Ile Val Arg Ala Val Asp Gly Gly Val Gly His Asn Gln Lys	
228 233 238 243	
act ggc atc gcc acc gta aac atc acc ctc ctg gac atc aac gac aac	822
Thr Gly Ile Ala Thr Val Asn Ile Thr Leu Leu Asp Ile Asn Asp Asn	
244 249 254 259	
cac ccc acg tgg aag gac gca ccc tac tac atc aac ctg gtg gag atg	870
His Pro Thr Trp Lys Asp Ala Pro Tyr Tyr Ile Asn Leu Val Glu Met	
260 265 270 275	
acc cct cca gac tct gac gtg acc acg gtg gtg gct gtt gac cca gac	918
Thr Pro Pro Asp Ser Asp Val Thr Thr Val Val Ala Val Asp Pro Asp	
276 281 286 291	
ctg ggg gag aat ggc acc ctg gtg tac agc atc cag cca ccc aac aag	966
Leu Gly Glu Asn Gly Thr Leu Val Tyr Ser Ile Gln Pro Pro Asn Lys	
292 297 302 307	
ttc tac agc ctc aac agc acc acg ggc aag atc cgc acc acc cac gcc	1014
Phe Tyr Ser Leu Asn Ser Thr Thr Gly Lys Ile Arg Thr Thr His Ala	
308 313 318 323	
atg ctg gac cgg gag aac ccc gac ccc cat gag gcc gag ctg atg cgc	1062
Met Leu Asp Arg Glu Asn Pro Asp Pro His Glu Ala Glu Leu Met Arg	

324	329	334	339	
aaa atc gtc gtc tct gtt act gac tgt ggc agg ccc cct ctg aaa gcc				1110
Lys Ile Val Val Ser Val Thr Asp Cys Gly Arg Pro Pro Leu Lys Ala				
340	345	350	355	
acc agc agt gcc aca gtg ttt gtg aac ctc ttg gat ctc aat gac aat				1158
Thr Ser Ser Ala Thr Val Phe Val Asn Leu Leu Asp Leu Asn Asp Asn				
356	361	366	371	
gac ccc acc ttt cag aac ctg cct ttt gtg gcc gag gtg ctt gaa ggc				1206
Asp Pro Thr Phe Gln Asn Leu Pro Phe Val Ala Glu Val Leu Glu Gly				
372	377	382	387	
atc ccg gcg ggg gtc tcc atc tac caa gtg gtg gcc atc gac ctc gat				1254
Ile Pro Ala Gly Val Ser Ile Tyr Gln Val Val Ala Ile Asp Leu Asp				
388	393	398	403	
gag gcc ctg aac gcc ctg gtg tcc tac cgc atg ccg gtg gcc atg ccc				1302
Glu Gly Leu Asn Gly Leu Val Ser Tyr Arg Met Pro Val Gly Met Pro				
404	409	414	419	
cgc atg gac ttc ctc atc aac agc agc agc ggc gtg gtg gtc acc acc				1350
Arg Met Asp Phe Leu Ile Asn Ser Ser Ser Gly Val Val Val Thr Thr				
420	425	430	435	
acc gag ctg gac cgc gag cgc atc gcg gag tac cag ctg cgg gtg gtg				1398
Thr Glu Leu Asp Arg Glu Arg Ile Ala Glu Tyr Gln Leu Arg Val Val				
436	441	446	451	
gcc agt gat gca gcc acg ccc acc aag agc tcc acc agc acg ctc acc				1446
Ala Ser Asp Ala Gly Thr Pro Thr Lys Ser Ser Thr Ser Thr Leu Thr				
452	457	462	467	
atc cat gtg ctg gat gtg aac gac gag acg ccc acc ttc ttc ccg gcc				1494
Ile His Val Leu Asp Val Asn Asp Glu Thr Pro Thr Phe Phe Pro Ala				
468	473	478	483	
gtg tac aat gtg tct gtg tcc gag gac gtg cca cgc gag ttc cgg gtg				1542
Val Tyr Asn Val Ser Val Ser Glu Asp Val Pro Arg Glu Phe Arg Val				
484	489	494	499	
gtc tgg ctg aac tgc acg gac aac gac gtg gcc ctc aat gca gag ctc				1590
Val Trp Leu Asn Cys Thr Asp Asn Asp Val Gly Leu Asn Ala Glu Leu				
500	505	510	515	
agc tac ttc atc aca ggt gct gcc ccg gcc tcc acc cac ctg tgc agg				1638
Ser Tyr Phe Ile Thr Gly Ala Ala Pro Ala Ser Thr His Leu Cys Arg				
516	521	526	531	
cct cct ggg gcc ctg cct cca ccc ctc cca gat gga cag cca gac tag				1686
Pro Pro Gly Ala Leu Pro Pro Pro Leu Pro Asp Gly Gln Pro Asp *				
532	537	542	547	
gtgggggcag gtgaggggtgg aaaagaggtc agggctctac tggtgggctt tagcctctgg				1746
tggtgcctcc cgaggatttg ctctggctc ttcccaaggg ctttgcagct ggatcactct				1806

ggactggctc cctggggacc tcctgaacct gttggttgca gggacgggga gcatctacca 1866
 aggttcattc tagagggagg taaggcccca tgattcctag ggaggagccc tgagcccccac 1926
 tccccgcccc aagtctgggt gacagagcag tgacttggag gaatgtggcc tcatccttcc 1986
 ttggggacct gttgagaatt cccacctgtt tagaggcaga tggttttgat ctccctaaat 2046
 gaaatggttt tagctcaaaa aaaaaa 2072

<210> 80
 <211> 2534
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (399)..(2534)

<400> 80
 cggccgctgg ggctgctggt accgccgagc cggggcgccgc agcggtcct cctggggcct 60
 acatttgccc cgccagcccg tgtccggagc ccccttcgcg gggtacataa ccaggctccc 120
 ggccgagtgg gcgaagccca gcacatttcg ggggcggggg gcaggtgagg gtccccagat 180
 gtcccttcag tgettccgaa gacaccggag gggagtaccc cgcgtagagc gcagctggac 240
 cctcggggtg cgggcccctc tccttgtcct gcttttcagc atctttggca attgcgcaaa 300
 gttgcttggg ttgcaatggt ggggtgcagg gggcgctcgg ctgctgcacc tgtagtgct 360
 gggcccaggt tgagaggcga cctccagccc ccacaata atg tcc cgg gct ctc 413
 Met Ser Arg Ala Leu
 1
 tgg ttt ggg tcc tcg cag cgc ccg att gac cgc cag cga tac gac gag 461
 Trp Phe Gly Ser Ser Gln Arg Pro Ile Asp Arg Gln Arg Tyr Asp Glu
 6 11 16 21
 aac gag gac ttg tcg gac gtg gag gag atc gtc agc gtc cgc ggc ttc 509
 Asn Glu Asp Leu Ser Asp Val Glu Glu Ile Val Ser Val Arg Gly Phe
 22 27 32 37
 agc ctg gag gag aag ctt cgc agc cag ctg tac cag ggg gac ttc gtg 557
 Ser Leu Glu Glu Lys Leu Arg Ser Gln Leu Tyr Gln Gly Asp Phe Val
 38 43 48 53
 cac gcc atg gag ggc aaa gat ttc aac tat gag tac gta cag aga gaa 605
 His Ala Met Glu Gly Lys Asp Phe Asn Tyr Glu Tyr Val Gln Arg Glu
 54 59 64 69
 gct ctc agg gtt ccc ctg ata ttt cga gaa aag gat gga ctg gga att 653

Ala	Leu	Arg	Val	Pro	Leu	Ile	Phe	Arg	Glu	Lys	Asp	Gly	Leu	Gly	Ile	
70					75					80					85	
aag	atg	cct	gac	cct	gat	ttc	aca	gtc	cga	gac	gtc	aaa	ctc	cta	gtg	701
Lys	Met	Pro	Asp	Pro	Asp	Phe	Thr	Val	Arg	Asp	Val	Lys	Leu	Leu	Val	
86					91					96					101	
ggg	agc	cgg	cgg	ctt	gtg	gac	gtg	atg	gat	gtg	aac	acc	cag	aag	ggc	749
Gly	Ser	Arg	Arg	Leu	Val	Asp	Val	Met	Asp	Val	Asn	Thr	Gln	Lys	Gly	
102					107					112					117	
acg	gag	atg	agc	atg	tcc	cag	ttt	gtg	cgt	tac	tac	gag	acg	ccc	gag	797
Thr	Glu	Met	Ser	Met	Ser	Gln	Phe	Val	Arg	Tyr	Tyr	Glu	Thr	Pro	Glu	
118					123					128					133	
gcc	cag	cgg	gac	aag	ctg	tac	aac	gtc	atc	agc	cta	gag	ttc	agc	cac	845
Ala	Gln	Arg	Asp	Lys	Leu	Tyr	Asn	Val	Ile	Ser	Leu	Glu	Phe	Ser	His	
134					139					144					149	
acc	aag	ctg	gag	cac	ttg	gtc	aag	cgt	ccg	act	gtg	gta	gac	ctg	gtg	893
Thr	Lys	Leu	Glu	His	Leu	Val	Lys	Arg	Pro	Thr	Val	Val	Asp	Leu	Val	
150					155					160					165	
gac	tgg	gtg	gac	aac	atg	tgg	ccc	cag	cat	ctg	aag	gag	aag	cag	aca	941
Asp	Trp	Val	Asp	Asn	Met	Trp	Pro	Gln	His	Leu	Lys	Glu	Lys	Gln	Thr	
166					171					176					181	
gaa	gcc	acg	aac	gcc	att	gca	gag	atg	aag	tac	ccg	aaa	gtg	aaa	aag	989
Glu	Ala	Thr	Asn	Ala	Ile	Ala	Glu	Met	Lys	Tyr	Pro	Lys	Val	Lys	Lys	
182					187					192					197	
tac	tgt	ctg	atg	agc	gtg	aaa	ggt	tgt	ttc	acc	gac	ttc	cac	atc	gac	1037
Tyr	Cys	Leu	Met	Ser	Val	Lys	Gly	Cys	Phe	Thr	Asp	Phe	His	Ile	Asp	
198					203					208					213	
ttt	gga	ggc	act	tcc	gtt	tgg	tac	cat	gtt	ttc	cgg	ggg	ggg	aag	att	1085
Phe	Gly	Gly	Thr	Ser	Val	Trp	Tyr	His	Val	Phe	Arg	Gly	Gly	Lys	Ile	
214					219					224					229	
ttt	tgg	ctg	att	cct	cca	acg	ctg	cac	aat	ttg	gcg	ctg	tac	gag	gag	1133
Phe	Trp	Leu	Ile	Pro	Pro	Thr	Leu	His	Asn	Leu	Ala	Leu	Tyr	Glu	Glu	
230					235					240					245	
tgg	gtg	ctg	tca	ggc	aaa	cag	agt	gac	atc	ttt	ctg	gga	gac	cgt	gtg	1181
Trp	Val	Leu	Ser	Gly	Lys	Gln	Ser	Asp	Ile	Phe	Leu	Gly	Asp	Arg	Val	
246					251					256					261	
gaa	cga	tgc	caa	aga	att	gag	ctg	aag	cag	ggc	tac	aca	ttt	ttc	atc	1229
Glu	Arg	Cys	Gln	Arg	Ile	Glu	Leu	Lys	Gln	Gly	Tyr	Thr	Phe	Phe	Ile	
262					267					272					277	

294	299	304	309	
atc tac gag atc gag gac agg acg cgg gtg	cag ccc aaa ttc cgt tac	1373		
Ile Tyr Glu Ile Glu Asp Arg Thr Arg Val	Gln Pro Lys Phe Arg Tyr			
310	315	320	325	
ccc ttc tac tat gag atg tgc tgg tat gtc	ctg gag aga tac gtg tac	1421		
Pro Phe Tyr Tyr Glu Met Cys Trp Tyr Val	Leu Glu Arg Tyr Val Tyr			
326	331	336	341	
tgt gtg acc cag cgc tcc cac ctc act cag	gaa tac cag agg gag tcg	1469		
Cys Val Thr Gln Arg Ser His Leu Thr Gln	Glu Tyr Gln Arg Glu Ser			
342	347	352	357	
atg ctt att gat gcc ccg agg aag ccc agc	ata gac ggc ttc tct tcg	1517		
Met Leu Ile Asp Ala Pro Arg Lys Pro Ser	Ile Asp Gly Phe Ser Ser			
358	363	368	373	
gat tcc tgg ctg gag atg gag gag gag gcc	tgt gat cag cag cct cag	1565		
Asp Ser Trp Leu Glu Met Glu Glu Glu Ala	Cys Asp Gln Gln Pro Gln			
374	379	384	389	
gag gag gag gag aag gac gag gag ggc gag	ggc agg gac agg gca ccc	1613		
Glu Glu Glu Glu Lys Asp Glu Glu Gly Glu	Gly Arg Asp Arg Ala Pro			
390	395	400	405	
aaa ccg ccc acc gat ggc tcc act tca ccc	acc agc acg ccc tct gag	1661		
Lys Pro Pro Thr Asp Gly Ser Thr Ser Pro	Thr Ser Thr Pro Ser Glu			
406	411	416	421	
gac cag gag gcc ctc ggg aag aag ccc aaa	gca cct gcc ctg cga ttc	1709		
Asp Gln Glu Ala Leu Gly Lys Lys Pro Lys	Ala Pro Ala Leu Arg Phe			
422	427	432	437	
ctc aaa agg act ttg tct aat gag tcg gag	gaa agt gtg aag tcc acc	1757		
Leu Lys Arg Thr Leu Ser Asn Glu Ser Glu	Glu Ser Val Lys Ser Thr			
438	443	448	453	
aca ttg gcc gta gac tac ccc aag acc ccc	acc ggc tct ccc gcc acg	1805		
Thr Leu Ala Val Asp Tyr Pro Lys Thr Pro	Thr Gly Ser Pro Ala Thr			
454	459	464	469	
gag gtc tct gcc aaa tgg acc cat ctc act	gag ttt gaa ctg aag ggc	1853		
Glu Val Ser Ala Lys Trp Thr His Leu Thr	Glu Phe Glu Leu Lys Gly			
470	475	480	485	
ctg aaa gct ctg gtg gag aaa ctg gaa tcc	ctc ccg gag aac aag aag	1901		
Leu Lys Ala Leu Val Glu Lys Leu Glu Ser	Leu Pro Glu Asn Lys Lys			
486	491	496	501	
tgt gtc ccc gag ggc atc gag gac ccc cag	gca ctc ctg gag ggt gtg	1949		
Cys Val Pro Glu Gly Ile Glu Asp Pro Gln	Ala Leu Leu Glu Gly Val			
502	507	512	517	
aag aac gtc ctg aag gag cac gca gat gat	gac cct agt ctg gcc atc	1997		
Lys Asn Val Leu Lys Glu His Ala Asp Asp	Asp Pro Ser Leu Ala Ile			
518	523	528	533	

act ggg gtc cct gtg gtg act tgg cca aag aag act cca aag aac cgg	2045
Thr Gly Val Pro Val Val Thr Trp Pro Lys Lys Thr Pro Lys Asn Arg	
534 539 544 549	
gct gtg ggt cgg ccc aag ggg aag ctg ggc ccg gcc tcc gcg gtg aag	2093
Ala Val Gly Arg Pro Lys Gly Lys Leu Gly Pro Ala Ser Ala Val Lys	
550 555 560 565	
ttg gcc gcc aac cgg aca acg gca gga gct cgg cgg cgc cgg acg cga	2141
Leu Ala Ala Asn Arg Thr Thr Ala Gly Ala Arg Arg Arg Arg Thr Arg	
566 571 576 581	
tgc cgc aag tgc gag gcc tgc ctg cgg acc gag tgc gga gag tgc cac	2189
Cys Arg Lys Cys Glu Ala Cys Leu Arg Thr Glu Cys Gly Glu Cys His	
582 587 592 597	
ttc tgc aag gac atg aag aag ttc ggg ggc ccc ggg cgc atg aag cag	2237
Phe Cys Lys Asp Met Lys Lys Phe Gly Gly Pro Gly Arg Met Lys Gln	
598 603 608 613	
agc tgc atc atg cgg cag tgc atc gcg cca gtg ctg ccc cac acc gcc	2285
Ser Cys Ile Met Arg Gln Cys Ile Ala Pro Val Leu Pro His Thr Ala	
614 619 624 629	
gtg tgc ctt gtg tgt ggc gag gcg ggg aag gaa gac acg gtg gaa gag	2333
Val Cys Leu Val Cys Gly Glu Ala Gly Lys Glu Asp Thr Val Glu Glu	
630 635 640 645	
gag gaa ggc aag ttt aac ctc atg ctc atg gag tgc tcc atc tgc aat	2381
Glu Glu Gly Lys Phe Asn Leu Met Leu Met Glu Cys Ser Ile Cys Asn	
646 651 656 661	
gaa atc atc cac cct gga tgc ctt aag gtg agt ggc cca gtg ggg aca	2429
Glu Ile Ile His Pro Gly Cys Leu Lys Val Ser Gly Pro Val Gly Thr	
662 667 672 677	
ggg ggt gct gac gct ctg ggg cag gta ggg ttg ctg gag atg ctg gtg	2477
Gly Gly Ala Asp Ala Leu Gly Gln Val Gly Leu Leu Glu Met Leu Val	
678 683 688 693	
aga tgg tgg gat gca ggt cgt gca gtg aat tcc tgg agg acc cct gag	2525
Arg Trp Trp Asp Ala Gly Arg Ala Val Asn Ser Trp Arg Thr Pro Glu	
694 699 704 709	
tct ggg tga	2534
Ser Gly *	
710	

<210> 81
 <211> 4100/
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (105)..(4100)

<400> 81

atacagttga tacttatgac agtggcgatg attgggaaaa tcggggttga aatttaataa 60

ttgatttgga cgctgatttg gagaaggaca gacagaaatt tgag atg aat aat tcc 116
Met Asn Asn Ser

1

acc acc acc act agt agc agc aac tcc aag gat tgt gga ggt ccg gcc 164
Thr Thr Thr Thr Ser Ser Ser Asn Ser Lys Asp Cys Gly Gly Pro Ala
5 10 15 20

tcc agt ggg gct ggt gct acc gca gcc tta gct gat ggc cta aaa ttt 212
Ser Ser Gly Ala Gly Ala Thr Ala Ala Leu Ala Asp Gly Leu Lys Phe
21 26 31 36

gct tct gtt cag gcc tct gct ccc cag ggg aat tca cac aaa gag acc 260
Ala Ser Val Gln Ala Ser Ala Pro Gln Gly Asn Ser His Lys Glu Thr
37 42 47 52

agc aaa tca aaa gtg aaa agg agt aaa act tct aag gat gct aat aaa 308
Ser Lys Ser Lys Val Lys Arg Ser Lys Thr Ser Lys Asp Ala Asn Lys
53 58 63 68

tct ctg cct tct gct gcc ttg tat ggg att ccc gag atc agc agc act 356
Ser Leu Pro Ser Ala Ala Leu Tyr Gly Ile Pro Glu Ile Ser Ser Thr
69 74 79 84

ggc aag agg cag gaa gtc caa ggg cgc cct gga gag gca act ggc atg 404
Gly Lys Arg Gln Glu Val Gln Gly Arg Pro Gly Glu Ala Thr Gly Met
85 90 95 100

aat tca gcg ctg ggt caa agt gtg agc agc ggc ggc agc ggc aac cca 452
Asn Ser Ala Leu Gly Gln Ser Val Ser Ser Gly Gly Ser Gly Asn Pro
101 106 111 116

aac agc aat agt acc agc acc agc acc tct gcc gcc acc gcg ggg gca 500
Asn Ser Asn Ser Thr Ser Thr Ser Thr Ser Ala Ala Thr Ala Gly Ala
117 122 127 132

ggc tcc tgt ggg aaa agc aaa gag gag aag cca ggt aaa agc cag agc 548
Gly Ser Cys Gly Lys Ser Lys Glu Glu Lys Pro Gly Lys Ser Gln Ser
133 138 143 148

agc cga ggc gcc aag cgg gat aag gat gcg ggg aaa tcc agg aag gac 596
Ser Arg Gly Ala Lys Arg Asp Lys Asp Ala Gly Lys Ser Arg Lys Asp
149 154 159 164

aag cac gac ctg ctt cag ggc cac cag aat ggc agt ggc agc cag gcc 644
Lys His Asp Leu Leu Gln Gly His Gln Asn Gly Ser Gly Ser Gln Ala
165 170 175 180

cct tcc ggg ggg cac ctc tat ggc ttt ggg gcc aag agc aat gga ggt 692

Pro Ser Gly Gly His Leu Tyr Gly Phe Gly Ala Lys Ser Asn Gly Gly	
181 186 191 196	
ggc gcg agc ccc ttc cac tgc ggg ggc act ggg agt ggc agc gtc gcc	740
Gly Ala Ser Pro Phe His Cys Gly Gly Thr Gly Ser Gly Ser Val Ala	
197 202 207 212	
gct gca ggg gaa gtt agc aaa agt gcc ccg gat tca ggg ctc atg gga	788
Ala Ala Gly Glu Val Ser Lys Ser Ala Pro Asp Ser Gly Leu Met Gly	
213 218 223 228	
aac tct atg ttg gta aag aag gaa gag gag gag gag gag agc cac agg	836
Asn Ser Met Leu Val Lys Lys Glu Glu Glu Glu Glu Glu Ser His Arg	
229 234 239 244	
cga atc aag aaa ctg aaa act gag aag gtt gac ccc ctg ttt aca gtg	884
Arg Ile Lys Lys Leu Lys Thr Glu Lys Val Asp Pro Leu Phe Thr Val	
245 250 255 260	
cca gcg cca cca ccg ccg att tcc agc agt ctc acg cct cag att cta	932
Pro Ala Pro Pro Pro Pro Ile Ser Ser Ser Leu Thr Pro Gln Ile Leu	
261 266 271 276	
ccc tcc tac ttt tcc cca tct tca tcc aat att gca gca ccg gtt gaa	980
Pro Ser Tyr Phe Ser Pro Ser Ser Ser Asn Ile Ala Ala Pro Val Glu	
277 282 287 292	
cag ctt ttg gtt cgg act cgt tct gtg ggt gtc aat aca tgt gaa gtt	1028
Gln Leu Leu Val Arg Thr Arg Ser Val Gly Val Asn Thr Cys Glu Val	
293 298 303 308	
gga gta gtg aca gag cca gag tgt ctt ggg ccc tgt gaa cct ggg acc	1076
Gly Val Val Thr Glu Pro Glu Cys Leu Gly Pro Cys Glu Pro Gly Thr	
309 314 319 324	
agt gtg aat ttg gaa ggg atc gtg tgg cat gaa aca gaa gaa ggt gtc	1124
Ser Val Asn Leu Glu Gly Ile Val Trp His Glu Thr Glu Glu Gly Val	
325 330 335 340	
cta gtg gtc aat gtc acg tgg agg aac aaa acg tac gtg gga acc cta	1172
Leu Val Val Asn Val Thr Trp Arg Asn Lys Thr Tyr Val Gly Thr Leu	
341 346 351 356	
ctg gac tgc acc aag cac gac tgg gcc cct ccc agg ttt tgt gag tca	1220
Leu Asp Cys Thr Lys His Asp Trp Ala Pro Pro Arg Phe Cys Glu Ser	
357 362 367 372	
ccg aca agt gac ctg gag atg aga ggg ggc ccg ggc aga ggg aag aga	1268
Pro Thr Ser Asp Leu Glu Met Arg Gly Gly Arg Gly Arg Gly Lys Arg	
373 378 383 388	
gcg agg tct gct gct gct gcc ccg ggc tcc gag gcc agc ttc aca gag	1316
Ala Arg Ser Ala Ala Ala Ala Pro Gly Ser Glu Ala Ser Phe Thr Glu	
389 394 399 404	
tcc aga ggg ctg cag aat aag aac aga ggg ggg gcc aat ggg aaa ggg	1364
Ser Arg Gly Leu Gln Asn Lys Asn Arg Gly Gly Ala Asn Gly Lys Gly	

405	410	415	420	
agg cgg ggc agc ctc aat gcc agc gga cga agg aca ccc cca aat tgt				1412
Arg Arg Gly Ser Leu Asn Ala Ser Gly Arg Arg Thr Pro Pro Asn Cys				
421	426	431	436	
gct gct gag gat atc aaa gcc agc cct tcc tcc acc aaa aaa aaa aaa				1460
Ala Ala Glu Asp Ile Lys Ala Ser Pro Ser Ser Thr Lys Lys Lys Lys				
437	442	447	452	
aac aag cct cca atg gag ctg gac ctg aac tcc agc tct gag gac aat				1508
Asn Lys Pro Pro Met Glu Leu Asp Leu Asn Ser Ser Ser Glu Asp Asn				
453	458	463	468	
aag cct gga aag cgt gtc cgc aca aat tcc aga agc act ccc act acc				1556
Lys Pro Gly Lys Arg Val Arg Thr Asn Ser Arg Ser Thr Pro Thr Thr				
469	474	479	484	
cct caa ggg aaa cca gag act act ttt ttg gac caa ggc tgc tct tct				1604
Pro Gln Gly Lys Pro Glu Thr Thr Phe Leu Asp Gln Gly Cys Ser Ser				
485	490	495	500	
cca gtg tta atc gac tgt ccc cac cca aac tgc aac aaa aag tac aag				1652
Pro Val Leu Ile Asp Cys Pro His Pro Asn Cys Asn Lys Lys Tyr Lys				
501	506	511	516	
cac att aac ggc ctg agg tac cac cag gct cat gca cac tta gac cca				1700
His Ile Asn Gly Leu Arg Tyr His Gln Ala His Ala His Leu Asp Pro				
517	522	527	532	
gaa aac aag ctg gag ttc gag cct gac agt gag gac aag atc tcg gac				1748
Glu Asn Lys Leu Glu Phe Glu Pro Asp Ser Glu Asp Lys Ile Ser Asp				
533	538	543	548	
tgt gag gaa gga ttg agt aat gtg gca ctt gaa tgc agt gag cca agc				1796
Cys Glu Glu Gly Leu Ser Asn Val Ala Leu Glu Cys Ser Glu Pro Ser				
549	554	559	564	
aca agt gta tct gct tat gac cag ttg aag gca ccg gca tcc cct ggt				1844
Thr Ser Val Ser Ala Tyr Asp Gln Leu Lys Ala Pro Ala Ser Pro Gly				
565	570	575	580	
gct gga aac cca cct ggg acc cca aag gga aag aga gag ctg atg agc				1892
Ala Gly Asn Pro Pro Gly Thr Pro Lys Gly Lys Arg Glu Leu Met Ser				
581	586	591	596	
aat ggc cca ggt tcc att att ggt gct aaa gct ggg aag aat tct ggc				1940
Asn Gly Pro Gly Ser Ile Ile Gly Ala Lys Ala Gly Lys Asn Ser Gly				
597	602	607	612	
aaa aag aag ggc ctt aac aat gaa ctg aac aac ctt cca gta atc tcc				1988
Lys Lys Lys Gly Leu Asn Asn Glu Leu Asn Asn Leu Pro Val Ile Ser				
613	618	623	628	
aac atg acg gct gcg tta gac agt tgc tcg gca gca gac ggc agt ttg				2036
Asn Met Thr Ala Ala Leu Asp Ser Cys Ser Ala Ala Asp Gly Ser Leu				
629	634	639	644	

gct gct gag atg cct aaa ctg gaa gca gaa gga tta att gac aag aaa	2084
Ala Ala Glu Met Pro Lys Leu Glu Ala Glu Gly Leu Ile Asp Lys Lys	
645 650 655 660	
aat tta gga gat aaa gaa aag ggc aaa aaa gct aac aac tgc aaa acg	2132
Asn Leu Gly Asp Lys Glu Lys Gly Lys Lys Ala Asn Asn Cys Lys Thr	
661 666 671 676	
gac aaa aac ctc tct aaa ctg aaa agt gcc cgg ccc att gcc cct gcc	2180
Asp Lys Asn Leu Ser Lys Leu Lys Ser Ala Arg Pro Ile Ala Pro Ala	
677 682 687 692	
cca gcc ccc act ccc ccg cag cta atc gct ata ccc act gca acc ttt	2228
Pro Ala Pro Thr Pro Pro Gln Leu Ile Ala Ile Pro Thr Ala Thr Phe	
693 698 703 708	
aca acg acc acc act ggg aca ata ccc gga ctg ccc tcc ctc aca aca	2276
Thr Thr Thr Thr Thr Gly Thr Ile Pro Gly Leu Pro Ser Leu Thr Thr	
709 714 719 724	
act gtt gtt cag gct aca cca aag agt cct ccg tta aaa ccc att caa	2324
Thr Val Val Gln Ala Thr Pro Lys Ser Pro Pro Leu Lys Pro Ile Gln	
725 730 735 740	
cca aag ccc aca att atg gga gag ccc atc acc gtg aac cca gct ctg	2372
Pro Lys Pro Thr Ile Met Gly Glu Pro Ile Thr Val Asn Pro Ala Leu	
741 746 751 756	
gtg tca ctc aaa gac aaa aag aaa aag gag aag cga aag cta aag gac	2420
Val Ser Leu Lys Asp Lys Lys Lys Lys Glu Lys Arg Lys Leu Lys Asp	
757 762 767 772	
aaa gaa ggg aaa gag acg gga agc cca aaa atg gat gcc aag ctg ggg	2468
Lys Glu Gly Lys Glu Thr Gly Ser Pro Lys Met Asp Ala Lys Leu Gly	
773 778 783 788	
aaa cta gag gac tcc aag ggg gcc agc aaa gat tta cct ggg cat ttt	2516
Lys Leu Glu Asp Ser Lys Gly Ala Ser Lys Asp Leu Pro Gly His Phe	
789 794 799 804	
tta aag gat cat ctc aac aag aat gaa ggg ctg gca aat gga ctg tcg	2564
Leu Lys Asp His Leu Asn Lys Asn Glu Gly Leu Ala Asn Gly Leu Ser	
805 810 815 820	
gag tct cag gag agc cgc atg gcc agt atc aaa gct gag gcc gat aag	2612
Glu Ser Gln Glu Ser Arg Met Ala Ser Ile Lys Ala Glu Ala Asp Lys	
821 826 831 836	
gtt tac act ttc aca gac aac gct ccc agc cct tcc ata ggg agc gcc	2660
Val Tyr Thr Phe Thr Asp Asn Ala Pro Ser Pro Ser Ile Gly Ser Ala	
837 842 847 852	
tcg agg ctg gaa tgc agc act ttg gtg aac ggg cag gca cca atg gca	2708
Ser Arg Leu Glu Cys Ser Thr Leu Val Asn Gly Gln Ala Pro Met Ala	
853 858 863 868	

ggg gcc ccg cct ctg cag gcg gag acc cca ggc agc gcg gtg gac tac	12816
Gly Ala Pro Pro Leu Gln Ala Glu Thr Pro Gly Ser Ala Val Asp Tyr	
4257 4262 4267 4272	
ccc ctg cat gac ctt gtc ctc cac acc aac tac acc gcc aca gtg cgt	12864
Pro Leu His Asp Leu Val Leu His Thr Asn Tyr Thr Ala Thr Val Arg	
4273 4278 4283 4288	
ggc ctg cgg ggc ccc aac ctc act tcc cca gcc agc atc acc ttc acc	12912
Gly Leu Arg Gly Pro Asn Leu Thr Ser Pro Ala Ser Ile Thr Phe Thr	
4289 4294 4299 4304	
aca ggg cta gag gcc cct cgg gac ttg gag gcc aag gaa gtg acc ccc	12960
Thr Gly Leu Glu Ala Pro Arg Asp Leu Glu Ala Lys Glu Val Thr Pro	
4305 4310 4315 4320	
cgc acc gcc ctg ctc act tgg act gag ccc cca gtc cgg ccc gca ggc	13008
Arg Thr Ala Leu Leu Thr Trp Thr Glu Pro Pro Val Arg Pro Ala Gly	
4321 4326 4331 4336	
tac ctg ctc agc ttc cac acc cct ggt gga cag aac cag gag atc ctg	13056
Tyr Leu Leu Ser Phe His Thr Pro Gly Gly Gln Asn Gln Glu Ile Leu	
4337 4342 4347 4352	
ctc cca gga ggg atc aca tct cac cag ctc ctt ggc ctc ttt ccc tcc	13104
Leu Pro Gly Gly Ile Thr Ser His Gln Leu Leu Gly Leu Phe Pro Ser	
4353 4358 4363 4368	
acc tcc tac aat gca cgg ctc cag gcc atg tgg ggc cag agc ctc ctg	13152
Thr Ser Tyr Asn Ala Arg Leu Gln Ala Met Trp Gly Gln Ser Leu Leu	
4369 4374 4379 4384	
ccg ccc gtg tcc acc tct ttc acc acg ggt ggg ctg cgg atc ccc ttc	13200
Pro Pro Val Ser Thr Ser Phe Thr Thr Gly Gly Leu Arg Ile Pro Phe	
4385 4390 4395 4400	
ccc agg gac tgc ggg gag gag atg cag aac gga gcc ggt gcc tcc agg	13248
Pro Arg Asp Cys Gly Glu Glu Met Gln Asn Gly Ala Gly Ala Ser Arg	
4401 4406 4411 4416	
acc agc acc atc ttc ctc aac ggc aac cgc gag cgg ccc ctg aac gtg	13296
Thr Ser Thr Ile Phe Leu Asn Gly Asn Arg Glu Arg Pro Leu Asn Val	
4417 4422 4427 4432	
ttt tgc gac atg gag act gat ggg ggc ggc tgg ctg gtg ttc cag cgc	13344
Phe Cys Asp Met Glu Thr Asp Gly Gly Trp Leu Val Phe Gln Arg	
4433 4438 4443 4448	
cgc atg gat gga cag aca gac ttc tgg agg gac tgg gag gac tat gcc	13392
Arg Met Asp Gly Gln Thr Asp Phe Trp Arg Asp Trp Glu Asp Tyr Ala	
4449 4454 4459 4464	
cat ggt ttt ggg aac atc tct gga gag ttc tgg ctg ggc aat gag gcc	13440
His Gly Phe Gly Asn Ile Ser Gly Glu Phe Trp Leu Gly Asn Glu Ala	
4465 4470 4475 4480	
ctg cac agc ctg aca cag gca ggt gac tac tcc atg cgc gtg gac ctg	13488

1317

1322

1327

1332

<210> 82
 <211> 2300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (514) .. (1419)

<400> 82

```

gtggaattac cgaccgcac ggaattcccg ggtcgacgat ttcgtgccgg aagagaccgg      60
accctgaaca gaatcgcata ttgccagccc ttttcccgac ccctacggaa agacgagtcc      120
agggggccgctc ctggcgagtt caaaacattt agtctgggtct tttcaggtga ggacttcccc      180
atccaggcac agtgccgggc caatccccct ttaatttccc atgactcctc gcgtcctgaa      240
gccccgcccc cagttcccca gccccgcccc gaagtttgag ggggtgtggac ggtttgtgac      300
ccccttagcc gaccctactc ctcaactggcc gggacaactg gtcttatcac ggaggctggg      360
gccaggcagc ccttcgggttc ggggtgggccc atggacccca gtccaacgcc gagggaatag      420
gaccatccaa aagcgggaacc ttcgcctcag aaaaagggtg cgggaccctt cctcaccgtg      480
cggtcacgcg tggaccctgc cagcagccag gcc atg gag ctc tct gat gtc acc      534
                               Met Glu Leu Ser Asp Val Thr
                               1                               5

ctc att gag ggt gtg ggt aat gag gtg atg gtg gtg gca ggt gtg gtg      582
Leu Ile Glu Gly Val Gly Asn Glu Val Met Val Val Ala Gly Val Val
   8                               13                               18                               23

gtg ctg att cta gcc ttg gtc cta gct tgg ctc tct acc tac gta gca      630
Val Leu Ile Leu Ala Leu Val Leu Ala Trp Leu Ser Thr Tyr Val Ala
  24                               29                               34                               39

gac agc ggt agc aac cag ctc ctg ggc gct att gtg tca gca ggc gac      678
Asp Ser Gly Ser Asn Gln Leu Leu Gly Ala Ile Val Ser Ala Gly Asp
  40                               45                               50                               55

aca toc gtc ctc cac ctg ggg cat gtg gac cac ctg gtg gca ggc caa      726
Thr Ser Val Leu His Leu Gly His Val Asp His Leu Val Ala Gly Gln
  56                               61                               66                               71

ggc aac ccc gag cca act gaa ctc ccc cat cca tca gag ggt aat gat      774
Gly Asn Pro Glu Pro Thr Glu Leu Pro His Pro Ser Glu Gly Asn Asp
  72                               77                               82                               87

gag aag gct gaa gag gcg ggt gaa ggt cgg gga gac tcc act ggg gag      822

```

Glu Lys Ala Glu Glu Ala Gly Glu Gly Arg Gly Asp Ser Thr Gly Glu	
88 93 98 103	
gct gga gct ggg ggt ggt gtt gag ccc agc ctt gag cat ctc ctt gac	870
Ala Gly Ala Gly Gly Gly Val Glu Pro Ser Leu Glu His Leu Leu Asp	
104 109 114 119	
atc caa ggc ctg ccc aaa aga caa gca ggt gca ggc agc agc agt cca	918
Ile Gln Gly Leu Pro Lys Arg Gln Ala Gly Ala Gly Ser Ser Ser Pro	
120 125 130 135	
gag gcc ccc ctg aga tct gag gat agc acc tgc ctc cct ccc agc cct	966
Glu Ala Pro Leu Arg Ser Glu Asp Ser Thr Cys Leu Pro Pro Ser Pro	
136 141 146 151	
ggc ctc atc act gtg cgg ctc aaa ttc ctc aat gat acc gag gag ctg	1014
Gly Leu Ile Thr Val Arg Leu Lys Phe Leu Asn Asp Thr Glu Glu Leu	
152 157 162 167	
gct gtg gct agg cca gag gat acc gtg ggt gcc ctg aag agc aaa tac	1062
Ala Val Ala Arg Pro Glu Asp Thr Val Gly Ala Leu Lys Ser Lys Tyr	
168 173 178 183	
ttc cct gga caa gaa agc cag atg aaa ctg atc tac cag ggc cgc ctg	1110
Phe Pro Gly Gln Glu Ser Gln Met Lys Leu Ile Tyr Gln Gly Arg Leu	
184 189 194 199	
cta caa gac cca gcc cgc aca ctg cgt tct ctg aac att acc gac aac	1158
Leu Gln Asp Pro Ala Arg Thr Leu Arg Ser Leu Asn Ile Thr Asp Asn	
200 205 210 215	
tgt gtg att cac tgc cac cgc tca ccc cca ggg tca gct gtt cca ggc	1206
Cys Val Ile His Cys His Arg Ser Pro Pro Gly Ser Ala Val Pro Gly	
216 221 226 231	
ccc tca gcc tcc ttg gcc ccc tcg gcc act gag cca ccc agc ctt ggt	1254
Pro Ser Ala Ser Leu Ala Pro Ser Ala Thr Glu Pro Pro Ser Leu Gly	
232 237 242 247	
gtc aat gtg ggc agc ctc atg gtg cct gtc ttt gtg gtg ctg ttg ggt	1302
Val Asn Val Gly Ser Leu Met Val Pro Val Phe Val Val Leu Leu Gly	
248 253 258 263	
gtg gtc tgg tac ttc cga atc aat tac cgc caa ttc ttc aca gca cct	1350
Val Val Trp Tyr Phe Arg Ile Asn Tyr Arg Gln Phe Phe Thr Ala Pro	
264 269 274 279	
gcc act gtc tcc ctg gtg gga gtc acc ttc ttc ttc agc ttc cta gta	1398
Ala Thr Val Ser Leu Val Gly Val Thr Phe Phe Phe Ser Phe Leu Val	
280 285 290 295	
ttt ggg atg tat gga cga taa gg acataggaag aaaatgaaag gcatgggtctt	1451
Phe Gly Met Tyr Gly Arg *	
296 301	
tctccttttat ggctcccca cttttcctgg ccagagctgg gcccaagggc cggggagggg	1511


```

ggggtggaaa ggatgtgatg gaaatctcct ccataggaca caggaggcaa gtatgcggcc 1571
tcccccttctc atccacagga gtacagatgt ccctcccggtg cgagcacaac tcaggtagaa 1631
atgaggatgt catcttcctt cacttttagg gtcctctgaa ggagttcaaa gctgctggcc 1691
aagctcagtg gggagcctgg gctctgagat tcctcccac ctgtggttct gactcttccc 1751
agtgtcctgc atgtctgccc ccagcaccca gggctgcctg caagggcagc tcagcatggc 1811
cccagcacia ctccgtaggg agcctggagt atccttccat ttctcagcca aatactcatc 1871
ttttgagact gaaatcacac tggcggaat gaagattgtg ccagccttct cttatgggca 1931
cctagccgcc ttcaccttct tctctaccc cttagcagga ataggggtgc ctcccttctt 1991
tcaaagcaact ttgcttgcat tttattttat tttttaaga gtccctcata gagctcagtc 2051
aggaagggga tggggcacca agccaagccc ccagcattgg gagcgccag gccacagctg 2111
ctgtcccggt agtcctcagg ctgtaagcaa gagacagcac tggcccttgg ccagcgtcct 2171
accctgcccc actccaagga ctgggtatgg attgctgggc cctaggctct tgcttctggg 2231
gctattggag ggtcagtgtc tgtgactgaa taaagttcca ttttgtggtc ctgcaaaaaa 2291
aaaaaaaaa 2300

```

```

<210> 83
<211> 2463
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (92) .. (892)

```

```

<400> 83
gaaattccgg ggcaccccg cgtccgccac gcgtccggaa ctgaggacag ggacagaggt 60

tatattatgg taccttgact ggcgagcact t atg aag aga aag agg atg aag 112
Met Lys Arg Lys Arg Met Lys
1 5

gcc aac att aag ctg gtt ggt tca gga ttt ccc ctt ccc tcc tct gat 160
Ala Asn Ile Lys Leu Val Gly Ser Gly Phe Pro Leu Pro Ser Ser Asp
8 13 18 23

ttg gat gac tct ctc act gaa gag ata gat gaa aag att gga ttc cga 208
Leu Asp Asp Ser Leu Thr Glu Glu Ile Asp Glu Lys Ile Gly Phe Arg
24 29 34 39

aat gat gca aat ttt gac tgg caa aat gtg gca gat ttc agg gat gca 256
Asn Asp Ala Asn Phe Asp Trp Gln Asn Val Ala Asp Phe Arg Asp Ala

```

40	45	50	55	
ggg gga tcc tta act gag gtc aag gtg gaa gag gaa gaa agg gat ccg				304
Gly Gly Ser Leu Thr Glu Val Lys Val Glu Glu Glu Glu Arg Asp Pro				
56	61	66	71	
cag agt cct gaa ttt gaa att gag gag gag gaa gaa atg ttg tca tcc				352
Gln Ser Pro Glu Phe Glu Ile Glu Glu Glu Glu Glu Met Leu Ser Ser				
72	77	82	87	
gtc ata cca gat tcc agg aga gaa aat gaa ctt ccc gat ttc ccc cac				400
Val Ile Pro Asp Ser Arg Arg Glu Asn Glu Leu Pro Asp Phe Pro His				
88	93	98	103	
att gat gag ttt ttt acc ctt aac tca aca cca tct aga tct gca tat				448
Ile Asp Glu Phe Phe Thr Leu Asn Ser Thr Pro Ser Arg Ser Ala Tyr				
104	109	114	119	
gat gag cct cat ttg ctc gta aat att gag aaa cag aaa cta gag ttg				496
Asp Glu Pro His Leu Leu Val Asn Ile Glu Lys Gln Lys Leu Glu Leu				
120	125	130	135	
gaa aaa cga cga ctg gat atc gag gcc gaa agg ctg cag gta gaa aag				544
Glu Lys Arg Arg Leu Asp Ile Glu Ala Glu Arg Leu Gln Val Glu Lys				
136	141	146	151	
gaa cgc cta caa atc gag aaa gag agg ctg cgg cat tta gac atg gaa				592
Glu Arg Leu Gln Ile Glu Lys Glu Arg Leu Arg His Leu Asp Met Glu				
152	157	162	167	
cat gag cgg ctt cag cta gag aag gag cgg ctg cag att gaa aga gaa				640
His Glu Arg Leu Gln Leu Glu Lys Glu Arg Leu Gln Ile Glu Arg Glu				
168	173	178	183	
aag ttg agg tta cag ata gtc aat tca gag aaa ccg tcc ttg gaa aat				688
Lys Leu Arg Leu Gln Ile Val Asn Ser Glu Lys Pro Ser Leu Glu Asn				
184	189	194	199	
gaa ctt ggt caa gga gaa aaa tcc atg ctt caa cca cag gac ata gaa				736
Glu Leu Gly Gln Gly Glu Lys Ser Met Leu Gln Pro Gln Asp Ile Glu				
200	205	210	215	
aca gag aag tta aaa ctt gag cga gaa cgc ttg caa ctg gaa aag gat				784
Thr Glu Lys Leu Lys Leu Glu Arg Glu Arg Leu Gln Leu Glu Lys Asp				
216	221	226	231	
agg ctg cag ttt ttg aag ttt gaa tct gag aag ctg cag att gaa aag				832
Arg Leu Gln Phe Leu Lys Phe Glu Ser Glu Lys Leu Gln Ile Glu Lys				
232	237	242	247	
gaa cgc tta cag gta gag aaa gac aga ctt cga att cag aaa gaa gga				880
Glu Arg Leu Gln Val Glu Lys Asp Arg Leu Arg Ile Gln Lys Glu Gly				
248	253	258	263	
cac ttg cag tga ttt ttccaggctt ccatttagca aatgtttgaa aactctagat				935
His Leu Gln *				
264				

ttttotcata tcaggtgata taatgatggt tgctggatta gctgtggttt cttgtcta	995
gtcagtgttc agtaggaaaa agttatatgt ggataactgt atgcctaagt agtatataaa	1055
agctgtgccc tagcgtaaac agtatagcag aaacttactg tgctggactc tttaccttat	1115
aatattacat agagtcttgt attgtctgtg taccagagt ttacaattat gtccatataa	1175
aattotagcc cagaagttct catctggggg agattttggc cttcagaaga ccaatttggt	1235
gatgtctgga gacatgttgg gttgtcaaaa ctgggggtggg gaaaagggtg ctactgtgca	1295
atgcatacct cctcaacacc cccccacact cagtaaagaa ttttccaacc caaaatatca	1355
ttagtctga gggtgagaaa ccctgtccta gcctaactgt gtacctctat agctatgttt	1415
tatagtttta gaatattaaa acctcagata tttatgtggg taggtactta aatggccaaa	1475
aactttaact atgaaatggt actgtgtagt atattgaata taggaagtga tgaagattat	1535
aggtatttta tcccatggt tccatctata aatagccttc tcagattcag aaaacaatac	1595
agagaacatc agaaattttc taaaatgggt cactttgaaa agaattcttt ttctcactat	1655
taatgcttta gaagcaagac gcaattttaa agcttttagtt ccttttcttt cagtcattgt	1715
cttagtttgg gtacaaaaat gtcatttcag taatgtactg aaatcttata agtgaatagt	1775
tgaagctagt aaaaatgata ccagtataaa aatgggtactt gtagtccatg agcttgaacc	1835
caatgactga ttgtttgact tttaaaataa gtaatagcag ccatttgagg gtagggggta	1895
gggtggggaag atgtactccg tatcaaataa taatgatggt gaaataatga tagtaggtat	1955
gtattatgga ttggagaagc acttattaca ctatctaacc taatatgtag aacaattctt	2015
gagagttgta tctgtcgtta tttctgaatg tgaagctcag agaagtgaca cagagtaa	2075
ggctgatctt ctatattgta gtatattttg tccttccttc ttccctgagg aacaaagcac	2135
gtatcttttag tctctttgat atttattctg agaccaaggg cttgcttgac ctgatgattt	2195
tccttcagct ctctgaaggt gctttttcca caatccaagt gattctgata cacactaaag	2255
ttgagaatca ctgcactaga tcactttgtg ttttctgatt ttcaagggtg atacatagct	2315
ttaatacagc tcttctgttg acagttatta ctttaatttt gcatttggtc cttgtaagaa	2375
tggttggaac ctgtgtgttg acatttgagg atgggtatgc aaggaaaaaa tatacttctg	2435
tttacttact ctgaaaaaaa aaaaaaaa	2463

<211> 2074
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (198)..(1778)

<400> 84

```

aggatgagat tgtaagcgta cgctgcggt accggcccgg aattcccggg tcgacgattt      60
cgtctagaag cgggctgtcg gtctccgtgt cgccgccgcc gcccggcacg gtggagctgg      120
ggcccccttt tgcctgggag tttttagtgc gcctagggtc agcggtgaca tcccaaaggg      180
caggccccggc agccgcc   atg gtg gcc aag gat tac ccc ttc tac ctc acg      230
                   Met Val Ala Lys Asp Tyr Pro Phe Tyr Leu Thr
                   1               5

gtc aag aga gcg aac tgc agc ctg gag cta cct ccg gcc agc ggt ccg      278
Val Lys Arg Ala Asn Cys Ser Leu Glu Leu Pro Pro Ala Ser Gly Pro
   12               17               22               27

gcc aag gac gct gag gag cct agt aat aaa cgg gtc aaa ccc ctt tcc      326
Ala Lys Asp Ala Glu Glu Pro Ser Asn Lys Arg Val Lys Pro Leu Ser
   28               33               38               43

cga gtc acg tcg cta gca aac ctc atc ccg ccc gtg aag gcc acg cca      374
Arg Val Thr Ser Leu Ala Asn Leu Ile Pro Pro Val Lys Ala Thr Pro
   44               49               54               59

tta aag cgc ttc agt caa acc ctg cag cgc tcc att agc ttc cgc agt      422
Leu Lys Arg Phe Ser Gln Thr Leu Gln Arg Ser Ile Ser Phe Arg Ser
   60               65               70               75

gag agc cgc cct gac atc ctc gcc ccc cga ccc tgg tcc aga aat gcc      470
Glu Ser Arg Pro Asp Ile Leu Ala Pro Arg Pro Trp Ser Arg Asn Ala
   76               81               86               91

gcc ccc tcg agc acg aaa cgg aga gat agc aag ctg tgg agt gag acc      518
Ala Pro Ser Ser Thr Lys Arg Arg Asp Ser Lys Leu Trp Ser Glu Thr
   92               97               102              107

ttc gat gtg tgc gtc aat cag atg ctt aca tcc aag gaa atc aaa cgt      566
Phe Asp Val Cys Val Asn Gln Met Leu Thr Ser Lys Glu Ile Lys Arg
  108               113               118               123

cag gag gcg atc ttt gag ctt tcc caa gga gaa gaa gac ttg ata gaa      614
Gln Glu Ala Ile Phe Glu Leu Ser Gln Gly Glu Glu Asp Leu Ile Glu
  124               129               134               139

gac ttg aaa tta gca aaa aag gcc tat cat gac ccc atg ctg aaa ctc      662
Asp Leu Lys Leu Ala Lys Lys Ala Tyr His Asp Pro Met Leu Lys Leu
  140               145               150               155

tcc ata atg aca gaa caa gag ttg aat caa att ttt gga aca ctg gac      710
Ser Ile Met Thr Glu Gln Glu Leu Asn Gln Ile Phe Gly Thr Leu Asp

```

156	161	166	171	
tct cta att cct cta cat gaa gag ctc ctt agt cag ctt cga gat gtt				758
Ser Leu Ile Pro Leu His Glu Glu Leu Leu Ser Gln Leu Arg Asp Val				
172	177	182	187	
agg aag cct gat ggc tgc act gaa cat gtt ggt ccc atc ctc gtg ggc				806
Arg Lys Pro Asp Gly Ser Thr Glu His Val Gly Pro Ile Leu Val Gly				
188	193	198	203	
tgg ctc cct tgc ctc agc tcc tat gat agc tac tgc agc aat caa gta				854
Trp Leu Pro Cys Leu Ser Ser Tyr Asp Ser Tyr Cys Ser Asn Gln Val				
204	209	214	219	
gcc gcc aaa gct ctg ctg gac cac aaa aag caa gat cac cga gtc cag				902
Ala Ala Lys Ala Leu Leu Asp His Lys Lys Gln Asp His Arg Val Gln				
220	225	230	235	
gat ttc cta cag cga tgt tta gaa tcc ccc ttt agc cgc aaa cta gat				950
Asp Phe Leu Gln Arg Cys Leu Glu Ser Pro Phe Ser Arg Lys Leu Asp				
236	241	246	251	
ctc tgg aat ttc ctc gat att cca aga agc cgc ctg gta aaa tac cct				998
Leu Trp Asn Phe Leu Asp Ile Pro Arg Ser Arg Leu Val Lys Tyr Pro				
252	257	262	267	
ctg ctt ctc cga gaa atc ttg agg cac aca cca aat gat aat cca gat				1046
Leu Leu Leu Arg Glu Ile Leu Arg His Thr Pro Asn Asp Asn Pro Asp				
268	273	278	283	
cag cag cac ttg gaa gaa gct ata aat atc att cag gga att gtg gca				1094
Gln Gln His Leu Glu Glu Ala Ile Asn Ile Ile Gln Gly Ile Val Ala				
284	289	294	299	
gaa atc aac acc aag act ggt gaa tct gaa tgc cgc tat tat aaa gag				1142
Glu Ile Asn Thr Lys Thr Gly Glu Ser Glu Cys Arg Tyr Tyr Lys Glu				
300	305	310	315	
cgg ctt ctt tac ttg gaa gaa ggc cag aaa gac tcc ctg atc gac agc				1190
Arg Leu Leu Tyr Leu Glu Glu Gly Gln Lys Asp Ser Leu Ile Asp Ser				
316	321	326	331	
tct cga gtc ttg tgt tgt cat ggt gaa ctg aag aac aat cgg ggc gtg				1238
Ser Arg Val Leu Cys Cys His Gly Glu Leu Lys Asn Asn Arg Gly Val				
332	337	342	347	
aaa ctg cat gtt ttc ctg ttc caa gaa gtg ctt gtg atc act cga gcc				1286
Lys Leu His Val Phe Leu Phe Gln Glu Val Leu Val Ile Thr Arg Ala				
348	353	358	363	
gtc acc cac aat gag cag ctt tgc tac cag ctg tac cgt cag cca atc				1334
Val Thr His Asn Glu Gln Leu Cys Tyr Gln Leu Tyr Arg Gln Pro Ile				
364	369	374	379	
ccc gtg aaa gac ctc ctg ctg gaa gac ctc cag gat gga gaa gtg agg				1382
Pro Val Lys Asp Leu Leu Leu Glu Asp Leu Gln Asp Gly Glu Val Arg				
380	385	390	395	

ctg ggt ggc tcc ctg cga ggg gca ttc agc aac aat gag aga att aaa	1430
Leu Gly Gly Ser Leu Arg Gly Ala Phe Ser Asn Asn Glu Arg Ile Lys	
396 401 406 411	
aac ttc ttc aga gtc agt ttc aaa aat gga tcc caa agt cag acc cac	1478
Asn Phe Phe Arg Val Ser Phe Lys Asn Gly Ser Gln Ser Gln Thr His	
412 417 422 427	
tcg cta caa gcc aat gac act ttc aac aaa cag cag tgg ctt aac tgt	1526
Ser Leu Gln Ala Asn Asp Thr Phe Asn Lys Gln Gln Trp Leu Asn Cys	
428 433 438 443	
att cgt caa gcc aaa gaa aca gtt ttg tgt gct gcc ggg caa gct ggg	1574
Ile Arg Gln Ala Lys Glu Thr Val Leu Cys Ala Ala Gly Gln Ala Gly	
444 449 454 459	
gtg ctt gac tcc gag gga tcg ttc cta aat ccc acc acc ggg agc aga	1622
Val Leu Asp Ser Glu Gly Ser Phe Leu Asn Pro Thr Thr Gly Ser Arg	
460 465 470 475	
gag cta cag gga gaa aca aaa ctt gag cag atg gac caa tcg gac agt	1670
Glu Leu Gln Gly Glu Thr Lys Leu Glu Gln Met Asp Gln Ser Asp Ser	
476 481 486 491	
gag tca gac tgt agt atg gac acg agt gag gtc agc ctc gac tgt gag	1718
Glu Ser Asp Cys Ser Met Asp Thr Ser Glu Val Ser Leu Asp Cys Glu	
492 497 502 507	
cgc atg gaa cag aca gac tct tcc tgt gga aac agc agg cac ggt gaa	1766
Arg Met Glu Gln Thr Asp Ser Ser Cys Gly Asn Ser Arg His Gly Glu	
508 513 518 523	
agt aac gtc tga cag aagcatgtgc acttcgggaa gcaggcctgc atcttacctg	1821
Ser Asn Val *	
524	
tacagtattt gcattccaca gatggaacgg tttggagaag cactttttca tacttttgtg	1881
aaagtataca tgttgGCCca gtctctcgta tctgtacctt tgtccctagt actgtaactg	1941
ccaatctgtc tgtgtaagct ggaatctgtg gcaactatta ccctgtgttg tatttcccaa	2001
gtgtctggat ggatggagag gtactcaaac aagttacttt cagttgtcct gctggatttt	2061
aaaaaaaaaa aaa	2074

<210> 85
 <211> 1550
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (46)..(1437)

<400> 85

ttgcacgacc	ggtcggaat	tcccgggtcg	aaacgtttca	tctaa	atg	gtg	tgc	54
					Met	Val	Cys	
					1			
aag	cgg	aag	ggg	gcc	ggt	gtt	ctt	102
Lys	Arg	Lys	Gly	Ala	Gly	Val	Leu	
4			9				14	19
ctc	tgc	cct	ccg	ccc	tct	tct	ccc	150
Leu	Cys	Pro	Pro	Pro	Ser	Ser	Pro	
20			25				30	35
gct	ggc	ggg	gac	gct	gtc	cga	gcc	198
Ala	Gly	Gly	Asp	Ala	Val	Arg	Ala	
36			41				46	51
cag	cag	cag	cat	gaa	tgt	ggc	gac	246
Gln	Gln	Gln	His	Glu	Cys	Gly	Asp	
52			57				62	67
aac	ccc	tgc	gac	tgt	cac	agg	gag	294
Asn	Pro	Cys	Asp	Cys	His	Arg	Glu	
68			73				78	83
aac	cag	ctg	ccg	ccg	tcc	atc	ctg	342
Asn	Gln	Leu	Pro	Pro	Ser	Ile	Leu	
84			89				94	99
ctg	gat	gag	cgt	tgc	ctt	tcc	gca	390
Leu	Asp	Glu	Arg	Cys	Leu	Ser	Ala	
100			105				110	115
gac	ctt	tgt	tta	gac	ttc	cag	ttt	438
Asp	Leu	Cys	Leu	Asp	Phe	Gln	Phe	
116			121				126	131
cgt	cag	cag	gtc	act	gat	gaa	ttg	486
Arg	Gln	Gln	Val	Thr	Asp	Glu	Leu	
132			137				142	147
cag	aat	ata	att	gaa	atc	aac	att	534
Gln	Asn	Ile	Ile	Glu	Ile	Asn	Ile	
148			153				158	163
aat	ggc	gta	tgt	gtt	tta	gca	ttt	582
Asn	Gly	Val	Cys	Val	Leu	Ala	Phe	
164			169				174	179
aca	gcc	tac	agg	tgt	aaa	cag	ctt	630
Thr	Ala	Tyr	Arg	Cys	Lys	Gln	Leu	
180			185				190	195
gcc	tct	cac	tgt	cct	tta	ctt	cag	678
Ala	Ser	His	Cys	Pro	Leu	Leu	Gln	

196	201	206	211	
aaa ctc act gat gaa gga ctc aag cag ctg ggc tca aaa tgc aga gaa				726
Lys Leu Thr Asp Glu Gly Leu Lys Gln Leu Gly Ser Lys Cys Arg Glu				
212	217	222	227	
ctc aaa gat att cat ttc ggc cag tgt tac aag atc tca gat gaa ggc				774
Leu Lys Asp Ile His Phe Gly Gln Cys Tyr Lys Ile Ser Asp Glu Gly				
228	233	238	243	
atg atc gtc ata gct aag ggc tgt ctg aaa tta caa agg ata tac atg				822
Met Ile Val Ile Ala Lys Gly Cys Leu Lys Leu Gln Arg Ile Tyr Met				
244	249	254	259	
cag gaa aac aaa tta gtg aca gat cag tca gtg aaa gca ttt gct gaa				870
Gln Glu Asn Lys Leu Val Thr Asp Gln Ser Val Lys Ala Phe Ala Glu				
260	265	270	275	
cac tgt cct gag ctt caa tat gta ggc ttc atg ggt tgt tca gtc act				918
His Cys Pro Glu Leu Gln Tyr Val Gly Phe Met Gly Cys Ser Val Thr				
276	281	286	291	
tct aaa gga gtc att cac cta acc aag cta aga aac ctt tcc agc ttg				966
Ser Lys Gly Val Ile His Leu Thr Lys Leu Arg Asn Leu Ser Ser Leu				
292	297	302	307	
gac cta cgt cat atc act gaa ctg gat aat gaa acc gtg atg gaa att				1014
Asp Leu Arg His Ile Thr Glu Leu Asp Asn Glu Thr Val Met Glu Ile				
308	313	318	323	
gtc aag agg tgc aaa aat ctt agc tct ctc aat ctc tgt ctg aac tgg				1062
Val Lys Arg Cys Lys Asn Leu Ser Ser Leu Asn Leu Cys Leu Asn Trp				
324	329	334	339	
atc ata aat gac agg tgt gtg gag gtc att gca aag gaa gga caa aac				1110
Ile Ile Asn Asp Arg Cys Val Glu Val Ile Ala Lys Glu Gly Gln Asn				
340	345	350	355	
ctg aaa gag cta tat ttg gtg tcc tgt aaa atc aca gat tat gca ctg				1158
Leu Lys Glu Leu Tyr Leu Val Ser Cys Lys Ile Thr Asp Tyr Ala Leu				
356	361	366	371	
ata gcc att ggg cga tac agc atg aca ata gag act gtg gat gtc gga				1206
Ile Ala Ile Gly Arg Tyr Ser Met Thr Ile Glu Thr Val Asp Val Gly				
372	377	382	387	
tgg tgt aaa gaa atc aca gac caa gga gcc acc ctg att gca cag agc				1254
Trp Cys Lys Glu Ile Thr Asp Gln Gly Ala Thr Leu Ile Ala Gln Ser				
388	393	398	403	
agc aag tct ctg aga tat ttg ggg ctg atg aga tgt gat aaa gtc aac				1302
Ser Lys Ser Leu Arg Tyr Leu Gly Leu Met Arg Cys Asp Lys Val Asn				
404	409	414	419	
gaa gtg acg gtg gaa cag ctg gtg cag cag tac ccc cac atc acc ttc				1350
Glu Val Thr Val Glu Gln Leu Val Gln Gln Tyr Pro His Ile Thr Phe				
420	425	430	435	

agc acc gtc ctg cag gac tgc aag agg acc ttg gag aga gcc tat cag 1398
 Ser Thr Val Leu Gln Asp Cys Lys Arg Thr Leu Glu Arg Ala Tyr Gln
 436 441 446 451

atg ggc tgg acc ccc aac atg tct gcc gcc tcc tcc tag cgctcctgcc 1447
 Met Gly Trp Thr Pro Asn Met Ser Ala Ala Ser Ser *
 452 457 462

tgcctagtc cactgggatac attcagcaga gcagaggaga attgtacatt tggggagctg 1507

atctctcgga agggtttttaa ctggcacctg tctgtgtgtg ttc 1550

<210> 86
 <211> 3215
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (264) .. (3128)

<400> 86

ggtccggaat tgccgggtcg acccacgcgt ccgctggcga actccaagcg cttgaatacc 60

tgtgacgtaa ccgcccactc ggaagaccgg tcccgctcgg gaggetctgc agtcgcgcct 120

ggggtcaggg ccggggggcga atgtggctcg cgttctaggc ctccctgggt tggaaaaaga 180

ctatgttagc aagtgtcacg ccatgctttt gccaaactttc caattaaagg ttgacattcc 240

tgcataagca tttctctgtg aaa atg tcc ttg cct ctt aca gag gag cag 290
 Met Ser Leu Pro Leu Thr Glu Glu Gln
 1 5

agg aaa aag att gaa gag aat cga caa aag gct ctg gcc cgc aga gct 338
 Arg Lys Lys Ile Glu Glu Asn Arg Gln Lys Ala Leu Ala Arg Arg Ala
 10 15 20 25

gag aag tta ttg gca gaa cag cat cag agg act agc tcg ggc acc tcc 386
 Glu Lys Leu Leu Ala Glu Gln His Gln Arg Thr Ser Ser Gly Thr Ser
 26 31 36 41

att gct ggc aac cca ttc cag gcc aag caa ggc cca tcc caa aat ttc 434
 Ile Ala Gly Asn Pro Phe Gln Ala Lys Gln Gly Pro Ser Gln Asn Phe
 42 47 52 57

cca agg gag tct tgt aag cca gtg agc cat ggt gtc att ttc aag caa 482
 Pro Arg Glu Ser Cys Lys Pro Val Ser His Gly Val Ile Phe Lys Gln
 58 63 68 73

cag aat ctc agt agc tca tct aat gct gac caa aga cct cat gat tcc 530
 Gln Asn Leu Ser Ser Ser Ser Asn Ala Asp Gln Arg Pro His Asp Ser
 74 79 84 89

cac agt ttt cag gca aag gga ata tgg aaa aag cca gaa gaa atg ccc His Ser Phe Gln Ala Lys Gly Ile Trp Lys Lys Pro Glu Glu Met Pro 90 95 100 105	578
aca gcc tgc cca ggc cac agt cca cgt agt caa atg gct ctc act gga Thr Ala Cys Pro Gly His Ser Pro Arg Ser Gln Met Ala Leu Thr Gly 106 111 116 121	626
atc tct cct ccc ttg gca caa agt cct cca gag gtc cct aaa caa cag Ile Ser Pro Pro Leu Ala Gln Ser Pro Pro Glu Val Pro Lys Gln Gln 122 127 132 137	674
ctc ttg agt tat gag tta ggt caa ggt cat gct cag gct tca cct gag Leu Leu Ser Tyr Glu Leu Gly Gln Gly His Ala Gln Ala Ser Pro Glu 138 143 148 153	722
atc agg ttc aca ccc ttt gct aac cca act cat aag cct ctg gcc aaa Ile Arg Phe Thr Pro Phe Ala Asn Pro Thr His Lys Pro Leu Ala Lys 154 159 164 169	770
cca aag agt tcc caa gag aca cca gct cat tcc tct gga cag cct ccc Pro Lys Ser Ser Gln Glu Thr Pro Ala His Ser Ser Gly Gln Pro Pro 170 175 180 185	818
agg gat gct aag tta gag gcc aag aca gca aaa gcc tcc cct tcg ggg Arg Asp Ala Lys Leu Glu Ala Lys Thr Ala Lys Ala Ser Pro Ser Gly 186 191 196 201	866
cag aac att tct tac atc cat tct agc tca gag agt gta acg ccc agg Gln Asn Ile Ser Tyr Ile His Ser Ser Ser Glu Ser Val Thr Pro Arg 202 207 212 217	914
aca gaa gga aga ctc cag cag aag tca ggg tcc tca gtc caa aaa gga Thr Glu Gly Arg Leu Gln Gln Lys Ser Gly Ser Ser Val Gln Lys Gly 218 223 228 233	962
gtg aac tct cag aag gga aag tgc gta agg aac ggc gat cgt ttc cag Val Asn Ser Gln Lys Gly Lys Cys Val Arg Asn Gly Asp Arg Phe Gln 234 239 244 249	1010
gtg ttg att ggg tac aat gcg gaa ctc att gca gtg ttt aag acc ctg Val Leu Ile Gly Tyr Asn Ala Glu Leu Ile Ala Val Phe Lys Thr Leu 250 255 260 265	1058
ccc agc aag aat tat gat cct gac acc aag acg tgg aac ttc agc atg Pro Ser Lys Asn Tyr Asp Pro Asp Thr Lys Thr Trp Asn Phe Ser Met 266 271 276 281	1106
aat gac tat agt gcc ctg atg aaa gca gcc cag agc ctc ccc acg gtc Asn Asp Tyr Ser Ala Leu Met Lys Ala Ala Gln Ser Leu Pro Thr Val 282 287 292 297	1154
aac ctg cag cct ctg gaa tgg gcc tat ggc agc agc gag tca ccc tcc Asn Leu Gln Pro Leu Glu Trp Ala Tyr Gly Ser Ser Glu Ser Pro Ser 298 303 308 313	1202

acc agc agt gag gga cag gcc ggc ctt cca tca gct cca tcc ctt tca	1250
Thr Ser Ser Glu Gly Gln Ala Gly Leu Pro Ser Ala Pro Ser Leu Ser	
314 319 324 329	
ttt gtc aaa ggg cga tgc atg ctc atc tcc agg gcc tac ttc gag gca	1298
Phe Val Lys Gly Arg Cys Met Leu Ile Ser Arg Ala Tyr Phe Glu Ala	
330 335 340 345	
gac atc agt tat tca cag gac ctt att gcg ctt ttt aaa cag atg gat	1346
Asp Ile Ser Tyr Ser Gln Asp Leu Ile Ala Leu Phe Lys Gln Met Asp	
346 351 356 361	
tcc aga aga tat gat gtc aag acc agg aag tgg agc ttt ctc ttg gaa	1394
Ser Arg Arg Tyr Asp Val Lys Thr Arg Lys Trp Ser Phe Leu Leu Glu	
362 367 372 377	
gag cac agt aaa cta att gca aag gtg cgc tgc ctc cca caa gtt cag	1442
Glu His Ser Lys Leu Ile Ala Lys Val Arg Cys Leu Pro Gln Val Gln	
378 383 388 393	
ctg gac cct ctg ccc acg act ctc acc ctg gcg ttt gct tct cag ctc	1490
Leu Asp Pro Leu Pro Thr Thr Leu Thr Leu Ala Phe Ala Ser Gln Leu	
394 399 404 409	
aag aag aca tct ctc agt ctc acg cca gat gtc cca gag gca gac ctt	1538
Lys Lys Thr Ser Leu Ser Leu Thr Pro Asp Val Pro Glu Ala Asp Leu	
410 415 420 425	
tct gaa gtg gac ccc aag ctc gtg tct aat ctg atg ccc ttt cag aga	1586
Ser Glu Val Asp Pro Lys Leu Val Ser Asn Leu Met Pro Phe Gln Arg	
426 431 436 441	
gct gga gtc aat ttt gcc ata gcc aaa gga ggc cgc ctg ctg ctc gct	1634
Ala Gly Val Asn Phe Ala Ile Ala Lys Gly Gly Arg Leu Leu Leu Ala	
442 447 452 457	
gac gac atg ggc ctg ggg aag acc atc caa gcc atc tgc atc gca gcc	1682
Asp Asp Met Gly Leu Gly Lys Thr Ile Gln Ala Ile Cys Ile Ala Ala	
458 463 468 473	
ttt tac cgg aag gag tgg ccg ctc ctg gtg gtg gtg cca tcc tcc gtg	1730
Phe Tyr Arg Lys Glu Trp Pro Leu Leu Val Val Val Pro Ser Ser Val	
474 479 484 489	
cgc ttc acc tgg gag cag gcc ttc ctt cgg tgg ctg cca tct ctg agc	1778
Arg Phe Thr Trp Glu Gln Ala Phe Leu Arg Trp Leu Pro Ser Leu Ser	
490 495 500 505	
cca gat tgc atc aac gtc gtg gtg act ggg aag gac cgc ctg aca gct	1826
Pro Asp Cys Ile Asn Val Val Val Thr Gly Lys Asp Arg Leu Thr Ala	
506 511 516 521	
ggc ctg atc aac att gtc agc ttt gac ctt ctt agc aag ttg gaa aaa	1874
Gly Leu Ile Asn Ile Val Ser Phe Asp Leu Leu Ser Lys Leu Glu Lys	
522 527 532 537	
cag cta aaa acc cct ttt aaa gtt gtc atc att gat gaa tct cac ttc	1922

Gln Leu Lys Thr Pro Phe Lys Val Val Ile Ile Asp Glu Ser His Phe	
538 543 548 553	
ctc aaa aac agt agg act gcc cgc tgt cga gca gct atg ccg gtc cta	1970
Leu Lys Asn Ser Arg Thr Ala Arg Cys Arg Ala Ala Met Pro Val Leu	
554 559 564 569	
aag gtt gcc aag agg gtg atc ctg ttg tcg ggc aca cca gcc atg tcc	2018
Lys Val Ala Lys Arg Val Ile Leu Leu Ser Gly Thr Pro Ala Met Ser	
570 575 580 585	
cgg ccc gca gag ctc tac acg cag atc atc gca gtc aag cca act ttc	2066
Arg Pro Ala Glu Leu Tyr Thr Gln Ile Ile Ala Val Lys Pro Thr Phe	
586 591 596 601	
ttc ccc cag ttt cat gcc ttt gga ctt cgc tac tgt gat gcc aaa cgg	2114
Phe Pro Gln Phe His Ala Phe Gly Leu Arg Tyr Cys Asp Ala Lys Arg	
602 607 612 617	
atg cct tgg ggg tgg gac tac tca ggt tcc tcc aac ctg gga gag ctg	2162
Met Pro Trp Gly Trp Asp Tyr Ser Gly Ser Ser Asn Leu Gly Glu Leu	
618 623 628 633	
aag ctc ctg ctg gag gaa gca gtc atg ctg cgg cgc ctc aag tcc gac	2210
Lys Leu Leu Leu Glu Glu Ala Val Met Leu Arg Arg Leu Lys Ser Asp	
634 639 644 649	
gtc ctt tcc cag ctg cct gcc aag cag cgc aag ata gtg gtg att gcc	2258
Val Leu Ser Gln Leu Pro Ala Lys Gln Arg Lys Ile Val Val Ile Ala	
650 655 660 665	
cca gga cgg atc aat gcc agg acc aga gct gcc ctg gat gct gca gcc	2306
Pro Gly Arg Ile Asn Ala Arg Thr Arg Ala Ala Leu Asp Ala Ala Ala	
666 671 676 681	
aag gaa atg acc acc aag gac aaa act aaa cag cag cag aaa gat gcc	2354
Lys Glu Met Thr Thr Lys Asp Lys Thr Lys Gln Gln Gln Lys Asp Ala	
682 687 692 697	
ctc att ctc ttc ttc aac aga aca gct gaa gct aaa atc cca tct gtc	2402
Leu Ile Leu Phe Phe Asn Arg Thr Ala Glu Ala Lys Ile Pro Ser Val	
698 703 708 713	
att gaa tat atc ttg gac cta ctg gaa agt gga aga gag aag ttt tta	2450
Ile Glu Tyr Ile Leu Asp Leu Leu Glu Ser Gly Arg Glu Lys Phe Leu	
714 719 724 729	
gta ttt gca cac cat aag gtg gtc ctg gac gca att acg caa gag ctt	2498
Val Phe Ala His His Lys Val Val Leu Asp Ala Ile Thr Gln Glu Leu	
730 735 740 745	
gag aga aag cac gtg cag cac atc cgc atc gat ggc tcc acc tca tca	2546
Glu Arg Lys His Val Gln His Ile Arg Ile Asp Gly Ser Thr Ser Ser	
746 751 756 761	
gct gag cgg gag gac ctg tgc cag cag ttc caa ctg tcg gag agg cat	2594
Ala Glu Arg Glu Asp Leu Cys Gln Gln Phe Gln Leu Ser Glu Arg His	

762	767	772	777	
gct gtg gcc gtg ctg tcc atc acc gct gcc aat atg ggc ctc acc ttc				2642
Ala Val Ala Val Leu Ser Ile Thr Ala Ala Asn Met Gly Leu Thr Phe				
778	783	788	793	
tcc tcg gct gac ctg gtg gtg ttt gct gag ctg ttt tgg aac cca ggg				2690
Ser Ser Ala Asp Leu Val Val Phe Ala Glu Leu Phe Trp Asn Pro Gly				
794	799	804	809	
gtg ctg atc cag gct gag gac cgc gtg cac cgc att gga cag acc agc				2738
Val Leu Ile Gln Ala Glu Asp Arg Val His Arg Ile Gly Gln Thr Ser				
810	815	820	825	
tcc gtg ggc att cac tac ctc gtg gca aag ggc aca gct gat gac tac				2786
Ser Val Gly Ile His Tyr Leu Val Ala Lys Gly Thr Ala Asp Asp Tyr				
826	831	836	841	
ctt tgg ccc ctg att caa gag aag att aaa gtt ctg gca gaa gcc ggg				2834
Leu Trp Pro Leu Ile Gln Glu Lys Ile Lys Val Leu Ala Glu Ala Gly				
842	847	852	857	
ctt tct gag acc aat ttt tca gaa atg aca gaa tcc act gat tac ctc				2882
Leu Ser Glu Thr Asn Phe Ser Glu Met Thr Glu Ser Thr Asp Tyr Leu				
858	863	868	873	
tac aag gac cca aag cag cag aag atc tac gac cta ttc cag aag tcc				2930
Tyr Lys Asp Pro Lys Gln Gln Lys Ile Tyr Asp Leu Phe Gln Lys Ser				
874	879	884	889	
ttt gag aaa gaa gga agt gat atg gag ctc ctg gaa gca gca gag tcc				2978
Phe Glu Lys Glu Gly Ser Asp Met Glu Leu Leu Glu Ala Ala Glu Ser				
890	895	900	905	
ttt gac cca gga agt gct tca gga aca tct gga agt agt tcc cag aac				3026
Phe Asp Pro Gly Ser Ala Ser Gly Thr Ser Gly Ser Ser Ser Gln Asn				
906	911	916	921	
atg gga gac acc ctg gat gaa agc tca ttg aca gcc agt cca cag aag				3074
Met Gly Asp Thr Leu Asp Glu Ser Ser Leu Thr Ala Ser Pro Gln Lys				
922	927	932	937	
aaa agg aga ttt gaa ttt ttt gat aac tgg gac agc ttt acg tct ccc				3122
Lys Arg Arg Phe Glu Phe Phe Asp Asn Trp Asp Ser Phe Thr Ser Pro				
938	943	948	953	
ctg taa aaggggcaaa aagaaaaaaa taaaaagcat tttaaaatca tggaattgaa				3178
Leu *				
954				
ataaaataat gtattttgtt ttaaaaaaaa aaaaaaa				3215

<210> 87
<211> 879

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (366)..(827)

<400> 87

```

caaccaccca gaggtgagga gatagtagag gaagaaggag aaggggggtg ggggggcgca      60
agcacaaaga gcaaaggcaa aggcaagcac agtgacagat gagacttgag aggtgccagg      120
ggccagggta tgcgaggcct tggaggccag catgcagtct aggatgaggc ctcctacctt      180
cagcctgcct gagggccagg agctggaggg aggcgagtga aggcccttct tcccgtgcct      240
gcagtaatgg ctcccaggac acctttgaag catgttacag cggcacgtcc acaccttctt      300
tccatggctc ccaactgcagc ggcagcgacc acagcagtct gggettgag cagttacagg      360

attac      atg gtc acg ttg cgg agt aag ctg ggg ccc ctc gag atc cag      407
           Met Val Thr Leu Arg Ser Lys Leu Gly Pro Leu Glu Ile Gln
           1              5              10

cag ttt gcg atg ctg ctg cgg gag tac cgg ctg ggg ctg ccc atc cag      455
Gln Phe Ala Met Leu Leu Arg Glu Tyr Arg Leu Gly Leu Pro Ile Gln
   15              20              25              30

gac tat tgc aca ggc ctg ctg aag ctc tac gga gac cgg cgc aag ttc      503
Asp Tyr Cys Thr Gly Leu Leu Lys Leu Tyr Gly Asp Arg Arg Lys Phe
   31              36              41              46

ctc ctc ctt ggg atg cgg ccc ttc atc ccg gac cag gac atc ggc tac      551
Leu Leu Leu Gly Met Arg Pro Phe Ile Pro Asp Gln Asp Ile Gly Tyr
   47              52              57              62

ttc gag ggc ttc ctg gag ggc gtg ggc atc cgc gag ggc ggc atc ctc      599
Phe Glu Gly Phe Leu Glu Gly Val Gly Ile Arg Glu Gly Gly Ile Leu
   63              68              73              78

act gac agc ttc ggc cgc atc aag cgc agc atg agc tcc acg tcg gcc      647
Thr Asp Ser Phe Gly Arg Ile Lys Arg Ser Met Ser Ser Thr Ser Ala
   79              84              89              94

tcc gca gtg cgc agc tac gat ggc gcg gcg cag cgg ccc gag gca cag      695
Ser Ala Val Arg Ser Tyr Asp Gly Ala Ala Gln Arg Pro Glu Ala Gln
   95              100             105             110

gcc ttc cac cgg ctg ctg gct gac atc acg cac gac atc gag gcg ctg      743
Ala Phe His Arg Leu Leu Ala Asp Ile Thr His Asp Ile Glu Ala Leu
  111              116             121             126

gcc ccc gat gac gac gac gac gag gat gag ccc cgg ggt cac agg      791
Ala Pro Asp Asp Asp Asp Asp Asp Glu Asp Glu Pro Arg Gly His Arg
  127              132             137             142

ggc ggg acc gac ccc gca gaa gac aac tac ctg tag ccac cgcccctgcg      841

```

Gly Gly Thr Asp Pro Ala Glu Asp Asn Tyr Leu *
 143 148 153

gacggcgtgg gttcagcagc ccacctctga gtctcacg

879

<210> 88
 <211> 4334
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (64)..(3810)

<400> 88

aggtgacact ataaaacaag tctgtacaaa aaagcaggct ggtaccgggc cggaattccc 60

ggg atg aag gag cct gcg gcg tgc agt gtg agg ggc ggg acc cgg ctg 108
 Met Lys Glu Pro Ala Ala Cys Ser Val Arg Gly Gly Thr Arg Leu
 1 5 10

ccg gcg gtg ggt cta gct ggg gga ggt cgg gcc atg ctg gtg ggc cag 156
 Pro Ala Val Gly Leu Ala Gly Gly Gly Arg Ala Met Leu Val Gly Gln
 16 21 26 31

ggc gcg ggg ctg ctg ggg ccc gcg gtg gtc acc gcc gcg gtg gtg ctg 204
 Gly Ala Gly Leu Leu Gly Pro Ala Val Val Thr Ala Ala Val Val Leu
 32 37 42 47

ctg ctg agc ggc gtg ggg ccg gcg cac ggc tcg gag gac atc gtg gtg 252
 Leu Leu Ser Gly Val Gly Pro Ala His Gly Ser Glu Asp Ile Val Val
 48 53 58 63

ggc tgc ggt ggc ttc gtc aag tcg gac gtg gag atc aac tac tct ctc 300
 Gly Cys Gly Gly Phe Val Lys Ser Asp Val Glu Ile Asn Tyr Ser Leu
 64 69 74 79

atc gag ata aag ctg tac acc aag cat ggg act ttg aaa tac cag aca 348
 Ile Glu Ile Lys Leu Tyr Thr Lys His Gly Thr Leu Lys Tyr Gln Thr
 80 85 90 95

gac tgt gcc cct aat aat ggt tac ttt atg atc cct ttg tat gat aag 396
 Asp Cys Ala Pro Asn Asn Gly Tyr Phe Met Ile Pro Leu Tyr Asp Lys
 96 101 106 111

ggg gat ttc att ctg aag att gag cct ccc cta ggg tgg agt ttt gag 444
 Gly Asp Phe Ile Leu Lys Ile Glu Pro Pro Leu Gly Trp Ser Phe Glu
 112 117 122 127

ccg acg acc gtg gag ctc cat gtg gat gga gtc agt gac atc tgc aca 492
 Pro Thr Thr Val Glu Leu His Val Asp Gly Val Ser Asp Ile Cys Thr
 128 133 138 / 143

aag ggt ggg gac atc aac ttt gtc ttc act ggg ttc tct gtg aat ggc 540

Lys Gly Gly Asp Ile Asn Phe Val Phe Thr Gly Phe Ser Val Asn Gly	
144 149 154 159	
aag gtc ctc agc aaa ggg cag ccc ctg ggt cct gcg gga gtt cag gtg	588
Lys Val Leu Ser Lys Gly Gln Pro Leu Gly Pro Ala Gly Val Gln Val	
160 165 170 175	
tct ctg aga aac act ggg acc gaa gca aag atc cag tcc aca gtt aca	636
Ser Leu Arg Asn Thr Gly Thr Glu Ala Lys Ile Gln Ser Thr Val Thr	
176 181 186 191	
cag cct ggc gga aag ttt gca ttt ttt aaa gtt ctg cct gga gat tat	684
Gln Pro Gly Gly Lys Phe Ala Phe Phe Lys Val Leu Pro Gly Asp Tyr	
192 197 202 207	
gaa atc ctc gca act cat cca acc tgg gcg ttg aaa gag gca agc acc	732
Glu Ile Leu Ala Thr His Pro Thr Trp Ala Leu Lys Glu Ala Ser Thr	
208 213 218 223	
aca gtg cgt gta acc aac tcc aat gcc aat gcg gcc agt ccc ctc ata	780
Thr Val Arg Val Thr Asn Ser Asn Ala Asn Ala Ala Ser Pro Leu Ile	
224 229 234 239	
gtt gct ggc tac aat gtg tct ggc tct gtc cga agt gat ggg gag ccc	828
Val Ala Gly Tyr Asn Val Ser Gly Ser Val Arg Ser Asp Gly Glu Pro	
240 245 250 255	
atg aaa ggc gtg aag ttt ctt ctc ttt tct tct tta gta act aaa gag	876
Met Lys Gly Val Lys Phe Leu Leu Phe Ser Ser Leu Val Thr Lys Glu	
256 261 266 271	
gat gtc ctg ggc tgc aat gtc tca cca gtg cct ggg ttc cag ccc caa	924
Asp Val Leu Gly Cys Asn Val Ser Pro Val Pro Gly Phe Gln Pro Gln	
272 277 282 287	
gac gag agt ctg gtg tat ttg tgc tac acg gtc tcc aga gaa gat ggc	972
Asp Glu Ser Leu Val Tyr Leu Cys Tyr Thr Val Ser Arg Glu Asp Gly	
288 293 298 303	
tcg ttc tct ttc tat tcc ttg cca agt ggg ggc tac act gtg att ccg	1020
Ser Phe Ser Phe Tyr Ser Leu Pro Ser Gly Gly Tyr Thr Val Ile Pro	
304 309 314 319	
ttc tat cga ggg gag agg att acc ttt gat gtg gcg cct tcc aga ctt	1068
Phe Tyr Arg Gly Glu Arg Ile Thr Phe Asp Val Ala Pro Ser Arg Leu	
320 325 330 335	
gac ttc aca gtg gag cat gac agc ttg aaa atc gag ccc gtg ttc cac	1116
Asp Phe Thr Val Glu His Asp Ser Leu Lys Ile Glu Pro Val Phe His	
336 341 346 351	
gtc atg gga ttc tcc gtc acc ggg agg gtc ttg aac gga ccc gaa gga	1164
Val Met Gly Phe Ser Val Thr Gly Arg Val Leu Asn Gly Pro Glu Gly	
352 357 362 367	
gat ggt gtt cca gaa gca gta gtc acc ctg aat aac caa atc aaa gtt	1212
Asp Gly Val Pro Glu Ala Val Val Thr Leu Asn Asn Gln Ile Lys Val	

368	373	378	383	
aaa aca aaa gct gat	ggc tca ttc cgc ctt	gag aac ata acc aca ggg	1260	
Lys Thr Lys Ala Asp	Gly Ser Phe Arg Leu	Glu Asn Ile Thr Thr Gly		
384	389	394	399	
aca tac acc atc cat	gct cag aaa gag cac	ctc tac ttt gaa acg gtc	1308	
Thr Tyr Thr Ile His	Ala Gln Lys Glu His	Leu Tyr Phe Glu Thr Val		
400	405	410	415	
acc atc aaa att gca	cag aac aca cct cag	ctg gct gac att gtt gca	1356	
Thr Ile Lys Ile Ala	Pro Asn Thr Pro Gln	Leu Ala Asp Ile Val Ala		
416	421	426	431	
aca ggg ttc agt gtc	tgt ggt cgg ata tca	atc att cgc ttc ccc gac	1404	
Thr Gly Phe Ser Val	Cys Gly Arg Ile Ser	Ile Ile Arg Phe Pro Asp		
432	437	442	447	
acc gtc aag cag atg	aat aaa tac aaa gtt	gtc ctg tca tct caa gac	1452	
Thr Val Lys Gln Met	Asn Lys Tyr Lys Val	Val Leu Ser Ser Gln Asp		
448	453	458	463	
aag gac aag tct ttg	gtc acc gtg gag aca	gat gct cat gga tca ttt	1500	
Lys Asp Lys Ser Leu	Val Thr Val Glu Thr	Asp Ala His Gly Ser Phe		
464	469	474	479	
tgt ttt aaa gca aaa	cca ggg act tac aaa	gtg cag gtg atg gtt cct	1548	
Cys Phe Lys Ala Lys	Pro Gly Thr Tyr Lys	Val Gln Val Met Val Pro		
480	485	490	495	
gag gca gaa acc aga	gca ggg ctg acg ttg	aaa ccc cag aca ttt cct	1596	
Glu Ala Glu Thr Arg	Ala Gly Leu Thr Leu	Lys Pro Gln Thr Phe Pro		
496	501	506	511	
ctt act gtg acc aac	agg ccc atg atg gat	gtg gcc ttt gta cag ttc	1644	
Leu Thr Val Thr Asn	Arg Pro Met Met Asp	Val Ala Phe Val Gln Phe		
512	517	522	527	
ttg gca tca gtt tct	ggg aaa gtc tct tgt	ttg gac acc tgt ggt gac	1692	
Leu Ala Ser Val Ser	Gly Lys Val Ser Cys	Leu Asp Thr Cys Gly Asp		
528	533	538	543	
ttg ctg gtg act cta	cag tcc ctg agc cgc	cag ggt gag aag cgg agc	1740	
Leu Leu Val Thr Leu	Gln Ser Leu Ser Arg	Gln Gly Glu Lys Arg Ser		
544	549	554	559	
ctc cag ctc tcc ggc	aag gtc aac gcc atg	act ttc acc ttt gac aac	1788	
Leu Gln Leu Ser Gly	Lys Val Asn Ala Met	Thr Phe Thr Phe Asp Asn		
560	565	570	575	
gtg ctc cct gga aaa	tac aaa ata agc atc	atg cat gag gat tgg tgc	1836	
Val Leu Pro Gly Lys	Tyr Lys Ile Ser Ile	Met His Glu Asp Trp Cys		
576	581	586	591	
tgg aag aac aag agc	ctg gag gtg gaa gtg	ctg gag gat gac atg tct	1884	
Trp Lys Asn Lys Ser	Leu Glu Val Glu Val	Leu Glu Asp Asp Met Ser		
592	597	602	607	

gca gtt gag ttc agg cag acg ggc tac atg ctg aga tgt tcc ctg tct	1932
Ala Val Glu Phe Arg Gln Thr Gly Tyr Met Leu Arg Cys Ser Leu Ser	
608 613 618 623	
cac gcc atc act ctg gaa ttt tat cag gat gga aat ggg cgt gag aat	1980
His Ala Ile Thr Leu Glu Phe Tyr Gln Asp Gly Asn Gly Arg Glu Asn	
624 629 634 639	
gtg ggg att tat aac ctc tcc aaa gga gtc aac cga ttc tgc ctg tcc	2028
Val Gly Ile Tyr Asn Leu Ser Lys Gly Val Asn Arg Phe Cys Leu Ser	
640 645 650 655	
aag cct ggt gtg tac aaa gtg acc cct cgc tcc tgc cac cgg ttt gag	2076
Lys Pro Gly Val Tyr Lys Val Thr Pro Arg Ser Cys His Arg Phe Glu	
656 661 666 671	
caa gcg ttc tat atc tat gac acg tct tca cct agt atc ttg aca ttg	2124
Gln Ala Phe Tyr Ile Tyr Asp Thr Ser Ser Pro Ser Ile Leu Thr Leu	
672 677 682 687	
aca gcc att cgc cac cat gtc ctt gga act atc acc acc gac aaa atg	2172
Thr Ala Ile Arg His His Val Leu Gly Thr Ile Thr Thr Asp Lys Met	
688 693 698 703	
atg gat gtc act gtg act atc aag tct tcc atc gac agt gaa ccc gcc	2220
Met Asp Val Thr Val Thr Ile Lys Ser Ser Ile Asp Ser Glu Pro Ala	
704 709 714 719	
ttg gtc tta ggc cct ctg aag tct gtg cag gag ctg cgg agg gag cag	2268
Leu Val Leu Gly Pro Leu Lys Ser Val Gln Glu Leu Arg Arg Glu Gln	
720 725 730 735	
cag ctg gct gag atc gag gcc cgc agg cag gag agg gag aaa aac ggc	2316
Gln Leu Ala Glu Ile Glu Ala Arg Arg Gln Glu Arg Glu Lys Asn Gly	
736 741 746 751	
aat gag gaa ggc gaa gaa aga atg acc aag cct ccc gtg cag gag atg	2364
Asn Glu Glu Gly Glu Glu Arg Met Thr Lys Pro Pro Val Gln Glu Met	
752 757 762 767	
gta gat gag tta caa ggc ccc ttc tcg tat gat ttc tct tac tgg gcg	2412
Val Asp Glu Leu Gln Gly Pro Phe Ser Tyr Asp Phe Ser Tyr Trp Ala	
768 773 778 783	
cgg tct gga gag aaa atc act gtt aca ccg tca tct aaa gag ctg ctc	2460
Arg Ser Gly Glu Lys Ile Thr Val Thr Pro Ser Ser Lys Glu Leu Leu	
784 789 794 799	
ttt tat ccc cct tca atg gaa gcc gtt gtc agt gga gaa agc tgc cca	2508
Phe Tyr Pro Pro Ser Met Glu Ala Val Val Ser Gly Glu Ser Cys Pro	
800 805 810 815	
ggg aag ctg atc gag atc cat ggg aag gca ggc ctg ttt tta gaa ggc	2556
Gly Lys Leu Ile Glu Ile His Gly Lys Ala Gly Leu Phe Leu Glu Gly	
816 821 826 831	

cag atc cac ccc gag ttg gaa gga gtc gag att gtc atc agt gaa aag	2604
Gln Ile His Pro Glu Leu Glu Gly Val Glu Ile Val Ile Ser Glu Lys	
832 837 842 847	
ggg gca agt tca ccg ctg atc aca gtc ttt act gat gac aaa ggt gcc	2652
Gly Ala Ser Ser Pro Leu Ile Thr Val Phe Thr Asp Asp Lys Gly Ala	
848 853 858 863	
tac agt gtt ggc ccc ctg cac agt gac ctg gag tac acg gtg acc tca	2700
Tyr Ser Val Gly Pro Leu His Ser Asp Leu Glu Tyr Thr Val Thr Ser	
864 869 874 879	
cag aag gag ggc tat gtt ctg act gca gtg gaa gga acc atc gga gac	2748
Gln Lys Glu Gly Tyr Val Leu Thr Ala Val Glu Gly Thr Ile Gly Asp	
880 885 890 895	
ttc aag gcc tat gcc ctg gca ggc gta agc ttt gag ata aaa gct gag	2796
Phe Lys Ala Tyr Ala Leu Ala Gly Val Ser Phe Glu Ile Lys Ala Glu	
896 901 906 911	
gat gac cag ccc ctc ccg gga gtc ctc tta tcc ctg agt ggt ggc ctg	2844
Asp Asp Gln Pro Leu Pro Gly Val Leu Leu Ser Leu Ser Gly Gly Leu	
912 917 922 927	
ttt cgt tcc aac ctc ttg acc cag gac aac ggc att ctg aca ttc tca	2892
Phe Arg Ser Asn Leu Leu Thr Gln Asp Asn Gly Ile Leu Thr Phe Ser	
928 933 938 943	
aac ctg agc cct ggc cag tat tac ttc aaa ccc atg atg aag gag ttc	2940
Asn Leu Ser Pro Gly Gln Tyr Tyr Phe Lys Pro Met Met Lys Glu Phe	
944 949 954 959	
cgg ttt gag cca tcc tca cag atg atc gag gtg cag gaa ggc cag aac	2988
Arg Phe Glu Pro Ser Ser Gln Met Ile Glu Val Gln Glu Gly Gln Asn	
960 965 970 975	
ctg aag atc acc atc acg ggg tac cga acc gct tac agt tgc tat ggc	3036
Leu Lys Ile Thr Ile Thr Gly Tyr Arg Thr Ala Tyr Ser Cys Tyr Gly	
976 981 986 991	
aca gtg tct tcc tta aac gga gag ccc gaa caa ggg gtt gcc atg gaa	3084
Thr Val Ser Ser Leu Asn Gly Glu Pro Glu Gln Gly Val Ala Met Glu	
992 997 1002 1007	
gcg gtg ggc cag aac gac tgc agc att tac gga gaa gac acc gtg aca	3132
Ala Val Gly Gln Asn Asp Cys Ser Ile Tyr Gly Glu Asp Thr Val Thr	
1008 1013 1018 1023	
gac gaa gag ggc aag ttc aga tta cgt gga ttg ctg ccg gga tgt gtg	3180
Asp Glu Glu Gly Lys Phe Arg Leu Arg Gly Leu Leu Pro Gly Cys Val	
1024 1029 1034 1039	
tac cac gtt cag ctc aag gca gaa ggc aac gac cac att gag cgg gcg	3228
Tyr His Val Gln Leu Lys Ala Glu Gly Asn Asp His Ile Glu Arg Ala	
1040 1045 1050 1055	
ctc ccc cac cat agg gtg att gag gtt ggg aat aat gac atc gat gat	3276

Leu Pro His His Arg Val Ile Glu Val Gly Asn Asn Asp Ile Asp Asp	
1056	1061 1066 1071
gta aac atc ata gtt ttc cgg cag att aat caa ttt gat tta agt gga	3324
Val Asn Ile Ile Val Phe Arg Gln Ile Asn Gln Phe Asp Leu Ser Gly	
1072	1077 1082 1087
aat gtg atc act tcc tct gaa tac ctt cct aca tta tgg gtc aag ctt	3372
Asn Val Ile Thr Ser Ser Glu Tyr Leu Pro Thr Leu Trp Val Lys Leu	
1088	1093 1098 1103
tac aaa agc gaa aac ctc gac aat cca atc cag aca gtt tcc ctt ggc	3420
Tyr Lys Ser Glu Asn Leu Asp Asn Pro Ile Gln Thr Val Ser Leu Gly	
1104	1109 1114 1119
cag tcc ctg ttc ttc cat ttc ccc cca ctg ctc aga gac ggc gag aac	3468
Gln Ser Leu Phe Phe His Phe Pro Pro Leu Leu Arg Asp Gly Glu Asn	
1120	1125 1130 1135
tat gtt gtg ctt ctg gac tcc aca ctc ccc aga tcc cag tat gac tac	3516
Tyr Val Val Leu Leu Asp Ser Thr Leu Pro Arg Ser Gln Tyr Asp Tyr	
1136	1141 1146 1151
atc ttg cct caa gtt tct ttc acc gca gtg ggc tac cat aaa cac atc	3564
Ile Leu Pro Gln Val Ser Phe Thr Ala Val Gly Tyr His Lys His Ile	
1152	1157 1162 1167
acc ttg att ttt aat ccc acg agg aag ctg cct gaa cag gac atc gca	3612
Thr Leu Ile Phe Asn Pro Thr Arg Lys Leu Pro Glu Gln Asp Ile Ala	
1168	1173 1178 1183
caa gga tcc tac att gcc ctg cca ttg acg ctg ctg gtt ctg ctg gcc	3660
Gln Gly Ser Tyr Ile Ala Leu Pro Leu Thr Leu Leu Val Leu Leu Ala	
1184	1189 1194 1199
ggc tac aac cat gac aag ctc att cct ttg ctg ctg cag ttg aca agc	3708
Gly Tyr Asn His Asp Lys Leu Ile Pro Leu Leu Leu Gln Leu Thr Ser	
1200	1205 1210 1215
cgg cta cag gga gtc cgc gcg ctc ggc cag gca gcc tct gac aat agc	3756
Arg Leu Gln Gly Val Arg Ala Leu Gly Gln Ala Ala Ser Asp Asn Ser	
1216	1221 1226 1231
ggc cca gaa gat gca aag aga caa gcc aag aaa cag aag aca agg cgg	3804
Gly Pro Glu Asp Ala Lys Arg Gln Ala Lys Lys Gln Lys Thr Arg Arg	
1232	1237 1242 1247
act tga ggaggaaggg gacagttgca gtctcacttg ggacaggcca cagccagggg	3860
Thr *	
1248	
tcgggccact acccgcccgt gggataaaag ccaaaagcat gcgtcagcta acttcagcct	3920
gtgtgtgtgg gcccgcaccc catgtccctt gtcactgtgg catcctgcac ccacccctac	3980
ccctccgtag agccccctgt gcaatgcaat gaatggaccc tcctgtcact ctgctgaaca	4040

```

gaatttattt tctgagtcaa atataattta ttattatttt tgtcaaagaa gtattttaago 4100
tgtgctgtgg tgtgagaatg tcattcttga tcttcagcct tcgtttgcaa ggagagttcc 4160
agttgacgtg gtgtttgggt ccatggcggg gtaccctagg gattcatctg ttttcttcac 4220
ttccctttgc atctgagatc ctgctggaaa ccacagcaac ctgtatccac tattaggagg 4280
taaaaatcaa taaaatggcc cattcatttg tgtttagct caaaaaaaaa aaaa 4334

```

```

<210> 89
<211> 2108
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (167)..(1903)

```

```

<400> 89
gtagcgaggc ttgggtggcg aactcggcac gaggcccaaa ggtaggctca ggctccgacg 60
gtggccggcg ggggtcacga ggcttcgtag tggaggaacg ggtttggcgt gtgggacgca 120
gctgcctctg tactggggag tcacggagtg gccgggctcc agggac atg gcg gcg 175
Met Ala Ala
1
gcc tct gcg gtg tcg gtg ctg ctg gtg gcg gcg gag agg aac cgg tgg 223
Ala Ser Ala Val Ser Val Leu Leu Val Ala Ala Glu Arg Asn Arg Trp
4 9 14 19
cat cgt ctc ccg agc ctg ctc ctg ccg ccg agg aca tgg gtg tgg agg 271
His Arg Leu Pro Ser Leu Leu Leu Pro Pro Arg Thr Trp Val Trp Arg
20 25 30 35
caa aga acc atg aag tac aca aca gcc aca gga aga aac att acc aag 319
Gln Arg Thr Met Lys Tyr Thr Thr Ala Thr Gly Arg Asn Ile Thr Lys
36 41 46 51
gtc ctc att gca aac aga gga gaa att gcc tgc agg gtg atg cgc aca 367
Val Leu Ile Ala Asn Arg Gly Glu Ile Ala Cys Arg Val Met Arg Thr
52 57 62 67
gcc aaa aaa ctg ggt gta cag act gtg gcg gtt tat agt gag gct gac 415
Ala Lys Lys Leu Gly Val Gln Thr Val Ala Val Tyr Ser Glu Ala Asp
68 73 78 83
aga aat tcc atg cat gta gat atg gca gat gaa gca tat tcc atc ggc 463
Arg Asn Ser Met His Val Asp Met Ala Asp Glu Ala Tyr Ser Ile Gly
84 89 94 99
ccc gct ccc tcc cag cag agc tac cta tct atg gag aaa atc att caa 511
Pro Ala Pro Ser Gln Gln Ser Tyr Leu Ser Met Glu Lys Ile Ile Gln

```

100	105	110	115	
gtg gcc aag acc tct	gct gca cag gct atc	cat cca gga tgc ggt ttt	559	
Val Ala Lys Thr Ser	Ala Ala Gln Ala Ile	His Pro Gly Cys Gly Phe		
116	121	126	131	
ctt tca gaa aac atg	gaa ttt gct gaa ctt	tgt aag caa gaa gga att	607	
Leu Ser Glu Asn Met	Glu Phe Ala Glu Leu	Cys Lys Gln Glu Gly Ile		
132	137	142	147	
att ttt ata ggc cct	cct cca tct gca att	aga gac atg ggt ata aag	655	
Ile Phe Ile Gly Pro	Pro Pro Ser Ala Ile	Arg Asp Met Gly Ile Lys		
148	153	158	163	
agc aca tcc aaa tcc	ata atg gct gct gct	gga gta cct gtt gtg gag	703	
Ser Thr Ser Lys Ser	Ile Met Ala Ala Ala	Gly Val Pro Val Val Glu		
164	169	174	179	
ggg tat cat ggt gag	gac caa tca gac cag	tgc ctg aag gaa cac gcc	751	
Gly Tyr His Gly Glu	Asp Gln Ser Asp Gln	Cys Leu Lys Glu His Ala		
180	185	190	195	
agg aga att ggc tat	cct gtc atg att aaa	gcc gtc cgg ggt gga gga	799	
Arg Arg Ile Gly Tyr	Pro Val Met Ile Lys	Ala Val Arg Gly Gly Gly		
196	201	206	211	
gga aaa gga atg agg	att gtt aga tca gaa	caa gaa ttt caa gaa cag	847	
Gly Lys Gly Met Arg	Ile Val Arg Ser Glu	Gln Glu Phe Gln Glu Gln		
212	217	222	227	
tta gag tca gca cgg	aga gaa gct aag aag	tct ttc aat gat gat gct	895	
Leu Glu Ser Ala Arg	Arg Glu Ala Lys Lys	Ser Phe Asn Asp Asp Ala		
228	233	238	243	
atg ctg atc gag aag	ttt gta gac aca ccg	agg cat gta gaa gtc cag	943	
Met Leu Ile Glu Lys	Phe Val Asp Thr Pro	Arg His Val Glu Val Gln		
244	249	254	259	
gtg ttt ggt gat cac	cat ggc aat gct gtg	tac ttg ttt gaa aga gac	991	
Val Phe Gly Asp His	His Gly Asn Ala Val	Tyr Leu Phe Glu Arg Asp		
260	265	270	275	
tgt agt gtg cag agg	cga cat cag aag atc	att gag gag gcc cca gcg	1039	
Cys Ser Val Gln Arg	Arg His Gln Lys Ile	Ile Glu Glu Ala Pro Ala		
276	281	286	291	
cct ggt att aaa tct	gaa gta aga aaa aag	ctg gga gaa gct gca gtc	1087	
Pro Gly Ile Lys Ser	Glu Val Arg Lys Lys	Leu Gly Glu Ala Ala Val		
292	297	302	307	
aga gct gct aaa gct	gta aat tat gtt gga	gca ggg act gtg gag ttt	1135	
Arg Ala Ala Lys Ala	Val Asn Tyr Val Gly	Ala Gly Thr Val Glu Phe		
308	313	318	323	
att atg gac tca aaa	cat aat ttc tgt ttc	atg gag atg aat aca agg	1183	
Ile Met Asp Ser Lys	His Asn Phe Cys Phe	Met Glu Met Asn Thr Arg		
324	329	334	339	

ctg caa gtg gaa cat cct gtt act gag atg atc aca gga act gac ttg	1231
Leu Gln Val Glu His Pro Val Thr Glu Met Ile Thr Gly Thr Asp Leu	
340 345 350 355	
gtg gag tgg cag ctt aga att gca gca gga gag aag att cct ttg agc	1279
Val Glu Trp Gln Leu Arg Ile Ala Ala Gly Glu Lys Ile Pro Leu Ser	
356 361 366 371	
cag gaa gaa ata act ctg cag ggc cat gcc ttc gaa gct aga ata tat	1327
Gln Glu Glu Ile Thr Leu Gln Gly His Ala Phe Glu Ala Arg Ile Tyr	
372 377 382 387	
gca gaa gat cct agc aat aac ttc atg cct gtg gca ggc cca tta gtg	1375
Ala Glu Asp Pro Ser Asn Asn Phe Met Pro Val Ala Gly Pro Leu Val	
388 393 398 403	
cac ctc tct act cct cga gca gac cct tcc acc agg att gaa act gga	1423
His Leu Ser Thr Pro Arg Ala Asp Pro Ser Thr Arg Ile Glu Thr Gly	
404 409 414 419	
gta cgg caa gga gac gaa gtt tcc gtg cat tat gac ccc atg att gcg	1471
Val Arg Gln Gly Asp Glu Val Ser Val His Tyr Asp Pro Met Ile Ala	
420 425 430 435	
aag ctg gtc gtg tgg gca gca gat cgc cag gcg gca ttg aca aaa ctg	1519
Lys Leu Val Val Trp Ala Ala Asp Arg Gln Ala Ala Leu Thr Lys Leu	
436 441 446 451	
agg tac agc ctt cgt cag tac aat att gtt gga ctg ccc acc aac att	1567
Arg Tyr Ser Leu Arg Gln Tyr Asn Ile Val Gly Leu Pro Thr Asn Ile	
452 457 462 467	
gac ttc tta ctc aac ctg tct ggc cac cca gag ttt gaa gct ggg aac	1615
Asp Phe Leu Leu Asn Leu Ser Gly His Pro Glu Phe Glu Ala Gly Asn	
468 473 478 483	
gtg cac act gat ttc atc cct caa cac cac aaa cag ttg ttg ctc agt	1663
Val His Thr Asp Phe Ile Pro Gln His His Lys Gln Leu Leu Leu Ser	
484 489 494 499	
cgg aag gct gca gcc aaa gag tct tta tgc cag gca gcc ctg ggt ctc	1711
Arg Lys Ala Ala Ala Lys Glu Ser Leu Cys Gln Ala Ala Leu Gly Leu	
500 505 510 515	
atc ctc aag gag aaa gcc atg acc gac act ttc act ctt cag gca cat	1759
Ile Leu Lys Glu Lys Ala Met Thr Asp Thr Phe Thr Leu Gln Ala His	
516 521 526 531	
gat caa ttc tct cca ttt tcg tct agc agt gga aga aga ctg aat atc	1807
Asp Gln Phe Ser Pro Phe Ser Ser Ser Ser Gly Arg Arg Leu Asn Ile	
532 537 542 547	
tcg tat acc aga aac atg act ctt aaa gat ggt aaa aac aat gta gcc	1855
Ser Tyr Thr Arg Asn Met Thr Leu Lys Asp Gly Lys Asn Asn Val Ala	
548 553 558 563	

ata gct gta acg tat aac cat gat ggg tct tat agc atg cag aat taa 1903
 Ile Ala Val Thr Tyr Asn His Asp Gly Ser Tyr Ser Met Gln Asn *
 564 569 574 579

agataaaaact ttccaagtcc ttggtaatct ttacagcgag ggagactgca cttacctgaa 1963
 atgttctgtt aatggagttg ctagtaaagc gaagctgatt atcctggaaa acactattta 2023
 cctattttoc aaggaaggaa gtattgagat tgacattcca gtccccaat acttatcttc 2083
 tgtgagctca caaaaaaaaa aaaaa 2108

<210> 90
 <211> 2498
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (530) .. (2356)

<400> 90
 gcagggtaccg cgtccggaat tcccgggtcg acgatttcgt gtgactggaa tccagcttaa 60
 ccccaacaac catctacagc tgtattcttg ttcccttgat ggcacaatta aactgtggga 120
 ctatatagat ggcattctaa taaagacttt catagttgga tgtaaacttc atgccctctt 180
 tactcttgcc caagctgagg attctgtctt tgttatagtg aataaagaaa aaccagatat 240
 atttcagctg gtttcagtga aactgccaaa atcctcaagc caggaagtag aagccaagga 300
 gctgtccttt gttttggatt acataaacca gtcacccaag tgcattgcct ttggaaacga 360
 gggagtatat gttgctgcag tacgggaatt ttacttgtct gtttattttt tcaaaaagaa 420
 aacaacatca aggtttactt tatcatcatc aagaaataag aagcatgcta aaaaccattt 480
 tacgtgtgta gcatgtcacc ccacggaaga ccgcatcgca totggtcac atg gat 535
 Met Asp
 1

ggc caa att cgt ctt tgg agg aat ttt tat gat gat aag aaa tat acg 583
 Gly Gln Ile Arg Leu Trp Arg Asn Phe Tyr Asp Asp Lys Lys Tyr Thr
 3 8 13 18

tac aca tgt tta cat tgg cac cat gat atg gtt atg gat ttg gct ttt 631
 Tyr Thr Cys Leu His Trp His His Asp Met Val Met Asp Leu Ala Phe
 19 24 29 34

tca gtg aca ggc acc agt ctg ctg agt ggc ggt cgt gaa tct gta ctt 679
 Ser Val Thr Gly Thr Ser Leu Leu Ser Gly Gly Arg Glu Ser Val Leu
 35 40 45 50

gta gag tgg cgc gat gca aca gag aag aat aag gag ttt ctc ccg cgt	727
Val Glu Trp Arg Asp Ala Thr Glu Lys Asn Lys Glu Phe Leu Pro Arg	
51 56 61 66	
tta gga gct act att gaa cat atc tca gtc tgc cct gca gga gat tta	775
Leu Gly Ala Thr Ile Glu His Ile Ser Val Ser Pro Ala Gly Asp Leu	
67 72 77 82	
ttc tgc act tct cac tct gat aat aag ata ata att att cac cga aac	823
Phe Cys Thr Ser His Ser Asp Asn Lys Ile Ile Ile Ile His Arg Asn	
83 88 93 98	
ctt gaa gca tcc gca gta att caa ggc cta gtg aaa gat agg agt atc	871
Leu Glu Ala Ser Ala Val Ile Gln Gly Leu Val Lys Asp Arg Ser Ile	
99 104 109 114	
ttc act ggt ttg atg att gat cca aga act aaa gct ttg gtt ttg aat	919
Phe Thr Gly Leu Met Ile Asp Pro Arg Thr Lys Ala Leu Val Leu Asn	
115 120 125 130	
gga aaa cct ggc cac ctg cag ttt tat tct ctc cag agt gat aaa cag	967
Gly Lys Pro Gly His Leu Gln Phe Tyr Ser Leu Gln Ser Asp Lys Gln	
131 136 141 146	
tta tac aat tta gat att ata cag caa gaa tat att aat gat tat ggt	1015
Leu Tyr Asn Leu Asp Ile Ile Gln Gln Glu Tyr Ile Asn Asp Tyr Gly	
147 152 157 162	
ctg atc caa att gaa cta aca aag gct gca ttt ggc tgc ttt ggt aac	1063
Leu Ile Gln Ile Glu Leu Thr Lys Ala Ala Phe Gly Cys Phe Gly Asn	
163 168 173 178	
tgg ctt gca aca gtg gaa cag cgg caa gaa aag gaa act gag ctt gaa	1111
Trp Leu Ala Thr Val Glu Gln Arg Gln Glu Lys Glu Thr Glu Leu Glu	
179 184 189 194	
ttg caa atg aaa ctg tgg atg tat aat aag aaa aca caa ggg ttt att	1159
Leu Gln Met Lys Leu Trp Met Tyr Asn Lys Lys Thr Gln Gly Phe Ile	
195 200 205 210	
ctt aac act aaa att aac atg cca cac gaa gac tgc att aca gct ctc	1207
Leu Asn Thr Lys Ile Asn Met Pro His Glu Asp Cys Ile Thr Ala Leu	
211 216 221 226	
tgt ttc tgt aat gca gaa aaa tct gaa cag ccc acc ttg gtt aca gct	1255
Cys Phe Cys Asn Ala Glu Lys Ser Glu Gln Pro Thr Leu Val Thr Ala	
227 232 237 242	
agc aaa gat ggt tac ttc aaa gta tgg ata tta aca gat gac tct gac	1303
Ser Lys Asp Gly Tyr Phe Lys Val Trp Ile Leu Thr Asp Asp Ser Asp	
243 248 253 258	
ata tac aaa aaa gct gtt ggc tgg acc tgt gac ttg gtt ggt agt tat	1351
Ile Tyr Lys Lys Ala Val Gly Trp Thr Cys Asp Phe Val Gly Ser Tyr	
259 264 269 274	
cac aag tat caa gca act aac tgt tgt ttc tcc gaa gat ggt tct tta	1399

499	504	509	514	
cca gcc cat gtc ctg cca tct gct gct ttc ctg tgc tcc atg ttt gta				2119
Pro Ala His Val Leu Pro Ser Ala Ala Phe Leu Cys Ser Met Phe Val				
515	520	525	530	
aat tca ttg ctg ctg tct aaa gag act aag agt gct aag gaa att cct				2167
Asn Ser Leu Leu Leu Ser Lys Glu Thr Lys Ser Ala Lys Glu Ile Pro				
531	536	541	546	
gaa gat gta gat atg gaa gaa gaa aaa gaa agt gaa gat tca gat gaa				2215
Glu Asp Val Asp Met Glu Glu Glu Lys Glu Ser Glu Asp Ser Asp Glu				
547	552	557	562	
gaa aat gat ttt acc gaa aaa gtc cag gat aca agt aac aca ggt tta				2263
Glu Asn Asp Phe Thr Glu Lys Val Gln Asp Thr Ser Asn Thr Gly Leu				
563	568	573	578	
gga gaa gac att ata cat cag ttg tca aaa tct gaa gaa aaa gaa ctg				2311
Gly Glu Asp Ile Ile His Gln Leu Ser Lys Ser Glu Glu Lys Glu Leu				
579	584	589	594	
aga aaa ttt agg aaa ata gac tac agc tgg ata gct gcc ctt taa gcc				2359
Arg Lys Phe Arg Lys Ile Asp Tyr Ser Trp Ile Ala Ala Leu *				
595	600	605		
ttggagatgg ggaggatcct tggactttgt gtttttgatt gtatgttgat attctaaaaa				2419
catctatttt aatgttattt ctgttctaaa aataagataa taaatattaa caaactttgc				2479
ttttttaaaa aaaaaaaaaa				2498

<210> 91
 <211> 1024
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (216)..(698)

<400> 91	
cgatacgact cactataggg aatttggccc tcgaggcaag aattcggcac gaggctaaag	60
gatcccaacta agggctgttc acctgccccca gggactcaga acacacatga ctctccccac	120
ttgagctcag gatcccgcca ttacacgggg cgcgctgagc cccagatgtc cctaaccctt	180
ttccagcacc ctccagcctt gcagaagcag ccacc atg cca gtc tct aag tgc	233
Met Pro Val Ser Lys Cys	
1	
cca aaa aag tcg gag tcc ctg tgg aag ggg tgg gac cgg aag gcc cag	281
Pro Lys Lys Ser Glu Ser Leu Trp Lys Gly Trp Asp Arg Lys Ala Gln	

7	12	17	22	
agg aac ggc ctg cgg agc cag gta tac gct gtg aat ggc gac tac tat				329
Arg Asn Gly Leu Arg Ser Gln Val Tyr Ala Val Asn Gly Asp Tyr Tyr				
23	28	33	38	
gtg ggc gag tgg aag gac aac gtg aaa cac ggg aaa gga aca cag gtc				377
Val Gly Glu Trp Lys Asp Asn Val Lys His Gly Lys Gly Thr Gln Val				
39	44	49	54	
tgg aag aag aaa gga gcc atc tat gag ggg gac tgg aag ttt ggg aag				425
Trp Lys Lys Lys Gly Ala Ile Tyr Glu Gly Asp Trp Lys Phe Gly Lys				
55	60	65	70	
cga gac ggc tac ggc acc ctc agc ctt cct gac caa cag aca gga aag				473
Arg Asp Gly Tyr Gly Thr Leu Ser Leu Pro Asp Gln Gln Thr Gly Lys				
71	76	81	86	
tgc agg aga gtc tac tca ggc tgg tgg aaa ggt gat aag aaa tcg ggt				521
Cys Arg Arg Val Tyr Ser Gly Trp Trp Lys Gly Asp Lys Lys Ser Gly				
87	92	97	102	
tat ggg atc cag ttt ttc gga ccc aag gag tat tat gag ggt gac tgg				569
Tyr Gly Ile Gln Phe Phe Gly Pro Lys Glu Tyr Tyr Glu Gly Asp Trp				
103	108	113	118	
tgt ggc agc cag cgc agc ggg tgg ggc cgc atg tat tac agc aac ggc				617
Cys Gly Ser Gln Arg Ser Gly Trp Gly Arg Met Tyr Tyr Ser Asn Gly				
119	124	129	134	
gac atc tac gag gga cag tgg gag aac gac aag ccc aac ggg gag ggc				665
Asp Ile Tyr Glu Gly Gln Trp Glu Asn Asp Lys Pro Asn Gly Glu Gly				
135	140	145	150	
atg ctg cgc ctg agt caa aat cct aga ccc tga tgggtgtgc tggcggagcc				716
Met Leu Arg Leu Ser Gln Asn Pro Arg Pro *				
151	156	161		
ttggccatgt tcaggaagac agaggaagga gattgatgcc agagaacaca aacgcttcag				776
gagaaattca agcctgtgtc acccgatcgc tcagaccagt gcggctcttg ctggaggagt				836
cagcagcagc tccagggcatg accccggcac cctcataggg cccctcacta cccccagcac				896
tgggtcattt cttgccataa ggaaggctgg tgcttctctc ccaggctgtc ctcgggaccc				956
tcttcattct ctgatctcat cctggaatgc atgagaataa agaataacca agtggaaaaa				1016
aaaaaaaa				1024

<210> 92
 <211> 2818
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (449) .. (2818)

<400> 92

aaggatcctt aattaaatta atcccccccc cccccctggc tcgtctgaac ttgaagacac	60
cccacattcc aagatgcccc aggttctctgg gaatgcctgg ggttcttcga tccggaaaat	120
cctaccggca tcctcctagg gagggattat tattattatt tttctttaat ctggaagaga	180
agagaacaag ttgtgctttt ccccccttct tcttgctaaa tgccatggat ataactgaat	240
aagcggctca gggctttccc cgcgtggacg tccgaggcca ccatctgcct gcattcgccg	300
gagccgcggg aggggttagc tcgagtcctgt ctcgggcggg gaaggatgog tggccgagcc	360
ggggagcccc ggcgccccgc ggagccggcc tcgggtgccac ccagccgggg gtagatgctg	420
cctcgcccag gcgctgagtg accagacc atg gag acc ctg ctt ggt ggc ctg	472
Met Glu Thr Leu Leu Gly Gly Leu	
1 5	
cta gcg ttt ggc atg gcg ttt gcc gtg gtc gac gcc tgc ccc aag tac	520
Leu Ala Phe Gly Met Ala Phe Ala Val Val Asp Ala Cys Pro Lys Tyr	
9 14 19 24	
tgt gtc tgc cag aat ctg tct gag tca ctg ggg acc ctg tgc ccc tcc	568
Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr Leu Cys Pro Ser	
25 30 35 40	
aag ggg ctg ctc ttt gta ccc cct gat att gac cgg cgg aca gtg gag	616
Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg Arg Thr Val Glu	
41 46 51 56	
ctg cgc ctg ggc ggc aac ttc atc atc cac atc agc cgc cag gac ttt	664
Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser Arg Gln Asp Phe	
57 62 67 72	
gcc aac atg acg ggg ctg gtg gac ctg acc ctg tcc agg aac acc atc	712
Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser Arg Asn Thr Ile	
73 78 83 88	
agc cac atc cag ccc ttt tcc ttt ctg gac ctc gag agc ctc cgc tcc	760
Ser His Ile Gln Pro Phe Ser Phe Leu Asp Leu Glu Ser Leu Arg Ser	
89 94 99 104	
ctg cat ctt gac agc aat cgg ctg cca agc ctt ggg gag gac acc ctc	808
Leu His Leu Asp Ser Asn Arg Leu Pro Ser Leu Gly Glu Asp Thr Leu	
105 110 115 120	
cgg ggc ctg gtc aac ctg cag cac ctt atc gtg aac aac aac cag ctg	856
Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn Asn Asn Gln Leu	
121 126 131 136	
ggc ggc atc gca gat gag gct ttt gag gac ttc ctg ctg aca ttg gag	904

Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu Leu Thr Leu Glu	
137 142 147 152	
gat ctg gac ctc tcc tac aac aac ctc cat ggc ctg ccg tgg gac tcc	952
Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu Pro Trp Asp Ser	
153 158 163 168	
gtg cga cgc atg gtc aac ctc cac cag ctg agc ctg gac cac aac ctg	1000
Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu Asp His Asn Leu	
169 174 179 184	
ctg gat cac atc gcc gag ggc acc ttt gca gac ctg cag aaa ctg gcc	1048
Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu Gln Lys Leu Ala	
185 190 195 200	
cgc ctg gat ctc acc tcc aat cgg ctg cag aag ctg ccc cct gat ccc	1096
Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu Pro Pro Asp Pro	
201 206 211 216	
atc ttt gcc cgc tcc cag gct tcg gct ttg aca gcc aca ccc ttt gcc	1144
Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala Thr Pro Phe Ala	
217 222 227 232	
cca ccc ttg tcc ttt agt ttt ggg ggt aac cca ctt cac tgc aat tgt	1192
Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu His Cys Asn Cys	
233 238 243 248	
gag ctt ctc tgg ctg cgg agg ctc gag cgg gac gat gac ctg gaa acc	1240
Glu Leu Leu Trp Leu Arg Arg Leu Glu Arg Asp Asp Asp Leu Glu Thr	
249 254 259 264	
tgt ggc tcc cca ggg ggc ctc aag ggt cgc tac ttc tgg cat gtg cgt	1288
Cys Gly Ser Pro Gly Gly Leu Lys Gly Arg Tyr Phe Trp His Val Arg	
265 270 275 280	
gag gag gag ttt gtg tgc gag cgg cct ctc atc acc cag cac aca cac	1336
Glu Glu Glu Phe Val Cys Glu Pro Pro Leu Ile Thr Gln His Thr His	
281 286 291 296	
aag ttg ctg gtt ctg gag ggc cag gcg gcc aca ctc aag tgc aaa gcc	1384
Lys Leu Leu Val Leu Glu Gly Gln Ala Ala Thr Leu Lys Cys Lys Ala	
297 302 307 312	
att ggg gac ccc agc ccc ctt atc cac tgg gta gcc ccc gat gac cgc	1432
Ile Gly Asp Pro Ser Pro Leu Ile His Trp Val Ala Pro Asp Asp Arg	
313 318 323 328	
ctg gta ggg aac tcc tca agg acc gct gtc tat gac aat ggc acc ccg	1480
Leu Val Gly Asn Ser Ser Arg Thr Ala Val Tyr Asp Asn Gly Thr Pro	
329 334 339 344	
gac atc ttc atc acc aca tct cag gac agt ggt gcc ttc acc tgc att	1528
Asp Ile Phe Ile Thr Thr Ser Gln Asp Ser Gly Ala Phe Thr Cys Ile	
345 350 355 360	
gct gcc aat gct gcc gga gag gcc acg gcc atg gtg gag gtc tcc atc	1576
Ala Ala Asn Ala Ala Gly Glu Ala Thr Ala Met Val Glu Val Ser Ile	

361	366	371	376	
gtc cag ctg cca cac ctc agc aac agc acc agc cgc act gca ccc ccc				1624
Val Gln Leu Pro His Leu Ser Asn Ser Thr Ser Arg Thr Ala Pro Pro				
377	382	387	392	
aag tcc cgc ctc tca gac atc act ggc tcc agc aag acc agc cgg gga				1672
Lys Ser Arg Leu Ser Asp Ile Thr Gly Ser Ser Lys Thr Ser Arg Gly				
393	398	403	408	
ggt gga ggc agt ggg ggc gga gag cct ccc aaa agc ccc ccg gaa cgg				1720
Gly Gly Gly Ser Gly Gly Gly Glu Pro Pro Lys Ser Pro Pro Glu Arg				
409	414	419	424	
gct gtg ctt gtg tct gaa gtg acc acc acc tcg gcc ctg gtc aag tgg				1768
Ala Val Leu Val Ser Glu Val Thr Thr Thr Ser Ala Leu Val Lys Trp				
425	430	435	440	
tct gtc agc aag tca gca ccc cgg gtg aag atg tac cag ctg cag tac				1816
Ser Val Ser Lys Ser Ala Pro Arg Val Lys Met Tyr Gln Leu Gln Tyr				
441	446	451	456	
aac tgc tct gac gat gag gta ctg att tac agg atg atc cca gcc tcc				1864
Asn Cys Ser Asp Asp Glu Val Leu Ile Tyr Arg Met Ile Pro Ala Ser				
457	462	467	472	
aac aag gcc ttc gtg gtc aac aac ctg gtg tca ggg act ggc tac gac				1912
Asn Lys Ala Phe Val Val Asn Asn Leu Val Ser Gly Thr Gly Tyr Asp				
473	478	483	488	
ttg tgt gtg ctg gcc atg tgg gat gac aca gcc acg aca ctc acg gcc				1960
Leu Cys Val Leu Ala Met Trp Asp Asp Thr Ala Thr Thr Leu Thr Ala				
489	494	499	504	
acc aac atc gtg ggc tgc gcc cag ttc ttc acc aag gct gac tac ccg				2008
Thr Asn Ile Val Gly Cys Ala Gln Phe Phe Thr Lys Ala Asp Tyr Pro				
505	510	515	520	
cag tgc cag tcc atg cac agc cag att ctg ggc ggc acc atg atc ctg				2056
Gln Cys Gln Ser Met His Ser Gln Ile Leu Gly Gly Thr Met Ile Leu				
521	526	531	536	
gtc atc ggg ggc atc atc gtg gcc acg ctg ctg gtc ttc atc gtc atc				2104
Val Ile Gly Gly Ile Ile Val Ala Thr Leu Leu Val Phe Ile Val Ile				
537	542	547	552	
ctc atg gtg cgc tac aag gtc tgc aac cac gag gcc ccc agc aag atg				2152
Leu Met Val Arg Tyr Lys Val Cys Asn His Glu Ala Pro Ser Lys Met				
553	558	563	568	
gca gcg gcc gtg agc aat gtg tac tcg cag acc aac ggc gcc cag cca				2200
Ala Ala Ala Val Ser Asn Val Tyr Ser Gln Thr Asn Gly Ala Gln Pro				
569	574	579	584	
ccg cct cca agc agc gca cca gcc ggg gcc ccg ccg cag ggc ccg ccg				2248
Pro Pro Pro Ser Ser Ala Pro Ala Gly Ala Pro Pro Gln Gly Pro Pro				
585	590	595	600	

aag gtg gtg gtg cgc aac gag ctc ctg gac ttc acc gcc agc ctg gcc	2296
Lys Val Val Val Arg Asn Glu Leu Leu Asp Phe Thr Ala Ser Leu Ala	
601 606 611 616	
cgc gcc agt gac tcc tct tcc tcc agc tcc ctg ggc agt ggg gag gct	2344
Arg Ala Ser Asp Ser Ser Ser Ser Ser Ser Leu Gly Ser Gly Glu Ala	
617 622 627 632	
gcg ggg ctg gga cgg gcc ccc tgg agg atc cca ccc tcc gcc ccg cgc	2392
Ala Gly Leu Gly Arg Ala Pro Trp Arg Ile Pro Pro Ser Ala Pro Arg	
633 638 643 648	
ccc aag ccc agc ctt gac cgc ctg atg ggg gcc ttc gcc tcc ctg gac	2440
Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala Phe Ala Ser Leu Asp	
649 654 659 664	
ctc aag agt cag aga aag gag gag ctg ctg gac tcc agg act cca gcc	2488
Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp Ser Arg Thr Pro Ala	
665 670 675 680	
ggg aga ggg gct ggg acg tcg gcc cgg ggc cac cac tcg gac cga gag	2536
Gly Arg Gly Ala Gly Thr Ser Ala Arg Gly His His Ser Asp Arg Glu	
681 686 691 696	
cca ctg ctg ggg ccc cct gcg gcc cgg gcc agg agc ctg ctc ccc ttg	2584
Pro Leu Leu Gly Pro Pro Ala Ala Arg Ala Arg Ser Leu Leu Pro Leu	
697 702 707 712	
ccg ttg gag ggc aag gcc aaa cgc agc cac tcc ttc gac atg ggg gac	2632
Pro Leu Glu Gly Lys Ala Lys Arg Ser His Ser Phe Asp Met Gly Asp	
713 718 723 728	
ttt gct gct gcg gcg gcg gga ggg gtc gtg ccg ggc ggc tac agt cct	2680
Phe Ala Ala Ala Ala Ala Gly Gly Val Val Pro Gly Gly Tyr Ser Pro	
729 734 739 744	
cct cgg aag gtc tcg aac atc tgg acg aag cgc agc ctc tct gtc aac	2728
Pro Arg Lys Val Ser Asn Ile Trp Thr Lys Arg Ser Leu Ser Val Asn	
745 750 755 760	
ggc atg ctc ttg ccc ttt gag gag agt gac ctg gtg ggg gcc cgg ggg	2776
Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu Val Gly Ala Arg Gly	
761 766 771 776	
act ttt ggc agc tcc gaa tgg gtg atg gag agc acg gtc tag	2818
Thr Phe Gly Ser Ser Glu Trp Val Met Glu Ser Thr Val *	
777 782 787	

<210> 93
 <211> 3626
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (296)..(3325)

<400> 93

gtgaaaaatt tattgctgta cgcctgcagg accgggtccgg aattcccggg tcgacgattt	60
cgtggagggg gcgcgcgtcg cgcagatcgt cgcggagcca cggcaggagg aggcaggggc	120
cgcgggagag cctgcgctgg gccggccgag ggtcaagggtg gaagggtccaa ggactgagaa	180
agaccctcga aggcattccac tttagtccctc cattccattc ctagagactg atcaggagtc	240
aggcttcaga aggagtcccc tggaaggcct ccacaacctc acgctagagt caaga atg	298
	Met
	1
gat atg ttc agc ttg gat atg atc atc agt gac cca gct gca gaa gcc	346
Asp Met Phe Ser Leu Asp Met Ile Ile Ser Asp Pro Ala Ala Glu Ala	
2 7 12 17	
agc agg gct ggg aag aag cag ctc aga ggt gtt cag aac cct tgc cca	394
Ser Arg Ala Gly Lys Lys Gln Leu Arg Gly Val Gln Asn Pro Cys Pro	
18 23 28 33	
tct gcc aga gcc aga ccc cgg cac aag tcc ctc aac ata aag gac aag	442
Ser Ala Arg Ala Arg Pro Arg His Lys Ser Leu Asn Ile Lys Asp Lys	
34 39 44 49	
ata tca gaa tgg gaa ggg aag aaa gag gtg ccc act cct gca ccc agc	490
Ile Ser Glu Trp Glu Gly Lys Lys Glu Val Pro Thr Pro Ala Pro Ser	
50 55 60 65	
agg aga gca gac gga cag gag gat tat ctg ccg tcc tct acg gtg gag	538
Arg Arg Ala Asp Gly Gln Glu Asp Tyr Leu Pro Ser Ser Thr Val Glu	
66 71 76 81	
agg agg agt agt gat ggg gtg aga act cag gtc aca gag gct aag aat	586
Arg Arg Ser Ser Asp Gly Val Arg Thr Gln Val Thr Glu Ala Lys Asn	
82 87 92 97	
gga atg agg cca gga aca gag agc aca gag aag gag agg aat aaa gga	634
Gly Met Arg Pro Gly Thr Glu Ser Thr Glu Lys Glu Arg Asn Lys Gly	
98 103 108 113	
gca gtg aac gtc ggg gga cag gac cca gag ccg ggg caa gac cta agc	682
Ala Val Asn Val Gly Gly Gln Asp Pro Glu Pro Gly Gln Asp Leu Ser	
114 119 124 129	
cag cca gaa cgg gaa gtg gat cct agc tgg ggc cga ggc cga gag cca	730
Gln Pro Glu Arg Glu Val Asp Pro Ser Trp Gly Arg Gly Arg Glu Pro	
130 135 140 145	
aga ctt ggc aag cta cgc ttt cag aac gat cac ctc tcc gtg ctg aag	778
Arg Leu Gly Lys Leu Arg Phe Gln Asn Asp His Leu Ser Val Leu Lys	
146 151 156 161	

cag gtc aag aaa ctc gag cag gct ttg aag gat ggg tcg gca ggg ctg	826
Gln Val Lys Lys Leu Glu Gln Ala Leu Lys Asp Gly Ser Ala Gly Leu	
162 167 172 177	
gat ccc cag tta cca ggg act tgt tac tcc cca cac tgc cct cct gac	874
Asp Pro Gln Leu Pro Gly Thr Cys Tyr Ser Pro His Cys Pro Pro Asp	
178 183 188 193	
aag gca gag gca ggg tcc acc ctt cct gag aac ctg gga ggc ggg agt	922
Lys Ala Glu Ala Gly Ser Thr Leu Pro Glu Asn Leu Gly Gly Gly Ser	
194 199 204 209	
ggc tca gaa gtc agc cag agg gtc cac ccc tcg gac ctg gaa ggc agg	970
Gly Ser Glu Val Ser Gln Arg Val His Pro Ser Asp Leu Glu Gly Arg	
210 215 220 225	
gag ccc acc cct gag ctt gtg gag gac agg aaa ggt tca tgc aga agg	1018
Glu Pro Thr Pro Glu Leu Val Glu Asp Arg Lys Gly Ser Cys Arg Arg	
226 231 236 241	
ccc tgg gac cgg agc ctt gag aac gtg tat agg ggc tcg gag ggt tcc	1066
Pro Trp Asp Arg Ser Leu Glu Asn Val Tyr Arg Gly Ser Glu Gly Ser	
242 247 252 257	
ccc aca aag ccc ttc atc aac cct ctg cca aaa ccc cgg aga acg ttc	1114
Pro Thr Lys Pro Phe Ile Asn Pro Leu Pro Lys Pro Arg Arg Thr Phe	
258 263 268 273	
aaa cat gcc gga gaa ggg gac aaa gat ggg aag cct ggc atc ggc ttc	1162
Lys His Ala Gly Glu Gly Asp Lys Asp Gly Lys Pro Gly Ile Gly Phe	
274 279 284 289	
agg aaa gag aaa aga aat ctg cct cct ctg ccc tct cta cct ccc ccg	1210
Arg Lys Glu Lys Arg Asn Leu Pro Pro Leu Pro Ser Leu Pro Pro Pro	
290 295 300 305	
cct ctg ccc tcc tct ccc cca cct tcc tct gtg aac aga aga ctg tgg	1258
Pro Leu Pro Ser Ser Pro Pro Pro Ser Ser Val Asn Arg Arg Leu Trp	
306 311 316 321	
acc ggg aga cag aaa tcc agt gca gac cac aga aag tcc tat gag ttt	1306
Thr Gly Arg Gln Lys Ser Ser Ala Asp His Arg Lys Ser Tyr Glu Phe	
322 327 332 337	
gaa gat tta ctg cag tct tcc tct gag agc agc agg gtg gac tgg tac	1354
Glu Asp Leu Leu Gln Ser Ser Ser Glu Ser Ser Arg Val Asp Trp Tyr	
338 343 348 353	
gcg cag act aag ctg ggg ctg aca cgc act tta tcg gag gag aac gtc	1402
Ala Gln Thr Lys Leu Gly Leu Thr Arg Thr Leu Ser Glu Glu Asn Val	
354 359 364 369	
tat gaa gac att cta gat ccg cca atg aag gag aac cct tat gag gac	1450
Tyr Glu Asp Ile Leu Asp Pro Pro Met Lys Glu Asn Pro Tyr Glu Asp	
370 375 380 385	

atc gag tta cat ggt cgc tgc ctg gga aag aag tgt gtc ttg aat ttt	1498
Ile Glu Leu His Gly Arg Cys Leu Gly Lys Lys Cys Val Leu Asn Phe	
386 391 396 401	
cct gct tct ccc acc tct tcc atc cct gac aca ctc acc aag cag tca	1546
Pro Ala Ser Pro Thr Ser Ser Ile Pro Asp Thr Leu Thr Lys Gln Ser	
402 407 412 417	
ttg tcc aaa cct gct ttt ttc cga caa aat tca gag agg agg aac ttc	1594
Leu Ser Lys Pro Ala Phe Phe Arg Gln Asn Ser Glu Arg Arg Asn Phe	
418 423 428 433	
aag ctg ctg gac act agg aag ctg agt cgg gat gga act ggg tcc cct	1642
Lys Leu Leu Asp Thr Arg Lys Leu Ser Arg Asp Gly Thr Gly Ser Pro	
434 439 444 449	
tcc aaa atc agc cct ccc tcc act ccc agc agc cct gat gac att ttc	1690
Ser Lys Ile Ser Pro Pro Ser Thr Pro Ser Ser Pro Asp Asp Ile Phe	
450 455 460 465	
ttt aac ctt gga gac cca cag aac ggc agg aag aag aga aag ata ccc	1738
Phe Asn Leu Gly Asp Pro Gln Asn Gly Arg Lys Lys Arg Lys Ile Pro	
466 471 476 481	
aag ctg gtg ttg cga atc aac gcc att tat gag gtc cgg aga gga aag	1786
Lys Leu Val Leu Arg Ile Asn Ala Ile Tyr Glu Val Arg Arg Gly Lys	
482 487 492 497	
aaa cgg gtg aag agg ctg tcc cag tca atg gag agc aac tca gga aaa	1834
Lys Arg Val Lys Arg Leu Ser Gln Ser Met Glu Ser Asn Ser Gly Lys	
498 503 508 513	
gtg aca gat gag aac agt gag tct gac agt gac aca gag gag aag ctg	1882
Val Thr Asp Glu Asn Ser Glu Ser Asp Ser Asp Thr Glu Glu Lys Leu	
514 519 524 529	
aaa gct cac agc cag cgc ctg gtc aac gtg aag tcc cgg ctg aag cag	1930
Lys Ala His Ser Gln Arg Leu Val Asn Val Lys Ser Arg Leu Lys Gln	
530 535 540 545	
gcg cct cgg tac cca tca ctt gcc cgg gaa ctc atc gag tac cag gag	1978
Ala Pro Arg Tyr Pro Ser Leu Ala Arg Glu Leu Ile Glu Tyr Gln Glu	
546 551 556 561	
agg cag ctc ttc gag tac ttt gtg gtt gtg tct ttg cac aag aag cag	2026
Arg Gln Leu Phe Glu Tyr Phe Val Val Val Ser Leu His Lys Lys Gln	
562 567 572 577	
gcc ggg gct gcc tac gtg cca gaa ctc acc caa cag ttc cct ctg aag	2074
Ala Gly Ala Ala Tyr Val Pro Glu Leu Thr Gln Gln Phe Pro Leu Lys	
578 583 588 593	
ttg gaa agg tct ttc aag ttc atg aga gaa gct gag gac caa ctg aag	2122
Leu Glu Arg Ser Phe Lys Phe Met Arg Glu Ala Glu Asp Gln Leu Lys	
594 599 604 609	
gcc att ccc cag ttc tgt ttt ccc gat gcc aag gat tgg gtt cct gtc	2170

Ala Ile Pro Gln Phe Cys Phe Pro Asp Ala Lys Asp Trp Val Pro Val	
610 615 620 625	
cag cag ttc acc agt gaa aca ttc tgc ttt gtc tta act gga gaa gat	2218
Gln Gln Phe Thr Ser Glu Thr Phe Ser Phe Val Leu Thr Gly Glu Asp	
626 631 636 641	
ggg agc aga agg ttc ggt tac tgc cga aga ctg ctg cct gga ggc aaa	2266
Gly Ser Arg Arg Phe Gly Tyr Cys Arg Arg Leu Leu Pro Gly Gly Lys	
642 647 652 657	
ggg aag cgc ctt cct gaa gtt tac tgc att gtg agc cgc ctg gga tgc	2314
Gly Lys Arg Leu Pro Glu Val Tyr Cys Ile Val Ser Arg Leu Gly Cys	
658 663 668 673	
ttc agc ctc ttt tca agg atc ttg gat gag gtg gaa aaa aga cga ggc	2362
Phe Ser Leu Phe Ser Arg Ile Leu Asp Glu Val Glu Lys Arg Arg Gly	
674 679 684 689	
atc tct cct gcc ctg gtt cag cca ctc atg aga agt gtc atg gaa gcc	2410
Ile Ser Pro Ala Leu Val Gln Pro Leu Met Arg Ser Val Met Glu Ala	
690 695 700 705	
cct ttc cca gcc ctg ggc aaa acc atc ctt gtc aag aac ttc ctg cca	2458
Pro Phe Pro Ala Leu Gly Lys Thr Ile Leu Val Lys Asn Phe Leu Pro	
706 711 716 721	
ggt tca gga act gag gtg atc gaa ctg tgc cgc ccg ctg gac tcc cgg	2506
Gly Ser Gly Thr Glu Val Ile Glu Leu Cys Arg Pro Leu Asp Ser Arg	
722 727 732 737	
gtc gag cac gtg gac ttt gag tct ctc ttc tcc tcc ctc agc gtc cgc	2554
Val Glu His Val Asp Phe Glu Ser Leu Phe Ser Ser Leu Ser Val Arg	
738 743 748 753	
cac ctg gtc tgt gtg ttt gcc tcc ctg ctt ctg gag agg agg gtc atc	2602
His Leu Val Cys Val Phe Ala Ser Leu Leu Leu Glu Arg Arg Val Ile	
754 759 764 769	
ttc att gca gac aag ctc agc atc ctg tcc aag tgc tgc cac gcg atg	2650
Phe Ile Ala Asp Lys Leu Ser Ile Leu Ser Lys Cys Cys His Ala Met	
770 775 780 785	
gtg gcg ctg atc tac ccc ttc gcc tgg cag cac acc tac atc ccg gtg	2698
Val Ala Leu Ile Tyr Pro Phe Ala Trp Gln His Thr Tyr Ile Pro Val	
786 791 796 801	
ctg cca ccc gcc atg gtc gac atc gtg tgc tgc ccg acg ccc ttc ctc	2746
Leu Pro Pro Ala Met Val Asp Ile Val Cys Ser Pro Thr Pro Phe Leu	
802 807 812 817	
atc ggg ctg ctc tcc agc tgc ctg cca ctg ctc agg gag ctg ccg ctg	2794
Ile Gly Leu Leu Ser Ser Ser Leu Pro Leu Leu Arg Glu Leu Pro Leu	
818 823 828 833	
gaa gag gtc ctt gtg gtt gac ctc gtc aac agc cgg ttc ctc aga cag	2842
Glu Glu Val Leu Val Val Asp Leu Val Asn Ser Arg Phe Leu Arg Gln	

834	839	844	849	
atg gac gat gag gac tcc atc ctg ccc cgg aag ctt cag gtg gcc ctg				2890
Met Asp Asp Glu Asp Ser Ile Leu Pro Arg Lys Leu Gln Val Ala Leu				
850	855	860	865	
gaa cac att ctg gaa cag agg aac gag ctg gct tgt gag cag gac gaa				2938
Glu His Ile Leu Glu Gln Arg Asn Glu Leu Ala Cys Glu Gln Asp Glu				
866	871	876	881	
ggg ccc cta gac ggc agg cac ggt cca gag tcc agc ccc ttg aac gag				2986
Gly Pro Leu Asp Gly Arg His Gly Pro Glu Ser Ser Pro Leu Asn Glu				
882	887	892	897	
gtg gtg tct gaa gcc ttt gtc cgc ttc ttc gtg gag att gtg gga cac				3034
Val Val Ser Glu Ala Phe Val Arg Phe Phe Val Glu Ile Val Gly His				
898	903	908	913	
tac tct ttg ttc ctg acg tcg ggc gag cgt gag gag aga acc ctg cag				3082
Tyr Ser Leu Phe Leu Thr Ser Gly Glu Arg Glu Glu Arg Thr Leu Gln				
914	919	924	929	
cgg gag gcc ttc cgc aaa gct gtc tcc tcc aag agc ctc cgc cac ttc				3130
Arg Glu Ala Phe Arg Lys Ala Val Ser Ser Lys Ser Leu Arg His Phe				
930	935	940	945	
ctg gag gtc ttc atg gag act cag atg ttt cgg ggc ttc atc cag gag				3178
Leu Glu Val Phe Met Glu Thr Gln Met Phe Arg Gly Phe Ile Gln Glu				
946	951	956	961	
cgg gag ctg cgc cgg cag gat gcc aaa ggt ctg ttt gag gtc cga gcc				3226
Arg Glu Leu Arg Arg Gln Asp Ala Lys Gly Leu Phe Glu Val Arg Ala				
962	967	972	977	
caa gag tat ctg gaa aca ctc ccc agt gga gag cac agc ggt gtc aat				3274
Gln Glu Tyr Leu Glu Thr Leu Pro Ser Gly Glu His Ser Gly Val Asn				
978	983	988	993	
aag ttc ctg aag gga cta ggc aat aaa atg aaa ttt ctc cac aag aaa				3322
Lys Phe Leu Lys Gly Leu Gly Asn Lys Met Lys Phe Leu His Lys Lys				
994	999	1004	1009	
taa ctct cagcctcaag ggaaaacttc ctctagtgc agccctatgc tttaaaaaca				3379
*				
1010				
gttctctggtg gcctttctga aaggctgggt ccaggttgt cacggtgcgg aactggaggc				3439
cgcggtggct tctggccgag gctgggctct tccctggatg aggacctggg agccgcctgg				3499
gaggacagcc ccagaaaggg agcccgagac caggcgtgtc gccgacatgc aaatgggttg				3559
ttttggtggt tgggtttttt tttttatctt agatattaaa agtaagaaaa atgtgaaaaa				3619
aaaaaaa				3626

[illegible][illegible]

Thr Arg Val Ala Phe Arg Gly Ser Asp Glu Ile Phe Cys Arg Val Tyr	
100 105 110 115	
atg cct gac cac tct tat gtg acc ata cgc agc cgc ctt tca gca tct	919
Met Pro Asp His Ser Tyr Val Thr Ile Arg Ser Arg Leu Ser Ala Ser	
116 121 126 131	
gtg cag gac att ctg ggc tct gtg acg gag aaa ctt caa tat tca gag	967
Val Gln Asp Ile Leu Gly Ser Val Thr Glu Lys Leu Gln Tyr Ser Glu	
132 137 142 147	
gag ccc gcg ggg cgt gag gat tcc ctc atc ctg gta gct gtg tcc tcc	1015
Glu Pro Ala Gly Arg Glu Asp Ser Leu Ile Leu Val Ala Val Ser Ser	
148 153 158 163	
tct gga gag aag gtc ctt ctc cag ccc act gag gac tgt gtt ttc acc	1063
Ser Gly Glu Lys Val Leu Leu Gln Pro Thr Glu Asp Cys Val Phe Thr	
164 169 174 179	
gca ctg ggc atc aac agc cac ctg ttt gcc tgt act cgg gac agc tat	1111
Ala Leu Gly Ile Asn Ser His Leu Phe Ala Cys Thr Arg Asp Ser Tyr	
180 185 190 195	
gag gct ctg gtg ccc ctc ccc gag gag atc cag gtc tcc cct gga gac	1159
Glu Ala Leu Val Pro Leu Pro Glu Glu Ile Gln Val Ser Pro Gly Asp	
196 201 206 211	
aca gag atc cac cga gtg gag cct gag gac gtt gcc aac cac cta act	1207
Thr Glu Ile His Arg Val Glu Pro Glu Asp Val Ala Asn His Leu Thr	
212 217 222 227	
gcc ttc cac tgg gag ctg ttc cga tgt gtg cat gag ctg gag ttc gtg	1255
Ala Phe His Trp Glu Leu Phe Arg Cys Val His Glu Leu Glu Phe Val	
228 233 238 243	
gac tac gtg ttc cac ggg gag cgc gcc cgc cgg gag acg gcc aac ttg	1303
Asp Tyr Val Phe His Gly Glu Arg Gly Arg Arg Glu Thr Ala Asn Leu	
244 249 254 259	
gag ctg ctg ctg cag cgc tgc agc gag gtc acg cac tgg gtg gcc acc	1351
Glu Leu Leu Leu Gln Arg Cys Ser Glu Val Thr His Trp Val Ala Thr	
260 265 270 275	
gaa gtg ctg ctc tgc gag gcc ccg ggc aag cgc gcg cag ctg ctc aag	1399
Glu Val Leu Leu Cys Glu Ala Pro Gly Lys Arg Ala Gln Leu Leu Lys	
276 281 286 291	
aag ttc atc aag atc gcg gcc ctc tgc aag cag aac cag gac ctg ctg	1447
Lys Phe Ile Lys Ile Ala Ala Leu Cys Lys Gln Asn Gln Asp Leu Leu	
292 297 302 307	
tct ttc tac gcc gtg gtc atg ggg ctg gac aac gcc gct gtc agc cgc	1495
Ser Phe Tyr Ala Val Val Met Gly Leu Asp Asn Ala Ala Val Ser Arg	
308 313 318 323	
ctt cga ctc acc tgg gag aag ctg cca ggg aaa ttc aag aac ttg ttt	1543
Leu Arg Leu Thr Trp Glu Lys Leu Pro Gly Lys Phe Lys Asn Leu Phe	

324	329	334	339	
cgc aaa ttt gag aac ctg acg gac ccc tgc agg aac cac aaa agc tac				1591
Arg Lys Phe Glu Asn Leu Thr Asp Pro Cys Arg Asn His Lys Ser Tyr				
340	345	350	355	
cga gaa gtg atc tcc aaa atg aag ccc cct gtg att ccc ttc gtg cct				1639
Arg Glu Val Ile Ser Lys Met Lys Pro Pro Val Ile Pro Phe Val Pro				
356	361	366	371	
ctg atc ctc aaa gac ctg act ttc ctg cac gaa ggg agt aag acc ctt				1687
Leu Ile Leu Lys Asp Leu Thr Phe Leu His Glu Gly Ser Lys Thr Leu				
372	377	382	387	
gta gat ggt ttg gtg aac atc gag aag ctg cat tca gtg gcc gaa aaa				1735
Val Asp Gly Leu Val Asn Ile Glu Lys Leu His Ser Val Ala Glu Lys				
388	393	398	403	
gtg agg aca atc cgc aaa tac cgg agc cgg ccc ctt tgc ctg gac atg				1783
Val Arg Thr Ile Arg Lys Tyr Arg Ser Arg Pro Leu Cys Leu Asp Met				
404	409	414	419	
gag gca tcc ccc aat cac ctg cag acc aag gcc tat gtg cgc cag ttt				1831
Glu Ala Ser Pro Asn His Leu Gln Thr Lys Ala Tyr Val Arg Gln Phe				
420	425	430	435	
cag gtc atc gac aac cag aac ctc ctc ttc gag ctc tcc tac aag ctg				1879
Gln Val Ile Asp Asn Gln Asn Leu Leu Phe Glu Leu Ser Tyr Lys Leu				
436	441	446	451	
gag gca aac agt cag tga				1897
Glu Ala Asn Ser Gln *				
452	457			

<210> 95
 <211> 2894
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (372) .. (2894)

<400> 95	
atttggccct cgaggccaag aattcggcac gagctggcct gtctggagcc agcctgtagg	60
gttggggagc ctttctctcc atagttccag ggtttggtga agcatcttac accagtaagt	120
attgattgaa cgtctgtcag tgacctctgc aaactctgct tttgtttag gaagcagtag	180
aggttttgat taagcactca gctgatgtca atgcaaggga caagaactgg cagaccctc	240
ttcatgtggc agcagccaac aaggctgtca aatgtgcaga agtgatcatt cccctgctga	300

gcagtggtcaa tgtctccgac cgaggggggc gcacagcctt gcaccatgcg gctctgaacg 360

gccacgtgga g atg gtc aat tta ctc ttg gcc aaa ggg gca aat atc aat 410
Met Val Asn Leu Leu Leu Ala Lys Gly Ala Asn Ile Asn
1 5 10

gca ttt gac aag aag gac cgg cgt gct ctg cac tgg gca gca tac atg 458
Ala Phe Asp Lys Lys Asp Arg Arg Ala Leu His Trp Ala Ala Tyr Met
14 19 24 29

ggc cac ttg gat gtt gta gca ttg ctc att aac cat ggc gca gaa gtg 506
Gly His Leu Asp Val Val Ala Leu Leu Ile Asn His Gly Ala Glu Val
30 35 40 45

acc tgt aag gat aag aag ggt tat acc cct ctg cat gct gca gcc tcc 554
Thr Cys Lys Asp Lys Lys Gly Tyr Thr Pro Leu His Ala Ala Ala Ser
46 51 56 61

aat gga cag att aat gtt gtc aag cat ctc ctg aac ctg ggg gtg gag 602
Asn Gly Gln Ile Asn Val Val Lys His Leu Leu Asn Leu Gly Val Glu
62 67 72 77

att gat gaa atc aat gtc tat gga aat aca gcg ctt cac atc gcc tgc 650
Ile Asp Glu Ile Asn Val Tyr Gly Asn Thr Ala Leu His Ile Ala Cys
78 83 88 93

tac aat gga cag gat gct gtg gtt aac gag ttg att gac tac ggt gct 698
Tyr Asn Gly Gln Asp Ala Val Val Asn Glu Leu Ile Asp Tyr Gly Ala
94 99 104 109

aac gtg aac cag cca aac aat aat ggg ttc acc cct ttg cat ttt gct 746
Asn Val Asn Gln Pro Asn Asn Asn Gly Phe Thr Pro Leu His Phe Ala
110 115 120 125

gct gcc tcc act cat ggt gct ttg tgt ctt gaa ttg tta gta aac aac 794
Ala Ala Ser Thr His Gly Ala Leu Cys Leu Glu Leu Leu Val Asn Asn
126 131 136 141

ggg gca gat gtt aac att cag agt aaa gat ggc aaa agt cca ctg cac 842
Gly Ala Asp Val Asn Ile Gln Ser Lys Asp Gly Lys Ser Pro Leu His
142 147 152 157

atg aca gct gtc cat gga agg ttc aca cgg tca cag acc ctc att cag 890
Met Thr Ala Val His Gly Arg Phe Thr Arg Ser Gln Thr Leu Ile Gln
158 163 168 173

aat gga ggt gaa att gac tgt gtg gat aag gac ggc aac act cct ctc 938
Asn Gly Gly Glu Ile Asp Cys Val Asp Lys Asp Gly Asn Thr Pro Leu
174 179 184 189

cat gtg gct gca aga tac ggt cat gag ctt ttg att aac acc tta ata 986
His Val Ala Ala Arg Tyr Gly His Glu Leu Leu Ile Asn Thr Leu Ile
190 195 200 205

acc agc gga gct gac aca gcc aag tgt gga atc cat agc atg ttc cct 1034
Thr Ser Gly Ala Asp Thr Ala Lys Cys Gly Ile His Ser Met Phe Pro

206	211	216	221	
tta cat tta gct gcc cta aat gct cac tct gac tgc tgc aga aag ttg				1082
Leu His Leu Ala Ala Leu Asn Ala His Ser Asp Cys Cys Arg Lys Leu				
222	227	232	237	
tta tca tcg gga caa aag tat agc ata gta tcc ttg ttt agt aat gag				1130
Leu Ser Ser Gly Gln Lys Tyr Ser Ile Val Ser Leu Phe Ser Asn Glu				
238	243	248	253	
cac gtg ctg tct gca ggc ttt gaa ata gac acc cca gat aaa ttt gga				1178
His Val Leu Ser Ala Gly Phe Glu Ile Asp Thr Pro Asp Lys Phe Gly				
254	259	264	269	
aga acg tgc ctt cat gct gct gct gca gga ggt aat gtg gaa tgt ata				1226
Arg Thr Cys Leu His Ala Ala Ala Ala Gly Gly Asn Val Glu Cys Ile				
270	275	280	285	
aaa ctc ttg cag agc agc gga gca gat ttc cat aaa aag gac aag tgt				1274
Lys Leu Leu Gln Ser Ser Gly Ala Asp Phe His Lys Lys Asp Lys Cys				
286	291	296	301	
ggg agg acc cct ttg cac tat gca gct gcg aat tgt cat ttc cac tgt				1322
Gly Arg Thr Pro Leu His Tyr Ala Ala Ala Asn Cys His Phe His Cys				
302	307	312	317	
att gag aca tta gtg acc aca ggg gcc aac gtt aat gaa aca gat gac				1370
Ile Glu Thr Leu Val Thr Thr Gly Ala Asn Val Asn Glu Thr Asp Asp				
318	323	328	333	
tgg gga cgc aca gct ttg cat tac gcc gct gca tca gac atg gat aga				1418
Trp Gly Arg Thr Ala Leu His Tyr Ala Ala Ala Ser Asp Met Asp Arg				
334	339	344	349	
aat aag act atc tta gga aat gcc cat gat aat tca gaa gaa ctt gaa				1466
Asn Lys Thr Ile Leu Gly Asn Ala His Asp Asn Ser Glu Glu Leu Glu				
350	355	360	365	
aga gcc agg gag ctg aag gaa aag gaa gcc aca cta tgt cta gag ttt				1514
Arg Ala Arg Glu Leu Lys Glu Lys Glu Ala Thr Leu Cys Leu Glu Phe				
366	371	376	381	
ctg ctt caa aat gat gca aat cca tct atc cgg gac aag gaa ggt tac				1562
Leu Leu Gln Asn Asp Ala Asn Pro Ser Ile Arg Asp Lys Glu Gly Tyr				
382	387	392	397	
aat agc ata cat tat gct gcc gcc tat ggg cac agg cag tgt ctg gaa				1610
Asn Ser Ile His Tyr Ala Ala Ala Tyr Gly His Arg Gln Cys Leu Glu				
398	403	408	413	
ttg ctt ttg gaa aga aca aac agt gga ttt gaa gaa tca gat tct ggt				1658
Leu Leu Leu Glu Arg Thr Asn Ser Gly Phe Glu Glu Ser Asp Ser Gly				
414	419	424	429	
gct act aag agt cca ctc cac tta gct gcc tac aat ggg cac cat caa				1706
Ala Thr Lys Ser Pro Leu His Leu Ala Ala Tyr Asn Gly His His Gln				
430	435	440	445	

gcc ttg gaa gtc ctt ctg cag tgc ttg gtg gac ctg gac atc agg gat	1754
Ala Leu Glu Val Leu Leu Gln Ser Leu Val Asp Leu Asp Ile Arg Asp	
446 451 456 461	
gag aaa ggc cgc act gct ctg gat ctg gct gcc ttt aaa gga cac aca	1802
Glu Lys Gly Arg Thr Ala Leu Asp Leu Ala Phe Lys Gly His Thr	
462 467 472 477	
gaa tgt gtg gaa ggc ctt atc aat cag ggc gca tcc atc ttt gtg aaa	1850
Glu Cys Val Glu Ala Leu Ile Asn Gln Gly Ala Ser Ile Phe Val Lys	
478 483 488 493	
gac aat gta acc aaa aga acc cca ctt cat gcc tca gta att aat ggt	1898
Asp Asn Val Thr Lys Arg Thr Pro Leu His Ala Ser Val Ile Asn Gly	
494 499 504 509	
cac aca ctg tgt tta cgg ctg ttg cta gaa att gca gac aac ccg gag	1946
His Thr Leu Cys Leu Arg Leu Leu Leu Glu Ile Ala Asp Asn Pro Glu	
510 515 520 525	
gcg gtc gat gtg aaa gat gcc aaa gga caa aca cca ctg atg ctt gca	1994
Ala Val Asp Val Lys Asp Ala Lys Gly Gln Thr Pro Leu Met Leu Ala	
526 531 536 541	
gta gca tat gga cat att gac gct gtt tca ttg tta ctt gaa aag gaa	2042
Val Ala Tyr Gly His Ile Asp Ala Val Ser Leu Leu Leu Glu Lys Glu	
542 547 552 557	
gcc aac gta gac act gtt gac atc cta gga tgc aca gct tta cac aga	2090
Ala Asn Val Asp Thr Val Asp Ile Leu Gly Cys Thr Ala Leu His Arg	
558 563 568 573	
ggg att atg aca gga cac gag gaa tgt gtg caa atg ctg ctg gaa caa	2138
Gly Ile Met Thr Gly His Glu Glu Cys Val Gln Met Leu Leu Glu Gln	
574 579 584 589	
gaa gtg tca att ctc tgt aaa gat tcc aga ggg agg acg ccc ttg cac	2186
Glu Val Ser Ile Leu Cys Lys Asp Ser Arg Gly Arg Thr Pro Leu His	
590 595 600 605	
tat gca gct gct cgt ggc cac gcc acg tgg ctg agc gag ctg ctc caa	2234
Tyr Ala Ala Ala Arg Gly His Ala Thr Trp Leu Ser Glu Leu Leu Gln	
606 611 616 621	
atg gct ctt tct gag gag gac tgt tgt ttc aaa gat aac caa ggc tac	2282
Met Ala Leu Ser Glu Glu Asp Cys Cys Phe Lys Asp Asn Gln Gly Tyr	
622 627 632 637	
acg ccg ctg cac tgg gct tgt tac aat ggt aat gaa aac tgt ata gag	2330
Thr Pro Leu His Trp Ala Cys Tyr Asn Gly Asn Glu Asn Cys Ile Glu	
638 643 648 653	
gta ctt ttg gag caa aaa tgt ttt cgc aaa ttt atc ggt aat ccc ttt	2378
Val Leu Leu Glu Gln Lys Cys Phe Arg Lys Phe Ile Gly Asn Pro Phe	
654 659 664 669	

act cca ctg cac tgt gca ata atc aat gat cat ggg aat tgt gca tca	2426
Thr Pro Leu His Cys Ala Ile Ile Asn Asp His Gly Asn Cys Ala Ser	
670 675 680 685	
ttg ctg ctt ggg gcc ata gat tcc agt atc gtc agt tgt aga gat gac	2474
Leu Leu Leu Gly Ala Ile Asp Ser Ser Ile Val Ser Cys Arg Asp Asp	
686 691 696 701	
aaa ggc agg aca ccc ctt cat gcg gca gca ttt gct gat cat gtg gag	2522
Lys Gly Arg Thr Pro Leu His Ala Ala Ala Phe Ala Asp His Val Glu	
702 707 712 717	
tgc ttg cag ctt ctt ctg aga cac agt gct cca gtg aac gca gta gat	2570
Cys Leu Gln Leu Leu Leu Arg His Ser Ala Pro Val Asn Ala Val Asp	
718 723 728 733	
aat tca ggg aaa aca gca ctg atg atg gct gct gag aat ggg cag gca	2618
Asn Ser Gly Lys Thr Ala Leu Met Met Ala Ala Glu Asn Gly Gln Ala	
734 739 744 749	
ggc gct gtg gat att ttg gtg aac agt gcc cag gct gat ctg act gta	2666
Gly Ala Val Asp Ile Leu Val Asn Ser Ala Gln Ala Asp Leu Thr Val	
750 755 760 765	
aag gat aag gac ttg aat aca ccc tta cat ttg gct tgt agt aaa ggt	2714
Lys Asp Lys Asp Leu Asn Thr Pro Leu His Leu Ala Cys Ser Lys Gly	
766 771 776 781	
cat gaa aaa tgt gcc ttg tta ata ctt gac aag ata caa gac gag agc	2762
His Glu Lys Cys Ala Leu Leu Ile Leu Asp Lys Ile Gln Asp Glu Ser	
782 787 792 797	
ctt att aat gaa aaa aat aat gca ctg cag aca ccc ctc cac gtc gct	2810
Leu Ile Asn Glu Lys Asn Asn Ala Leu Gln Thr Pro Leu His Val Ala	
798 803 808 813	
gcg cgc aat ggc tta aag gtg gta gtt gag gag ttg ctg gcc aaa ggg	2858
Ala Arg Asn Gly Leu Lys Val Val Val Glu Glu Leu Leu Ala Lys Gly	
814 819 824 829	
gcc tgt gta ctt gct gta gat gaa aat ggc tgt taa	2894
Ala Cys Val Leu Ala Val Asp Glu Asn Gly Cys *	
830 835 840	

<210> 96
 <211> 1522
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (158)..(1303)

<400> 96

atttggccct cgaggccaaa aattcggcac gagggattat ttacaaaatg gactgcttag	60
tacgtgtoga gaactttctc gagccactgc cgaattggaa cgagcatgga gagaatatga	120
taagttagaa tacgatgtaa ctgttaccag gaaccag atg caa gag cag ctg gat	175
Met Gln Glu Gln Leu Asp	
1	
cac ctt ggt gaa gtt cag acg gaa tca gca gga att cag cgt gca cag	223
His Leu Gly Glu Val Gln Thr Glu Ser Ala Gly Ile Gln Arg Ala Gln	
7 12 17 22	
att cag aaa gaa ctt tgg cga att cag gat gtc atg gaa ggg ctg agt	271
Ile Gln Lys Glu Leu Trp Arg Ile Gln Asp Val Met Glu Gly Leu Ser	
23 28 33 38	
aaa cat aag cag caa aga ggt act aca gaa ata ggt atg ata gga tca	319
Lys His Lys Gln Gln Arg Gly Thr Thr Glu Ile Gly Met Ile Gly Ser	
39 44 49 54	
aag cct ttc tca aca gtt aag tac aaa aat gag ggt cca gat tat aga	367
Lys Pro Phe Ser Thr Val Lys Tyr Lys Asn Glu Gly Pro Asp Tyr Arg	
55 60 65 70	
ctc tac aag agt gaa cca gag tta aca aca gtg gca gaa gtt gat gaa	415
Leu Tyr Lys Ser Glu Pro Glu Leu Thr Thr Val Ala Glu Val Asp Glu	
71 76 81 86	
tct aat gga gaa gaa aaa tca gaa cct gtt tca gag ata gaa act tca	463
Ser Asn Gly Glu Glu Lys Ser Glu Pro Val Ser Glu Ile Glu Thr Ser	
87 92 97 102	
gtt gtt aaa ggt tcc cac ttt cct gtt gga gta gtc cct cca aga gca	511
Val Val Lys Gly Ser His Phe Pro Val Gly Val Val Pro Pro Arg Ala	
103 108 113 118	
aaa tca cca aca ccc gaa tct tcg aca ata gct tcc tat gta acc ttg	559
Lys Ser Pro Thr Pro Glu Ser Ser Thr Ile Ala Ser Tyr Val Thr Leu	
119 124 129 134	
agg aaa act aag aag atg atg gat cta aga acg gaa aga cca aga agt	607
Arg Lys Thr Lys Lys Met Met Asp Leu Arg Thr Glu Arg Pro Arg Ser	
135 140 145 150	
gca gtg gaa cag ctc tgt ttg gct gaa agt act cga cca agg atg act	655
Ala Val Glu Gln Leu Cys Leu Ala Glu Ser Thr Arg Pro Arg Met Thr	
151 156 161 166	
gtg gaa gag caa atg gaa aga ata aga aga cat caa caa gcg tgc ctg	703
Val Glu Glu Gln Met Glu Arg Ile Arg Arg His Gln Gln Ala Cys Leu	
167 172 177 182	
agg gag aag aaa aaa ggg tta aat gtt atc ggt gct tca gac cag tca	751
Arg Glu Lys Lys Lys Gly Leu Asn Val Ile Gly Ala Ser Asp Gln Ser	
183 188 193 198	

ccc tta caa agc cct tca aat tta agg gat aat cca ttt agg act act	799
Pro Leu Gln Ser Pro Ser Asn Leu Arg Asp Asn Pro Phe Arg Thr Thr	
199 204 209 214	
cag act cga agg agg gat gat aag gaa ctg gac act gcc att aga gaa	847
Gln Thr Arg Arg Arg Asp Asp Lys Glu Leu Asp Thr Ala Ile Arg Glu	
215 220 225 230	
aat gat gta aag cca gac cat gaa act cct gca aca gaa att gtt caa	895
Asn Asp Val Lys Pro Asp His Glu Thr Pro Ala Thr Glu Ile Val Gln	
231 236 241 246	
cta aaa gaa acc gaa ccc caa aat gtg gac ttc agc aaa gag tta aaa	943
Leu Lys Glu Thr Glu Pro Gln Asn Val Asp Phe Ser Lys Glu Leu Lys	
247 252 257 262	
aaa act gaa aac att tca tat gaa atg ctt ttt gaa cct gag cca aat	991
Lys Thr Glu Asn Ile Ser Tyr Glu Met Leu Phe Glu Pro Glu Pro Asn	
263 268 273 278	
gga gta aat tct gtg gaa atg atg gat aaa gaa aga aac aaa gac aaa	1039
Gly Val Asn Ser Val Glu Met Met Asp Lys Glu Arg Asn Lys Asp Lys	
279 284 289 294	
atg cct gag gat gtt aca ttc agc cct caa gat gaa aca cag acc gca	1087
Met Pro Glu Asp Val Thr Phe Ser Pro Gln Asp Glu Thr Gln Thr Ala	
295 300 305 310	
aat cat aaa cca gaa gag cat cct gaa gaa aat aca aag aac agt gtt	1135
Asn His Lys Pro Glu Glu His Pro Glu Glu Asn Thr Lys Asn Ser Val	
311 316 321 326	
gac gaa cag gaa gaa act gtt att tct tac gaa tca act cct gag gtt	1183
Asp Glu Gln Glu Glu Thr Val Ile Ser Tyr Glu Ser Thr Pro Glu Val	
327 332 337 342	
tct aga gga aat caa aca atg gca gtg aaa agt ctg tcc cca tct cct	1231
Ser Arg Gly Asn Gln Thr Met Ala Val Lys Ser Leu Ser Pro Ser Pro	
343 348 353 358	
gag tcc tcg gca tcg cca gtt cca tcc act cag ccg cag ctc aca gaa	1279
Glu Ser Ser Ala Ser Pro Val Pro Ser Thr Gln Pro Gln Leu Thr Glu	
359 364 369 374	
gga tca cat ttc atg tgt gtg tag tcttagaaga actatactga cttctgttga	1333
Gly Ser His Phe Met Cys Val *	
375 380	
aaccattcaa agctaaagac atggaccttc agcagtgtaa gaagatattg tacagtatat	1393
tttaaattcta tgaaattcat agttctgatg cttttgggtca cagagcatca ttttatcact	1453
tctggaaaaa tgtttattcc aaaacagctt taatggccca tatgtacacc ttcgtaatct	1513
tcaaggtta	1522

<210> 97
 <211> 1202
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (155) .. (976)

<400> 97

```

atttggccct cgaggccaag aattcggcac gagaactgga agagcaggtg aagaggctcc      60
ttgggtgggc acccctggcg tctctccatg agggcagcct cacaggggtg tctgcctgtg      120
agttttgtta cagggcctca ccaagagagg gcct      atg gag gcc gag gac cag      172
                                         Met Glu Ala Glu Asp Gln
                                         1
ggg gag ctt ttc ctg cac ctc cgg tca gtg gca cgt gcc ccc cag acc      220
Gly Glu Leu Phe Leu His Leu Arg Ser Val Ala Arg Ala Pro Gln Thr
   7              12              17              22
tta tct atg cac cga ctc cag aga aag ctg aag gag gca gcc aga aaa      268
Leu Ser Met His Arg Leu Gln Arg Lys Leu Lys Glu Ala Ala Arg Lys
  23              28              33              38
atc atc agc ctc cgc ctg gag aaa gag cag ctc atc gag atg ggg aac      316
Ile Ile Ser Leu Arg Leu Glu Lys Glu Gln Leu Ile Glu Met Gly Asn
  39              44              49              54
agg ctc cgt gca gag ctg ggc cga ccc gaa agg tgg ctg ttg cac cac      364
Arg Leu Arg Ala Glu Leu Gly Arg Pro Glu Arg Trp Leu Leu His His
  55              60              65              70
gcc ctc cct cct gcc cct gag gcc cgg aag cca ggc gag gag ccc agg      412
Ala Leu Pro Pro Ala Pro Glu Ala Arg Lys Pro Gly Glu Glu Pro Arg
  71              76              81              86
agg cct ttg gat cgc agc cca cct ttg gga cag gtg cag ccc cat ttt      460
Arg Pro Leu Asp Arg Ser Pro Pro Leu Gly Gln Val Gln Pro His Phe
  87              92              97              102
aca tct cag gac gcc aag agt gcc gag gat gag gct cct tcc aga cac      508
Thr Ser Gln Asp Ala Lys Ser Ala Glu Asp Glu Ala Pro Ser Arg His
 103              108              113              118
ttg gga aag cac cag ccc cgc tca gca cag gtg ggc agc aga ctt gac      556
Leu Gly Lys His Gln Pro Arg Ser Ala Gln Val Gly Ser Arg Leu Asp
 119              124              129              134
gcc ctg caa ggc ccg aag aca caa cac agc atc cac acg gtg acc tgt      604
Ala Leu Gln Gly Pro Lys Thr Gln His Ser Ile His Thr Val Thr Cys
 135              140              145              150
aaa tca cct cgg cag aaa gaa gac agg tcc cca aag cca ccc cag gct      652

```

Lys Ser Pro Arg Gln Lys Glu Asp Arg Ser Pro Lys Pro Pro Gln Ala	
151 156 161 166	
ccc cag cac cct gag gag cat ggt cgc caa tcc cac agc tcc tcc tcc	700
Pro Gln His Pro Glu Glu His Gly Arg Gln Ser His Ser Ser Ser Ser	
167 172 177 182	
ttt gcc agt ggc acc ctc cag gac atg tgg agg ttg cta gac ctg gga	748
Phe Ala Ser Gly Thr Leu Gln Asp Met Trp Arg Leu Leu Asp Leu Gly	
183 188 193 198	
tcc agc cct tct ggt gtc acc tcc cag ggt gac tca act cca gag ctc	796
Ser Ser Pro Ser Gly Val Thr Ser Gln Gly Asp Ser Thr Pro Glu Leu	
199 204 209 214	
cca gct cct oca gca gcc gac agg agg ccc gtc aag atg cag gca ggc	844
Pro Ala Pro Pro Ala Ala Asp Arg Arg Pro Val Lys Met Gln Ala Gly	
215 220 225 230	
att gcc acc cca ggg atg aag aca gca gcc cag gca aag gcc aag acc	892
Ile Ala Thr Pro Gly Met Lys Thr Ala Ala Gln Ala Lys Ala Lys Thr	
231 236 241 246	
aca gga gcc tcc cgg tct cat cct gca aaa gct aaa ggc tgc cag agg	940
Thr Gly Ala Ser Arg Ser His Pro Ala Lys Ala Lys Gly Cys Gln Arg	
247 252 257 262	
ccc ccc aag atc cgt aac tac aac att atg gac tga cttc ctccccccac	990
Pro Pro Lys Ile Arg Asn Tyr Asn Ile Met Asp *	
263 268 273	
ccccccccac taaggggtgc tcgggggcctc cgcattggtgc ctgtgctttc acctacgtgt	1050
tgtggggggg tgtgggcaca gcgtgcaggg tggaggcagg gagctgcagg gcaggctccc	1110
aaatgctgct gaggcgaccc tgctgactga aggcctccct gagcacaggg cccattaaaa	1170
ccaggttcct ccctggggaa aaaaaaaaaa aa	1202

<210> 98
 <211> 6314
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(5379)

<400> 98	
atg gcc cca gaa tcc cat ata tta gct tct aac acc atg gag acc cat	48
Met Ala Pro Glu Ser His Ile Leu Ala Ser Asn Thr Met Glu Thr His	
1 5 10	
ata tta gca tcc aac acc atg gac tcc caa atg cta gcg tcc aac acc	96

Ile	Leu	Ala	Ser	Asn	Thr	Met	Asp	Ser	Gln	Met	Leu	Ala	Ser	Asn	Thr		
17					22					27					32		
atg	gac	tcc	cag	atg	cta	gca	tcc	aac	acc	atg	gac	tcc	cag	atg	tta	144	
Met	Asp	Ser	Gln	Met	Leu	Ala	Ser	Asn	Thr	Met	Asp	Ser	Gln	Met	Leu		
33					38					43					48		
gcg	tct	agc	acc	atg	gac	tcc	cag	atg	tta	gca	act	agc	tcc	atg	gac	192	
Ala	Ser	Ser	Thr	Met	Asp	Ser	Gln	Met	Leu	Ala	Thr	Ser	Ser	Met	Asp		
49					54					59					64		
tcc	caa	atg	cta	gcg	tcc	aac	acc	atg	gac	tcc	cag	atg	cta	gca	tcc	240	
Ser	Gln	Met	Leu	Ala	Ser	Asn	Thr	Met	Asp	Ser	Gln	Met	Leu	Ala	Ser		
65					70					75					80		
aac	acc	atg	gac	tcc	cag	atg	tta	gcg	tct	agc	acc	atg	gac	tcc	cag	288	
Asn	Thr	Met	Asp	Ser	Gln	Met	Leu	Ala	Ser	Ser	Thr	Met	Asp	Ser	Gln		
81					86					91					96		
atg	tta	gca	act	agc	tcc	atg	gac	tcc	cag	atg	tta	gca	act	agc	tcc	336	
Met	Leu	Ala	Thr	Ser	Ser	Met	Asp	Ser	Gln	Met	Leu	Ala	Thr	Ser	Ser		
97					102					107					112		
atg	gac	tcc	cag	atg	tta	gca	act	agc	act	atg	gac	tcc	cag	atg	tta	384	
Met	Asp	Ser	Gln	Met	Leu	Ala	Thr	Ser	Thr	Met	Asp	Ser	Gln	Met	Leu		
113					118					123					128		
gca	acc	agt	tcc	atg	gac	tcc	cag	atg	tta	gca	acc	agc	tcc	atg	gac	432	
Ala	Thr	Ser	Ser	Met	Asp	Ser	Gln	Met	Leu	Ala	Thr	Ser	Ser	Met	Asp		
129					134					139					144		
tcc	cag	atg	tta	gca	acc	agc	tcc	atg	gac	tcc	cag	atg	tta	gca	acc	480	
Ser	Gln	Met	Leu	Ala	Thr	Ser	Ser	Met	Asp	Ser	Gln	Met	Leu	Ala	Thr		
145					150					155					160		
agc	tcc	atg	gac	tcc	cag	atg	tta	gca	acc	agc	acc	atg	gat	tct	cag	528	
Ser	Ser	Met	Asp	Ser	Gln	Met	Leu	Ala	Thr	Ser	Thr	Met	Asp	Ser	Gln		
161					166					171					176		
atg	tta	gca	acc	agc	acc	atg	gac	tcc	cag	atg	tta	gca	act	agc	tca	576	
Met	Leu	Ala	Thr	Ser	Thr	Met	Asp	Ser	Gln	Met	Leu	Ala	Thr	Ser	Ser		
177					182					187					192		
atg	gat	tcc	cag	atg	tta	gca	tct	ggc	act	atg	gac	tct	caa	atg	tta	624	
Met	Asp	Ser	Gln	Met	Leu	Ala	Ser	Gly	Thr	Met	Asp	Ser	Gln	Met	Leu		
193					198					203					208		
gct	tct	ggc	acc	atg	gat	gct	cag	atg	tta	gcg	tct	ggg	acc	atg	gat	672	
Ala	Ser	Gly	Thr	Met	Asp	Ala	Gln	Met	Leu	Ala	Ser	Gly	Thr	Met	Asp		
209					214					219					224		
gcc	cag	atg	tta	gcg	tct	agt	acc	caa	gat	tct	gct	atg	ttg	ggg	tca	720	
Ala	Gln	Met	Leu	Ala	Ser	Ser	Thr	Gln	Asp	Ser	Ala	Met	Leu	Gly	Ser		
225					230					235					240		
aaa	tct	cct	gat	ccc	tat	agg	tta	gct	cag	gat	cct	tac	agg	tta	gct	768	
Lys	Ser	Pro	Asp	Pro	Tyr	Arg	Leu	Ala	Gln	Asp	Pro	Tyr	Arg	Leu	Ala		

241	246	251	256	
cag gat ccc tat agg ttg ggc cat gac ccc tat aga tta ggt cat gat				816
Gln Asp Pro Tyr Arg Leu Gly His Asp Pro Tyr Arg Leu Gly His Asp				
257	262	267	272	
gct tac agg tta gga caa gac cct tat aga tta ggc cat gat ccc tac				864
Ala Tyr Arg Leu Gly Gln Asp Pro Tyr Arg Leu Gly His Asp Pro Tyr				
273	278	283	288	
aga cta act cct gat ccc tat agg atg tca cct aga ccc tac agg ata				912
Arg Leu Thr Pro Asp Pro Tyr Arg Met Ser Pro Arg Pro Tyr Arg Ile				
289	294	299	304	
gca ccc agg tcc tat aga ata gca ccc agg cca tat agg tta gca cct				960
Ala Pro Arg Ser Tyr Arg Ile Ala Pro Arg Pro Tyr Arg Leu Ala Pro				
305	310	315	320	
aga ccc ctg atg tta gca tct aga cgt tct atg atg atg tcc tat gct				1008
Arg Pro Leu Met Leu Ala Ser Arg Arg Ser Met Met Met Ser Tyr Ala				
321	326	331	336	
gca gaa cgt tcc atg atg tca tct tac gaa cgc tct atg atg tct tat				1056
Ala Glu Arg Ser Met Met Ser Ser Tyr Glu Arg Ser Met Met Ser Tyr				
337	342	347	352	
gag cgg tct atg atg tcc cct atg gct gaa cgc tct atg atg tca gcc				1104
Glu Arg Ser Met Met Ser Pro Met Ala Glu Arg Ser Met Met Ser Ala				
353	358	363	368	
tac gag cgc tct atg atg tca gcc tac gag cgc tct atg atg tcc cct				1152
Tyr Glu Arg Ser Met Met Ser Ala Tyr Glu Arg Ser Met Met Ser Pro				
369	374	379	384	
atg gct gag cgc tct atg atg tca gct tat gaa cgc tcc atg atg tca				1200
Met Ala Glu Arg Ser Met Met Ser Ala Tyr Glu Arg Ser Met Met Ser				
385	390	395	400	
gct tat gaa cgc tcc atg atg tcc cca atg gct gat cga tct atg atg				1248
Ala Tyr Glu Arg Ser Met Met Ser Pro Met Ala Asp Arg Ser Met Met				
401	406	411	416	
tcc atg ggt gct gac cgg tct atg atg tcc tca tac tct gct gct gac				1296
Ser Met Gly Ala Asp Arg Ser Met Met Ser Ser Tyr Ser Ala Ala Asp				
417	422	427	432	
cgg tct atg atg tca tcc tac tct gca gct gac cga tct atg atg tca				1344
Arg Ser Met Met Ser Ser Tyr Ser Ala Ala Asp Arg Ser Met Met Ser				
433	438	443	448	
tct tat act gct gat cgt tca atg atg tct atg gct gct gat tct tac				1392
Ser Tyr Thr Ala Asp Arg Ser Met Met Ser Met Ala Ala Asp Ser Tyr				
449	454	459	464	
acc gat tct tac act gac aca tat aca gag gca tat atg gtg cca cct				1440
Thr Asp Ser Tyr Thr Asp Thr Tyr Thr Glu Ala Tyr Met Val Pro Pro				
465	470	475	480	

ttg cct cct gaa gag ccc cca aca atg cca ccg ttg cca cct gag gag	1488
Leu Pro Pro Glu Glu Pro Pro Thr Met Pro Pro Leu Pro Pro Glu Glu	
481 486 491 496	
cca cca atg aca cca cca ttg cct cct gag gaa cca cca gag ggt cca	1536
Pro Pro Met Thr Pro Pro Leu Pro Pro Glu Glu Pro Pro Glu Gly Pro	
497 502 507 512	
gca ttg ccc act gag cag tca gca tta aca gct gaa aat act tgg cct	1584
Ala Leu Pro Thr Glu Gln Ser Ala Leu Thr Ala Glu Asn Thr Trp Pro	
513 518 523 528	
aca gag gtg cca tca tta cca tct gaa gag tct gta tcg cag cct gag	1632
Thr Glu Val Pro Ser Leu Pro Ser Glu Glu Ser Val Ser Gln Pro Glu	
529 534 539 544	
cct cct gtg agt caa agt gag att tcg gag cct tca gca gtg cct act	1680
Pro Pro Val Ser Gln Ser Glu Ile Ser Glu Pro Ser Ala Val Pro Thr	
545 550 555 560	
gat tat tca gtg tca gca tca gat ccc tca gtt tta gta tca gag gct	1728
Asp Tyr Ser Val Ser Ala Ser Asp Pro Ser Val Leu Val Ser Glu Ala	
561 566 571 576	
gct gtg act gtt cca gaa cca cca cca gag cca gaa tct tca att acg	1776
Ala Val Thr Val Pro Glu Pro Pro Pro Glu Pro Glu Ser Ser Ile Thr	
577 582 587 592	
tta aca cct gta gag tct gca gta gta gca gaa gaa cat gaa gtt gtt	1824
Leu Thr Pro Val Glu Ser Ala Val Val Ala Glu Glu His Glu Val Val	
593 598 603 608	
cca gag aga cca gtg act tgt atg gta tct gaa act ccc gcc atg tca	1872
Pro Glu Arg Pro Val Thr Cys Met Val Ser Glu Thr Pro Ala Met Ser	
609 614 619 624	
gct gaa cca act gtg tta gca tca gag cct cct gtt atg tca gag aca	1920
Ala Glu Pro Thr Val Leu Ala Ser Glu Pro Pro Val Met Ser Glu Thr	
625 630 635 640	
gca gaa aca ttt gat tcc atg aga gcc tca gga cat gtt gcc tca gaa	1968
Ala Glu Thr Phe Asp Ser Met Arg Ala Ser Gly His Val Ala Ser Glu	
641 646 651 656	
gta tct aca tcc ttg ttg gtt cca gca gta act act cca gtg ctg gca	2016
Val Ser Thr Ser Leu Leu Val Pro Ala Val Thr Thr Pro Val Leu Ala	
657 662 667 672	
gag agc att ctg gag ccg cca gcc atg gct gcc cca gag tct tca gct	2064
Glu Ser Ile Leu Glu Pro Pro Ala Met Ala Ala Pro Glu Ser Ser Ala	
673 678 683 688	
atg gct gtc ctg gag tct tcg gct gtg acc gtc ctg gag tct tcg act	2112
Met Ala Val Leu Glu Ser Ser Ala Val Thr Val Leu Glu Ser Ser Thr	
689 694 699 704	

gtg act gtc ctg gag tct tcg act gta act gtc ctg gag cct tcg gtt	2160
Val Thr Val Leu Glu Ser Ser Thr Val Thr Val Leu Glu Pro Ser Val	
705 710 715 720	
gtg act gtc ccg gag cct cct gtt gtg gct gag cca gac tct gtt acc	2208
Val Thr Val Pro Glu Pro Pro Val Val Ala Glu Pro Asp Ser Val Thr	
721 726 731 736	
att cct gtg cca gtt gtt tct gcg ctg gag cct tct gtg cct gtt ctg	2256
Ile Pro Val Pro Val Val Ser Ala Leu Glu Pro Ser Val Pro Val Leu	
737 742 747 752	
gaa cca gcg gtg tca gtc ctt caa cct tct atg att gtt tca gaa cca	2304
Glu Pro Ala Val Ser Val Leu Gln Pro Ser Met Ile Val Ser Glu Pro	
753 758 763 768	
tct gtt tct gtc cag gaa tcg act gtg aca gtt tca gag cct gct gtc	2352
Ser Val Ser Val Gln Glu Ser Thr Val Thr Val Ser Glu Pro Ala Val	
769 774 779 784	
aca gtc tca gag cag act caa gta ata cca act gag gtg gct ata gag	2400
Thr Val Ser Glu Gln Thr Gln Val Ile Pro Thr Glu Val Ala Ile Glu	
785 790 795 800	
tcc aca cca atg ata ctg gaa tct agt atc atg tca tca cat gtt atg	2448
Ser Thr Pro Met Ile Leu Glu Ser Ser Ile Met Ser Ser His Val Met	
801 806 811 816	
aaa gga att aat cta tcc tct ggt gat caa att ctt gct cca gag att	2496
Lys Gly Ile Asn Leu Ser Ser Gly Asp Gln Ile Leu Ala Pro Glu Ile	
817 822 827 832	
ggc atg cag gag att gca ttg cat tca ggt gaa gaa cca cat gct gag	2544
Gly Met Gln Glu Ile Ala Leu His Ser Gly Glu Glu Pro His Ala Glu	
833 838 843 848	
gaa cac ctg aaa ggt gac ttt tac gaa agt gaa cat ggt ata aat ata	2592
Glu His Leu Lys Gly Asp Phe Tyr Glu Ser Glu His Gly Ile Asn Ile	
849 854 859 864	
gac ctt aat ata aat agt cat tta att gct aaa gag atg gaa cat aat	2640
Asp Leu Asn Ile Asn Ser His Leu Ile Ala Lys Glu Met Glu His Asn	
865 870 875 880	
aca gtg tgt gct gct ggt act agt cct gtt ggg gaa att ggt gaa gag	2688
Thr Val Cys Ala Ala Gly Thr Ser Pro Val Gly Glu Ile Gly Glu Glu	
881 886 891 896	
aaa att ttg ccc acc agt gag act aaa cag cgc aca gta ttg gat acc	2736
Lys Ile Leu Pro Thr Ser Glu Thr Lys Gln Arg Thr Val Leu Asp Thr	
897 902 907 912	
tac cct ggt gtt agt gaa gct gat gca gga gaa act cta tct tct act	2784
Tyr Pro Gly Val Ser Glu Ala Asp Ala Gly Glu Thr Leu Ser Ser Thr	
913 918 923 928	
ggc cct ttt gct ctg gaa cct gat gca aca gga act agt aag ggt att	2832

Gly	Pro	Phe	Ala	Leu	Glu	Pro	Asp	Ala	Thr	Gly	Thr	Ser	Lys	Gly	Ile	
929					934					939					944	
gaa ttt acc aca gca tct act ctc agt tta gtt aat aaa tat gat gtt																2880
Glu	Phe	Thr	Thr	Ala	Ser	Thr	Leu	Ser	Leu	Val	Asn	Lys	Tyr	Asp	Val	
945					950					955					960	
gat tta tct tta act act caa gat act gaa cat gac atg gta ata att																2928
Asp	Leu	Ser	Leu	Thr	Thr	Gln	Asp	Thr	Glu	His	Asp	Met	Val	Ile	Ile	
961					966					971					976	
tcc acc agt cct agt ggt ggt agt gaa gct gac att gaa ggg cct ttg																2976
Ser	Thr	Ser	Pro	Ser	Gly	Gly	Ser	Glu	Ala	Asp	Ile	Glu	Gly	Pro	Leu	
977					982					987					992	
cct gct aaa gat att cat ctt gat tta cca tct aat aat aac ctt gtt																3024
Pro	Ala	Lys	Asp	Ile	His	Leu	Asp	Leu	Pro	Ser	Asn	Asn	Asn	Leu	Val	
993					998					1003					1008	
agt aag gat aca gaa gaa cca tta cct gta aaa gag agt gac cag aca																3072
Ser	Lys	Asp	Thr	Glu	Glu	Pro	Leu	Pro	Val	Lys	Glu	Ser	Asp	Gln	Thr	
1009					1014					1019					1024	
ata gca gcc ttg ctc agc cct aaa gaa agt agt gga gga gaa aaa gaa																3120
Ile	Ala	Ala	Leu	Leu	Ser	Pro	Lys	Glu	Ser	Ser	Gly	Gly	Glu	Lys	Glu	
1025					1030					1035					1040	
gta cct ccc cct cct aaa gag aca ctg cct gat tca gga ttt tct gcc																3168
Val	Pro	Pro	Pro	Pro	Lys	Glu	Thr	Leu	Pro	Asp	Ser	Gly	Phe	Ser	Ala	
1041					1046					1051					1056	
aat att gag gat att aat gaa gca gat tta gtg aga ccg tta ctt cct																3216
Asn	Ile	Glu	Asp	Ile	Asn	Glu	Ala	Asp	Leu	Val	Arg	Pro	Leu	Leu	Pro	
1057					1062					1067					1072	
aag gac atg gaa cgt ctt aca agc ctt aga gct ggc att gaa gga cct																3264
Lys	Asp	Met	Glu	Arg	Leu	Thr	Ser	Leu	Arg	Ala	Gly	Ile	Glu	Gly	Pro	
1073					1078					1083					1088	
tta ctt gca agt gat gtt gga cgt gac aga tct gct gcc agc ccg gtt																3312
Leu	Leu	Ala	Ser	Asp	Val	Gly	Arg	Asp	Arg	Ser	Ala	Ala	Ser	Pro	Val	
1089					1094					1099					1104	
gta agt agt atg cca gaa aga gct tca gag tct tct tca gag gaa aaa																3360
Val	Ser	Ser	Met	Pro	Glu	Arg	Ala	Ser	Glu	Ser	Ser	Ser	Glu	Glu	Lys	
1105					1110					1115					1120	
gat gat tat gaa att ttt gta aaa gtt aag gac act cac gaa aaa agc																3408
Asp	Asp	Tyr	Glu	Ile	Phe	Val	Lys	Val	Lys	Asp	Thr	His	Glu	Lys	Ser	
1121					1126					1131					1136	
aag aaa aat aag aac cgt gat aag ggg gag aaa gag aag aaa aga gat																3456
Lys	Lys	Asn	Lys	Asn	Arg	Asp	Lys	Gly	Glu	Lys	Glu	Lys	Lys	Arg	Asp	
1137					1142					1147					1152	
cct cat tta aga tct cga agt aag cgt tcc aaa tct tct gaa cac aaa																3504
Pro	His	Leu	Arg	Ser	Arg	Ser	Lys	Arg	Ser	Lys	Ser	Ser	Glu	His	Lys	

1153	1158	1163	1168	
tca cgc aag cgt acc agt gaa tct cgt tct agg gca aga aag aga tca				3552
Ser Arg Lys Arg Thr Ser Glu Ser Arg Ser Arg Ala Arg Lys Arg Ser				
1169	1174	1179	1184	
tct aag tcc aag tct cat cgc tct cag aca cgt tca cgg tca cgt tca				3600
Ser Lys Ser Lys Ser His Arg Ser Gln Thr Arg Ser Arg Ser Arg Ser				
1185	1190	1195	1200	
aga cgc agg agg aga agc agc aga tca aga tca aag tct aga gga aga				3648
Arg Arg Arg Arg Arg Ser Ser Arg Ser Arg Ser Lys Ser Arg Gly Arg				
1201	1206	1211	1216	
aga tct gta tca aaa gag aag cgc aaa aga tct cca aag cac aga tcc				3696
Arg Ser Val Ser Lys Glu Lys Arg Lys Arg Ser Pro Lys His Arg Ser				
1217	1222	1227	1232	
aag tct agg gaa aga aaa aga aaa aga tca agc tcc agg gat aac cga				3744
Lys Ser Arg Glu Arg Lys Arg Lys Arg Ser Ser Ser Arg Asp Asn Arg				
1233	1238	1243	1248	
aag aca gtt aga gct cga agt cga acc cca agt cgt cgg agt cgg agt				3792
Lys Thr Val Arg Ala Arg Ser Arg Thr Pro Ser Arg Arg Ser Arg Ser				
1249	1254	1259	1264	
cat act cca agt cgt cga cga agg tct aga tct gtg ggt aga aga agg				3840
His Thr Pro Ser Arg Arg Arg Arg Ser Arg Ser Val Gly Arg Arg Arg				
1265	1270	1275	1280	
agc ttt agc att tcc cca agc cgc cgc agc cgc acc ccc agc cgc cgc				3888
Ser Phe Ser Ile Ser Pro Ser Arg Arg Ser Arg Thr Pro Ser Arg Arg				
1281	1286	1291	1296	
agc cgc acc ccc agc cgc cgc agc cgc acc ccc agc cgc cgc agc cgc				3936
Ser Arg Thr Pro Ser Arg Arg Ser Arg Thr Pro Ser Arg Arg Ser Arg				
1297	1302	1307	1312	
acc ccc agc cgc cgg agc cgc acc cct agc cgt cgg agc cgc acc cca				3984
Thr Pro Ser Arg Arg Ser Arg Thr Pro Ser Arg Arg Ser Arg Thr Pro				
1313	1318	1323	1328	
agc cgc cgg aga aga tca agg tct gtg gta aga aga cga agc ttc agt				4032
Ser Arg Arg Arg Arg Ser Arg Ser Val Val Arg Arg Arg Ser Phe Ser				
1329	1334	1339	1344	
atc tca cca gtc aga tta agg cga tca aga aca ccc tta aga aga agg				4080
Ile Ser Pro Val Arg Leu Arg Arg Ser Arg Thr Pro Leu Arg Arg Arg				
1345	1350	1355	1360	
ttt agc aga tct ccc atc cgt cgt aaa aga tcc agg tct tct gaa cga				4128
Phe Ser Arg Ser Pro Ile Arg Arg Lys Arg Ser Arg Ser Ser Glu Arg				
1361	1366	1371	1376	
ggc aga tca ccc aaa cgt ctg aca gat ttg gat aag gct caa tta ctt				4176
Gly Arg Ser Pro Lys Arg Leu Thr Asp Leu Asp Lys Ala Gln Leu Leu				
1377	1382	1387	1392	

gaa ata gcc aaa gct aat gca gct gcc atg tgt gct aag gct ggt gtc	4224
Glu Ile Ala Lys Ala Asn Ala Ala Ala Met Cys Ala Lys Ala Gly Val	
1393 1398 1403 1408	
cct tta cca cca aac cta aag cct gca cct cca cct act ata gtt gag	4272
Pro Leu Pro Pro Asn Leu Lys Pro Ala Pro Pro Pro Thr Ile Val Glu	
1409 1414 1419 1424	
aaa gtt gct aaa aag tca gga gga gct act ata gaa gaa cta act gag	4320
Lys Val Ala Lys Lys Ser Gly Gly Ala Thr Ile Glu Glu Leu Thr Glu	
1425 1430 1435 1440	
aaa tgt aaa cag atc gca cag agt aaa gaa gat gat gat gta ata gtg	4368
Lys Cys Lys Gln Ile Ala Gln Ser Lys Glu Asp Asp Asp Val Ile Val	
1441 1446 1451 1456	
aat aaa cct cat gtt tcg gat gaa gag gaa gaa gaa cct cct ttt tat	4416
Asn Lys Pro His Val Ser Asp Glu Glu Glu Glu Glu Pro Pro Phe Tyr	
1457 1462 1467 1472	
cat cat ccc ttt aaa ctc agt gaa ttt aaa cct att ttt ttc aat ctg	4464
His His Pro Phe Lys Leu Ser Glu Phe Lys Pro Ile Phe Phe Asn Leu	
1473 1478 1483 1488	
aat att gct gca gca aaa cca act cca cca aaa agc cag gta aca tta	4512
Asn Ile Ala Ala Ala Lys Pro Thr Pro Pro Lys Ser Gln Val Thr Leu	
1489 1494 1499 1504	
aca aaa gaa ttc cct gta tca tct gga tct caa cat cgg aaa aaa gaa	4560
Thr Lys Glu Phe Pro Val Ser Ser Gly Ser Gln His Arg Lys Lys Glu	
1505 1510 1515 1520	
gcg gat agt gtt tat gga gaa tgg gtt cct gtg gag aaa aat ggt gaa	4608
Ala Asp Ser Val Tyr Gly Glu Trp Val Pro Val Glu Lys Asn Gly Glu	
1521 1526 1531 1536	
gaa aac aaa gat gat gat aat gtt ttc agc agc aat ttg ccc tca gag	4656
Glu Asn Lys Asp Asp Asp Asn Val Phe Ser Ser Asn Leu Pro Ser Glu	
1537 1542 1547 1552	
cct gtg gac atc tct aca gca atg agt gaa cgg gca ctt gct cag aaa	4704
Pro Val Asp Ile Ser Thr Ala Met Ser Glu Arg Ala Leu Ala Gln Lys	
1553 1558 1563 1568	
aga ctc agt gag aat gca ttt gat ctt gaa gcc atg agc atg tta aat	4752
Arg Leu Ser Glu Asn Ala Phe Asp Leu Glu Ala Met Ser Met Leu Asn	
1569 1574 1579 1584	
aga gct cag gaa agg att gat gcc tgg gct cag ctg aac tct att cct	4800
Arg Ala Gln Glu Arg Ile Asp Ala Trp Ala Gln Leu Asn Ser Ile Pro	
1585 1590 1595 1600	
ggc cag ttc aca gga agt aca gga gta cag gtt ttg aca caa gaa cag	4848
Gly Gln Phe Thr Gly Ser Thr Gly Val Gln Val Leu Thr Gln Glu Gln	
1601 1606 1611 1616	

ttg gcc aat act ggt gcc caa gcc tgg att aaa aag gat cag ttc tta	4896
Leu Ala Asn Thr Gly Ala Gln Ala Trp Ile Lys Lys Asp Gln Phe Leu	
1617 1622 1627 1632	
aga gca gcc ccg gta act gga gga atg gga gcc gtt ttg atg aga aaa	4944
Arg Ala Ala Pro Val Thr Gly Gly Met Gly Ala Val Leu Met Arg Lys	
1633 1638 1643 1648	
atg ggc tgg aga gaa gga gaa gga tta gga aaa aac aaa gaa ggc aat	4992
Met Gly Trp Arg Glu Gly Glu Gly Leu Gly Lys Asn Lys Glu Gly Asn	
1649 1654 1659 1664	
aag gaa ccc atc cta gtt gat ttt aag aca gac cga aaa ggt ctt gtt	5040
Lys Glu Pro Ile Leu Val Asp Phe Lys Thr Asp Arg Lys Gly Leu Val	
1665 1670 1675 1680	
gca gta gga gaa aga gca caa aag agg tct ggg aac ttc tct gct gca	5088
Ala Val Gly Glu Arg Ala Gln Lys Arg Ser Gly Asn Phe Ser Ala Ala	
1681 1686 1691 1696	
atg aaa gat ctg tca ggc aaa cat cct gtg tct gct ttg atg gag atc	5136
Met Lys Asp Leu Ser Gly Lys His Pro Val Ser Ala Leu Met Glu Ile	
1697 1702 1707 1712	
tgt aat aaa aga agg tgg caa cca cct gaa ttt cta ttg gtc cat gat	5184
Cys Asn Lys Arg Arg Trp Gln Pro Pro Glu Phe Leu Leu Val His Asp	
1713 1718 1723 1728	
agt ggc cct gat cat cgc aaa cat ttt ctc ttt agg gta ttg ata aat	5232
Ser Gly Pro Asp His Arg Lys His Phe Leu Phe Arg Val Leu Ile Asn	
1729 1734 1739 1744	
gga agc gct tac cag ccc agc ttt gcc agc cct aat aag aag cat gct	5280
Gly Ser Ala Tyr Gln Pro Ser Phe Ala Ser Pro Asn Lys Lys His Ala	
1745 1750 1755 1760	
aaa gcc aca gca gct act gtg gtt ctt caa gca atg ggc ctt gta cca	5328
Lys Ala Thr Ala Ala Thr Val Val Leu Gln Ala Met Gly Leu Val Pro	
1761 1766 1771 1776	
aag gac ctc atg gct aat gcc act tgc ttc agg agt gcc tca cgt aga	5376
Lys Asp Leu Met Ala Asn Ala Thr Cys Phe Arg Ser Ala Ser Arg Arg	
1777 1782 1787 1792	
tag attg aggttttata ataatacattt cagaatttta ctctgcatca caatgtattt	5433
*	
1793	
cctctttaat gttgtaaata tttggcaatt taagacattg tgtaaaaagc aatctgtaaa	5493
aacatctcca ggctttgatt tttgtaccat ggaaattgta tttaaccata cagggttttg	5553
gtatgtttat attgtttacc ttagtgatgt atttgtttaa gtggctaaca tccaaacgac	5613
tgtttgaagg catcagagta atcttcagtg tggaatgtta aataacgctt ttatactgta	5673
ttttgtacta tgatgtaact ccccttcctt atggctaggo tactgtaaca cttgcctgta	5733

atcagtgaag ggctgtgcac cttgtactat ttcacaatgg gttctgctgg acagataatg 5793
ggccagtgtt attgaggtga tcaagatctg ttccacaggg ctaatgccac catctcccct 5853
caaaattttg tagaggttct aaaaagaaag tggatatgtg tgtgatgatc agcactaagt 5913
cctgcattcc tgtaaagcc acttgggtca taagaaggga gtaaaaaatg aagtctgact 5973
agaattctat tgcagaggcc aagtacattt agtatggcat tgagttgtga tatagtttta 6033
ctttgatgtg cattttgaat ttcagctaca cctagataga cgtaaaatga taattaaaat 6093
gctgtaacca acttatctaa taaaattggc aaccagccac tattttgttg actatgaaaa 6153
agttaaaagt ttatgttaat ttttagggtc tgatagaata tttcatgtgt attacagtgg 6213
tattcatatg ctatgtctct aaactttatt ttcaaaagct taaggcccaa atacaaactt 6273
ctctggaata aacgtggtgt tttatttaaa aaaaaaaaaa a 6314

<210> 99
<211> 1606
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (103)..(1071)

<400> 99
atttggccct cgaggccaag aattcggcac gagggcagct gcagggtctc gctggggggcc 60
gctcgggacc aattttgaag aggactgaga gtggctttca ca atg gaa ggg atc 114
Met Glu Gly Ile
1
agt aat ttc aag aca cca agc aaa tta tca gaa aaa aag aaa tct gta 162
Ser Asn Phe Lys Thr Pro Ser Lys Leu Ser Glu Lys Lys Lys Ser Val
5 10 15 20
tta tgt tca act cca act ata aat atc ccg gcc tct ccg ttt atg cag 210
Leu Cys Ser Thr Pro Thr Ile Asn Ile Pro Ala Ser Pro Phe Met Gln
21 26 31 36
aag ctt ggc ttt ggt act ggg gta aat gtg tac cta atg aaa aga tct 258
Lys Leu Gly Phe Gly Thr Gly Val Asn Val Tyr Leu Met Lys Arg Ser
37 42 47 52
cca aga ggt ttg tct cat tct cct tgg gct gta aaa aag att aat cct 306
Pro Arg Gly Leu Ser His Ser Pro Trp Ala Val Lys Lys Ile Asn Pro
53 58 63 68
ata tgt aat gat cat tat cga agt gtg tat caa aag aga cta atg gat 354

Ile Cys Asn Asp His Tyr Arg Ser Val Tyr Gln Lys Arg Leu Met Asp
69 74 79 84

gaa gct aag att ttg aaa agc ctt cat cat cca aac att gtt ggt tat 402
Glu Ala Lys Ile Leu Lys Ser Leu His His Pro Asn Ile Val Gly Tyr
85 90 95 100

cgt gct ttt act gaa gcc aat gat ggc agt ctg tgt ctt gct atg gaa 450
Arg Ala Phe Thr Glu Ala Asn Asp Gly Ser Leu Cys Leu Ala Met Glu
101 106 111 116

tat gga ggt gaa aag tct cta aat gac tta ata gaa gaa cga tat aaa 498
Tyr Gly Gly Glu Lys Ser Leu Asn Asp Leu Ile Glu Glu Arg Tyr Lys
117 122 127 132

gcc agc caa gat cct ttt cca gca gcc ata att tta aaa gtt gct ttg 546
Ala Ser Gln Asp Pro Phe Pro Ala Ala Ile Ile Leu Lys Val Ala Leu
133 138 143 148

aat atg gca aga ggg tta aag tat ctg cac caa gaa aag aaa ctg ctt 594
Asn Met Ala Arg Gly Leu Lys Tyr Leu His Gln Glu Lys Lys Leu Leu
149 154 159 164

cat gga gac ata aag tct tca aat gtt gta att aaa ggc gat ttt gaa 642
His Gly Asp Ile Lys Ser Ser Asn Val Val Ile Lys Gly Asp Phe Glu
165 170 175 180

aca att aaa atc tgt gat gta gga gtc tct cta cca ctg gat gaa aat 690
Thr Ile Lys Ile Cys Asp Val Gly Val Ser Leu Pro Leu Asp Glu Asn
181 186 191 196

atg act gtg act gac cct gag gct tgt tac att ggc aca gag cca tgg 738
Met Thr Val Thr Asp Pro Glu Ala Cys Tyr Ile Gly Thr Glu Pro Trp
197 202 207 212

aaa ccc aaa gaa gct gtg gag gag aat ggt gtt att act gac aag gca 786
Lys Pro Lys Glu Ala Val Glu Glu Asn Gly Val Ile Thr Asp Lys Ala
213 218 223 228

gac ata ttt gcc ttt ggc ctt act ttg tgg gaa atg atg act tta tcg 834
Asp Ile Phe Ala Phe Gly Leu Thr Leu Trp Glu Met Met Thr Leu Ser
229 234 239 244

att cca cac att aat ctt tca aat gat gat gat gat gaa gat aaa act 882
Ile Pro His Ile Asn Leu Ser Asn Asp Asp Asp Asp Glu Asp Lys Thr
245 250 255 260

ttt gat gaa agt gat ttt gat gat gaa gca tac tat gca gcg ttg gga 930
Phe Asp Glu Ser Asp Phe Asp Asp Glu Ala Tyr Tyr Ala Ala Leu Gly
261 266 271 276

act agg cca cct att aat atg gaa gaa ctg gat gaa tca tac cag aaa 978
Thr Arg Pro Pro Ile Asn Met Glu Glu Leu Asp Glu Ser Tyr Gln Lys
277 282 287 292

gta att gaa ctc ttc tct gta tgc act aat gaa gac cct aaa gat cgt 1026
Val Ile Glu Leu Phe Ser Val Cys Thr Asn Glu Asp Pro Lys Asp Arg

293	298	303	308	
cct tct gct gca cac att gtt gaa gct ctg gaa aca gat gtc tag tga				1074
Pro Ser Ala Ala His Ile Val Glu Ala Leu Glu Thr Asp Val *				
309	314	319		
tcattctcagc tgaagtgtgg cttgcataaa taactgttta ttccaaaata tttacatagt				1134
tactatcagt agttattaga ctctaaaatt ggcataatttg aggaccatag tttcttggtta				1194
acatatggat aactatttct aatatgaaat atgcttatat tggctataag cacttggaat				1254
tgtactgggt tttctgtaaa gttttagaaa ctagctacat aagtactttg atactgctca				1314
tgctgactta aaacactagc agtaaaacgc tgtaaactgt aacattaaat tgaatgacca				1374
ttacttttat taatgatctt tcttaaatat tctatatttt aatggatcta ctgacattag				1434
cactttgtac agtacaaaat aaagtctaca ttgttttaaa acaaaaaaaaaa aaaaaaaaaa				1494
ttgcggccgc tctagagtat ccctcaaaga ggcccaagct tacgcgtacc cagctttctt				1554
gtacaaagtg gtgccgatat gtgagacgaa tgatggctag atcgacgac gc				1606

<210> 100
 <211> 2275
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (770)..(2230)

<400> 100	
ccactttgta caagaaagct gggtacgcgt aagcttgggc ccctctaggg atactctaga	60
gcggccgccc tttttttttt tttttttttt taaacacatt tttttcctgg cttcggacct	120
cagactgctg cagccctaac cttoocaggg ctgagctctt tggagctgcc cattcctccg	180
gctgcgagaa aggacgcgcg ccctgcgtcg ggcgaagaaa agaagcaaaa cttgtcggga	240
gggtttcgtc atcaacctcc ttcccgcaaa cctaaacctc ctgccggggc catccctaga	300
cagaggaaag ttcttcgaga gccgaccagc cctagtggat ctggggcagg cagcggcgct	360
ggctgtggaa ttagatctgt tttgaacca gtggagcgca tcgctggggc tcggaagtca	420
ccgtccgcgg gcaccgggtt ggcgctgccc gagtgaacc gacagtttgc gagcctcggc	480
tgcaagtggc ctctcctccc cgcgggttgtt gttcagtgtc gggtgagggc tgcgagtgtg	540
gcaagttgca aagagagcct cagaggtccg aagagcgctg cgctcctact cgcgttcgct	600

tcttctctt ctcggttccc tactgtgaaa tcgcagcgac atttaciaag gcctccgggt	660
cctaccgaga ccgatccgca gcgtttggcc cggtcgcgcc tattgcatcg ggagcccccg	720
agcaccggcg aaggactggc ggggtggggta gggaggtggc ggcggcggc atg gcg	775
Met Ala	
1	
agg ttc ccg aag gcc gac ctg gcc gct gca gga gtt atg tta ctt tgc	823
Arg Phe Pro Lys Ala Asp Leu Ala Ala Ala Gly Val Met Leu Leu Cys	
3 8 13 18	
cac ttc ttc acg gac cag ttt cag ttc gcc gat ggg aaa ccc gga gac	871
His Phe Phe Thr Asp Gln Phe Gln Phe Ala Asp Gly Lys Pro Gly Asp	
19 24 29 34	
caa atc ctt gat tgg cag tat gga gtt act cag gcc ttc cct cac aca	919
Gln Ile Leu Asp Trp Gln Tyr Gly Val Thr Gln Ala Phe Pro His Thr	
35 40 45 50	
gag gag gag gtg gaa gtt gat tca cac gcg tac agc cac agg tgg aaa	967
Glu Glu Glu Val Glu Val Asp Ser His Ala Tyr Ser His Arg Trp Lys	
51 56 61 66	
aga aac ttg gac ttt ctc aag gcg gta gac acg aac cga gca agc gtc	1015
Arg Asn Leu Asp Phe Leu Lys Ala Val Asp Thr Asn Arg Ala Ser Val	
67 72 77 82	
ggc caa gac tct cct gag ccc aga agc ttc aca gac ctg ctg ctg gat	1063
Gly Gln Asp Ser Pro Glu Pro Arg Ser Phe Thr Asp Leu Leu Leu Asp	
83 88 93 98	
gat ggg cag gac aat aac act cag atc gag gag gat aca gac cac aat	1111
Asp Gly Gln Asp Asn Asn Thr Gln Ile Glu Glu Asp Thr Asp His Asn	
99 104 109 114	
tac tat ata tct cga ata tat ggt cca tct gat tct gcc agc cgg gat	1159
Tyr Tyr Ile Ser Arg Ile Tyr Gly Pro Ser Asp Ser Ala Ser Arg Asp	
115 120 125 130	
tta tgg gtg aac ata gac caa atg gaa aaa gat aaa gtg aag att cat	1207
Leu Trp Val Asn Ile Asp Gln Met Glu Lys Asp Lys Val Lys Ile His	
131 136 141 146	
gga ata ttg tcc aat act cat cgg caa gct gca aga gtg aat ctg tcc	1255
Gly Ile Leu Ser Asn Thr His Arg Gln Ala Ala Arg Val Asn Leu Ser	
147 152 157 162	
ttc gat ttt cca ttt tat ggc cac ttc cta cgt gaa atc act gtg gca	1303
Phe Asp Phe Pro Phe Tyr Gly His Phe Leu Arg Glu Ile Thr Val Ala	
163 168 173 178	
acc ggg ggt ttc ata tac act gga gaa gtc gta cat cga atg cta aca	1351
Thr Gly Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met Leu Thr	
179 184 189 194	
gcc aca cag tac ata gca cct tta atg gca aat ttc gat ccc agt gta	1399

Ala Thr Gln Tyr Ile	Ala Pro Leu Met Ala Asn Phe Asp Pro Ser Val	
195	200	205 210
tcc aga aat tca act gtc aga tat ttt gat aat ggc aca gca ctt gtg		1447
Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala Leu Val		
211	216	221 226
gtc cag tgg gac cat gta cat ctc cag gat aat tat aac ctg gga agc		1495
Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu Gly Ser		
227	232	237 242
ttc aca ttc cag gca acc ctg ctc atg gat gga cga atc atc ttt gga		1543
Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile Phe Gly		
243	248	253 258
tac aaa gaa att cct gtc ttg gtc aca cag ata agt tca acc aat cat		1591
Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr Asn His		
259	264	269 274
cca gtg aaa gtc gga ctg tcc gat gca ttt gtc gtt gtc cac agg atc		1639
Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His Arg Ile		
275	280	285 290
caa caa att ccc aat gtt cga aga aga aca att tat gaa tac cac cga		1687
Gln Gln Ile Pro Asn Val Arg Arg Arg Thr Ile Tyr Glu Tyr His Arg		
291	296	301 306
gta gag cta caa atg tca aaa att acc aac att tcg gct gtg gag atg		1735
Val Glu Leu Gln Met Ser Lys Ile Thr Asn Ile Ser Ala Val Glu Met		
307	312	317 322
acc cca tta ccc aca tgc ctc cag ttt aac aga tgt ggc ccc tgt gta		1783
Thr Pro Leu Pro Thr Cys Leu Gln Phe Asn Arg Cys Gly Pro Cys Val		
323	328	333 338
tct tct cag att ggc ttc aac tgc agt tgg tgt agt aaa ctt caa aga		1831
Ser Ser Gln Ile Gly Phe Asn Cys Ser Trp Cys Ser Lys Leu Gln Arg		
339	344	349 354
tgt tcc agt gga ttt gat cgt cat cgg cag gac tgg gtg gac agt gga		1879
Cys Ser Ser Gly Phe Asp Arg His Arg Gln Asp Trp Val Asp Ser Gly		
355	360	365 370
tgc cct gaa gag tca aaa gag aag atg tgt gag aat aca gaa cca gtg		1927
Cys Pro Glu Glu Ser Lys Glu Lys Met Cys Glu Asn Thr Glu Pro Val		
371	376	381 386
gaa act tct tct cga acc acc aca acc ata gga gcg aca acc acc cag		1975
Glu Thr Ser Ser Arg Thr Thr Thr Thr Ile Gly Ala Thr Thr Thr Gln		
387	392	397 402
ttc agg gtc cta act acc acc aga aga gca gtg act tct cag ttt ccc		2023
Phe Arg Val Leu Thr Thr Thr Arg Arg Ala Val Thr Ser Gln Phe Pro		
403	408	413 418
acc agc ctc cct aca gaa gat gat acc aag ata gca cta cat cta aaa		2071
Thr Ser Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu His Leu Lys		

419	424	429	434	
gat aat gga gct tct aca gat gac agt gca gct gag aag aaa ggg gga				2119
Asp Asn Gly Ala Ser Thr Asp Asp Ser Ala Ala Glu Lys Lys Gly Gly				
435	440	445	450	
acc ctc cac gct ggc ctc atc gtt gga atc ctc atc ctg gtc ctc att				2167
Thr Leu His Ala Gly Leu Ile Val Gly Ile Leu Ile Leu Val Leu Ile				
451	456	461	466	
gta gcc aca gcc att ctt gtg aca gtc tat atg tat cac cac cat gta				2215
Val Ala Thr Ala Ile Leu Val Thr Val Tyr Met Tyr His His His Val				
467	472	477	482	
ttg cgg ccg ctc tag aggatccaag cttacgtacg cgtgcatgcg ccgacgggtgc				2270
Leu Arg Pro Leu *				
483				
ttcat				2275

<210> 101
 <211> 2817
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (770) .. (2359)

<400> 101

ccacttttgta caagaaagct gggtagcgcgt aagcttgggc ccctctaggg atactctaga	60
gcgggcgcgcc tttttttttt tttttttttt taaacacatt tttttcctgg cttcggacct	120
cagactgctg cagccctaac cttcccaggg ctcagctctt tggagctgcc cattcctccg	180
gctgcgagaa aggacgcgcg ccctgcgtcg ggcgaagaaa agaagcaaaa cttgtcggga	240
gggtttcgtc atcaacctcc ttcccgcaaa cctaaacctc ctgccggggc catccctaga	300
cagaggaaag ttcctgcaga gccgaccagc ctagtggtat ctggggcagg cagcggcgct	360
ggctgtggaa ttagatctgt tttgaacca gtggagcgca tcgctggggc tcggaagtca	420
ccgtccgcgg gcaccgggtt ggcgctgccc gagtggaacc gacagtttgc gagcctcggc	480
tgcaagtggc ctctcctccc cgcggttgtt gttcagtgtc gggtgagggc tgcgagtgtg	540
gcaagttgca aagagagcct cagaggtccg aagagcgctg cgctcctact cgcgttcgct	600
tcttcctctt ctcggttccc tactgtgaaa tcgcagcgac atttaciaag gcctccgggt	660
cctaccgaga ccgatccgca gcgtttggcc cggtcgcgcc tattgcatcg ggagcccccg	720

agcacogggcg aaggactggc ggggtggggta gggaggtggc ggcggcggc atg gcg 775
Met Ala
1

agg ttc ccg aag gcc gac ctg gcc gct gca gga gtt atg tta ctt tgc 823
Arg Phe Pro Lys Ala Asp Leu Ala Ala Ala Gly Val Met Leu Leu Cys
3 8 13 18

cac ttc ttc acg gac cag ttt cag ttc gcc gat ggg aaa ccc gga gac 871
His Phe Phe Thr Asp Gln Phe Gln Phe Ala Asp Gly Lys Pro Gly Asp
19 24 29 34

caa atc ctt gat tgg cag tat gga gtt act cag gcc ttc cct cac aca 919
Gln Ile Leu Asp Trp Gln Tyr Gly Val Thr Gln Ala Phe Pro His Thr
35 40 45 50

gag gag gag gtg gaa gtt gat tca cac gcg tac agc cac agg tgg aaa 967
Glu Glu Glu Val Glu Val Asp Ser His Ala Tyr Ser His Arg Trp Lys
51 56 61 66

aga aac ttg gac ttt ctc aag gcg gta gac acg aac cga gca agc gtc 1015
Arg Asn Leu Asp Phe Leu Lys Ala Val Asp Thr Asn Arg Ala Ser Val
67 72 77 82

ggc caa gac tct cct gag ccc aga agc ttc aca gac ctg ctg ctg gat 1063
Gly Gln Asp Ser Pro Glu Pro Arg Ser Phe Thr Asp Leu Leu Leu Asp
83 88 93 98

gat ggg cag gac aat aac act cag atc gag gag gat aca gac cac aat 1111
Asp Gly Gln Asp Asn Asn Thr Gln Ile Glu Glu Asp Thr Asp His Asn
99 104 109 114

tac tat ata tct cga ata tat ggt cca tct gat tct gcc agc cgg gat 1159
Tyr Tyr Ile Ser Arg Ile Tyr Gly Pro Ser Asp Ser Ala Ser Arg Asp
115 120 125 130

tta tgg gtg aac ata gac caa atg gaa aaa gat aaa gtg aag att cat 1207
Leu Trp Val Asn Ile Asp Gln Met Glu Lys Asp Lys Val Lys Ile His
131 136 141 146

gga ata ttg tcc aat act cat cgg caa gct gca aga gtg aat ctg tcc 1255
Gly Ile Leu Ser Asn Thr His Arg Gln Ala Ala Arg Val Asn Leu Ser
147 152 157 162

ttc gat ttt cca ttt tat ggc cac ttc cta cgt gaa atc act gtg gca 1303
Phe Asp Phe Pro Phe Tyr Gly His Phe Leu Arg Glu Ile Thr Val Ala
163 168 173 178

acc ggg ggt ttc ata tac act gga gaa gtc gta cat cga atg cta aca 1351
Thr Gly Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met Leu Thr
179 184 189 194

gcc aca cag tac ata gca cct tta atg gca aat ttc gat ccc agt gta 1399
Ala Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro Ser Val
195 200 205 210

tcc aga aat tca act gtc aga tat ttt gat aat ggc aca gca ctt gtg 1447

Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala Leu Val	
211 216 221 226	
gtc cag tgg gac cat gta cat ctc cag gat aat tat aac ctg gga agc	1495
Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu Gly Ser	
227 232 237 242	
ttc aca ttc cag gca acc ctg ctc atg gat gga cga atc atc ttt gga	1543
Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile Phe Gly	
243 248 253 258	
tac aaa gaa att cct gtc ttg gtc aca cag ata agt tca acc aat cat	1591
Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr Asn His	
259 264 269 274	
cca gtg aaa gtc gga ctg tcc gat gca ttt gtc gtt gtc cac agg atc	1639
Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His Arg Ile	
275 280 285 290	
caa caa att ccc aat gtt cga aga aga aca att tat gaa tac cac cga	1687
Gln Gln Ile Pro Asn Val Arg Arg Arg Thr Ile Tyr Glu Tyr His Arg	
291 296 301 306	
gta gag cta caa atg tca aaa att acc aac att tcg gct gtg gag atg	1735
Val Glu Leu Gln Met Ser Lys Ile Thr Asn Ile Ser Ala Val Glu Met	
307 312 317 322	
acc cca tta ccc aca tgc ctc cag ttt aac aga tgt ggc ccc tgt gta	1783
Thr Pro Leu Pro Thr Cys Leu Gln Phe Asn Arg Cys Gly Pro Cys Val	
323 328 333 338	
tct tct cag att ggc ttc aac tgc agt tgg tgt agt aaa ctt caa aga	1831
Ser Ser Gln Ile Gly Phe Asn Cys Ser Trp Cys Ser Lys Leu Gln Arg	
339 344 349 354	
tgt tcc agt gga ttt gat cgt cat cgg cag gac tgg gtg gac agt gga	1879
Cys Ser Ser Gly Phe Asp Arg His Arg Gln Asp Trp Val Asp Ser Gly	
355 360 365 370	
tgc cct gaa gag tca aaa gag aag atg tgt gag aat aca gaa cca gtg	1927
Cys Pro Glu Glu Ser Lys Glu Lys Met Cys Glu Asn Thr Glu Pro Val	
371 376 381 386	
gaa act tct tct cga acc acc aca acc ata gga gcg aca acc acc cag	1975
Glu Thr Ser Ser Arg Thr Thr Thr Thr Ile Gly Ala Thr Thr Thr Gln	
387 392 397 402	
ttc agg gtc cta act acc acc aga aga gca gtg act tct cag ttt ccc	2023
Phe Arg Val Leu Thr Thr Thr Arg Arg Ala Val Thr Ser Gln Phe Pro	
403 408 413 418	
acc agc ctc cct aca gaa gat gat acc aag ata gca cta cat cta aaa	2071
Thr Ser Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu His Leu Lys	
419 424 429 434	
gat aat gga gct tct aca gat gac agt gca gct gag aag aaa ggg gga	2119
Asp Asn Gly Ala Ser Thr Asp Asp Ser Ala Ala Glu Lys Lys Gly Gly	

435	440	445	450	
acc ctc cac gct ggc ctc atc att gga atc ctc atc ctg gtc ctc att				2167
Thr Leu His Ala Gly Leu Ile Ile Gly Ile Leu Ile Leu Val Leu Ile				
451	456	461	466	
gta gcc aca gcc att ctt gtg aca gtc tat atg tat cac cac cca aca				2215
Val Ala Thr Ala Ile Leu Val Thr Val Tyr Met Tyr His His Pro Thr				
467	472	477	482	
tca gca gcc agc atc ttc ttt att gag aga cgc cca agc aga tgg cct				2263
Ser Ala Ala Ser Ile Phe Phe Ile Glu Arg Arg Pro Ser Arg Trp Pro				
483	488	493	498	
gcg atg aag ttt aga aga ggc tct gga cat cct gcc tat gct gaa gtt				2311
Ala Met Lys Phe Arg Arg Gly Ser Gly His Pro Ala Tyr Ala Glu Val				
499	504	509	514	
gaa cca gtt gga gag aaa gaa ggc ttt att gta tca gag cag tgc taa				2359
Glu Pro Val Gly Glu Lys Glu Gly Phe Ile Val Ser Glu Gln Cys *				
515	520	525	530	
aatttctagg acagaacaac accagtactg gtttacaggt gttaagacta aaattttgcc				2419
tataccttta agacaaacaa acaaacacac acacaaacaa gctctaagct gctgtagcct				2479
gaagaagaca agatttctgg acaagctcag ccaggaac aaagggtaaa caaaaaacta				2539
aaacttatac aagataccat ttacactgaa catagaattc cctagtggaa tgtcatctat				2599
agttcactcg gaacatctcc cgtggactta tctgaagtat gacaagatta taatgctttt				2659
ggcttaggtg caggggttgca aagggatcag aaaaaaaaaa tcataataaa gcttttagttc				2719
atgagggatc gaaaaaaaaa aaaaaaaagg gcggccgctc tagagtatcc ctcgaggggc				2779
ccaagottac gcgtaccag ctttcttgta caaagtgg				2817

<210> 102
 <211> 1156
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (251)..(904)

<400> 102	
taatgctgta cgcctgcacg taccgggtccg gaattcccgg gtcgacgatt tcgtacaagt	60
tgccggcagc tgagcgcgcg gcctcctcct gctcgcagcc cctacgccc acccggcggc	120
ggtggccagc gccaggacgc acatcccgcg gacaccgacc ccagatgtaa agcgggaccc	180

gacgcttcag caaaggcagc attgggtcacg gagttcaagg gaatagatga gtaagcaacg 974
 tttcaaattt gggatgaaaa gactgccaaa ctattggctg accaagggtt ttaaattcag 1034
 aagagcaatt ctaaattctaa agaaatgtat cattaagta attacgttac attgaaaaaa 1094
 aaaaaaaaaa aaacctatgc ggccgcaagc ttattccctt tagtgagggt atactaaaac 1154
 cg 1156

<210> 103
 <211> 3227
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (440)..(1747)

<400> 103
 atttggccct cgaggccaag aattcggcac gagatggcat ctccactctg tgacccagac 60
 tgccacttgg ccccaaaaga atattttctt tgacagtgga cagctgacat atcaccactt 120
 tcctttctact gtgagtgtct ctggatgggc agaaaggaat ggccagcccc tggttatggt 180
 catctaaggt cacctctgaa atgctgtgag cccctcttcc ttcctctcct ctgctatttc 240
 ccatctctgc tgttggcagg agaatagaac cctggctgcc agagatgcaa gtgtgtgacg 300
 atatgggtgc tggtgcatat ttagtatgtg cctgtgtcca gccatgtgca tgtgtgggtg 360
 tgtgagtgtg tgacccagcc cttccccogt ggccaagcag agagagtggc cttgaggaag 420
 ccatagcagc aggaccagc atg gcc tct gct gcc tct gtg acc agc ctg gca 472
 Met Ala Ser Ala Ala Ser Val Thr Ser Leu Ala
 1 5
 gat gaa gtc aac tgc ccc atc tgt cag ggt acc ctg agg gag ccg gtc 520
 Asp Glu Val Asn Cys Pro Ile Cys Gln Gly Thr Leu Arg Glu Pro Val
 12 17 22 27
 act atc gac tgc ggc cac aac ttc tgc cgg gcc tgc ctt acc cgc tac 568
 Thr Ile Asp Cys Gly His Asn Phe Cys Arg Ala Cys Leu Thr Arg Tyr
 28 33 38 43
 tgt gag ata cca ggc cca gac ctg gag gag tcc cct act tgc cca ctc 616
 Cys Glu Ile Pro Gly Pro Asp Leu Glu Glu Ser Pro Thr Cys Pro Leu
 44 49 54 59
 tgc aaa gaa ccc ttc cgt cct ggg agc ttc cgg ccc aac tgg cag ctg 664
 Cys Lys Glu Pro Phe Arg Pro Gly Ser Phe Arg Pro Asn Trp Gln Leu
 60 65 70 75

gct aac gtg gtg gag aac att gag cgc ctc cag ctg gtg tcc aca ctg	712
Ala Asn Val Val Glu Asn Ile Glu Arg Leu Gln Leu Val Ser Thr Leu	
76 81 86 91	
ggt ttg gga gag gag gat gtc tgc caa gag cac gga gag aag atc tac	760
Gly Leu Gly Glu Glu Asp Val Cys Gln Glu His Gly Glu Lys Ile Tyr	
92 97 102 107	
ttc ttc tgt gag gat gat gag atg cag ttg tgc gtg gtg tgc cgg gag	808
Phe Phe Cys Glu Asp Asp Glu Met Gln Leu Cys Val Val Cys Arg Glu	
108 113 118 123	
gct ggg gag cac gct acc cac acc atg cgc ttc ctg gag gat gca gcg	856
Ala Gly Glu His Ala Thr His Thr Met Arg Phe Leu Glu Asp Ala Ala	
124 129 134 139	
gct ccc tat agg gaa caa atc cat aag tgt ctt aaa tgt cta aga aaa	904
Ala Pro Tyr Arg Glu Gln Ile His Lys Cys Leu Lys Cys Leu Arg Lys	
140 145 150 155	
gag aga gag gag att caa gaa atc cag tca aga gaa aat aaa agg atg	952
Glu Arg Glu Glu Ile Gln Glu Ile Gln Ser Arg Glu Asn Lys Arg Met	
156 161 166 171	
caa gtc ctc ctg act cag gtg tcc acc aag aga caa cag gtg att tct	1000
Gln Val Leu Leu Thr Gln Val Ser Thr Lys Arg Gln Gln Val Ile Ser	
172 177 182 187	
gag ttc gca cac ctg agg aag ttt cta gag gaa cag cag agc atc ctc	1048
Glu Phe Ala His Leu Arg Lys Phe Leu Glu Glu Gln Gln Ser Ile Leu	
188 193 198 203	
tta gca caa ttg gag agc cag gat ggg gac atc ttg agg caa cgg gat	1096
Leu Ala Gln Leu Glu Ser Gln Asp Gly Asp Ile Leu Arg Gln Arg Asp	
204 209 214 219	
gaa ttt gat ttg ctg gtt gct ggg gag atc tgc cgg ttt agt gct ctt	1144
Glu Phe Asp Leu Leu Val Ala Gly Glu Ile Cys Arg Phe Ser Ala Leu	
220 225 230 235	
att gaa gaa ctg gag gag aag aat gag agg cca gca agg gag ctc ctg	1192
Ile Glu Glu Leu Glu Glu Lys Asn Glu Arg Pro Ala Arg Glu Leu Leu	
236 241 246 251	
acg gac atc aga agc act cta ata aga tgt gaa acc aga aag tgc cgg	1240
Thr Asp Ile Arg Ser Thr Leu Ile Arg Cys Glu Thr Arg Lys Cys Arg	
252 257 262 267	
aaa ccg gtg gct gtg tgc cca gag ctg ggc cag agg att cgg gac ttt	1288
Lys Pro Val Ala Val Ser Pro Glu Leu Gly Gln Arg Ile Arg Asp Phe	
268 273 278 283	
ccc cag cag gcc ctc ccg ctg cag agg gag atg aag atg ttt ctg gaa	1336
Pro Gln Gln Ala Leu Pro Leu Gln Arg Glu Met Lys Met Phe Leu Glu	
284 289 294 299	

aaa cta tgc ttt gag ttg gac tat gag cca gct cac att tct cta gac	1384
Lys Leu Cys Phe Glu Leu Asp Tyr Glu Pro Ala His Ile Ser Leu Asp	
300 305 310 315	
cct cag act tcc cac ccc aag ctc ctc ttg tcc gag gac cac cag cga	1432
Pro Gln Thr Ser His Pro Lys Leu Leu Leu Ser Glu Asp His Gln Arg	
316 321 326 331	
gct cag ttc tcc tac aaa tgg cag aac tca cca gac aac ccc cag cgt	1480
Ala Gln Phe Ser Tyr Lys Trp Gln Asn Ser Pro Asp Asn Pro Gln Arg	
332 337 342 347	
ttt gac cgg gcc acc tgt gtt ctg gcc cac act ggc atc aca ggg ggg	1528
Phe Asp Arg Ala Thr Cys Val Leu Ala His Thr Gly Ile Thr Gly Gly	
348 353 358 363	
aga cac acg tgg gtg gtg agt ata gac ctg gcc cat ggg ggc agc tgc	1576
Arg His Thr Trp Val Val Ser Ile Asp Leu Ala His Gly Gly Ser Cys	
364 369 374 379	
acc gtg ggc gtg gtg agc gag gat gtg cag cgg aag ggg gag ctt cgg	1624
Thr Val Gly Val Val Ser Glu Asp Val Gln Arg Lys Gly Glu Leu Arg	
380 385 390 395	
ctg cgg cca gag gag ggg gtg tgg gct gtg agg ctg gct tgg ggc ttc	1672
Leu Arg Pro Glu Glu Gly Val Trp Ala Val Arg Leu Ala Trp Gly Phe	
396 401 406 411	
gtc tcg gct ctg ggc tcc ttc ccc cac acg gct gac cct gaa gga gca	1720
Val Ser Ala Leu Gly Ser Phe Pro His Thr Ala Asp Pro Glu Gly Ala	
412 417 422 427	
gcc ccg gca ggt gag ggt gtc tct tga ctatg aggtgggctg ggtgaccttc	1772
Ala Pro Ala Gly Glu Gly Val Ser *	
428 433	
accaaagctg tcacccgaga gcccatctac accttcaactg cctccttcac taggaaggctc	1832
attccctttct ttgggctctg gggccgaggg tccagtttct ccctgagctc ctgagaagga	1892
gcagttacct actctctctt aagtacagga ctcatatcaa cccaagtacc atgtggactt	1952
gatccctggc tgaatcacct ggatgacttg gaatagaaat gactgcttta gaagatggga	2012
tggggccggg tggttaaggga tagaagagag gactctcaat ctactgatca agtcctttcc	2072
ccaatgccca gtggatggcc agggtaacctg gggactcagg ctgctgccag ttctgctcac	2132
caccatccgt gcttggcaca gaagtagctg catagaaagg gcactggatt tgaagtcaga	2192
agacctgggt tcttgaacca gcctgtcaac cagttgtatg acttttaaaca aggcattctca	2252
cctcttttca tcttgttttc ttccaataat gttagagttc atgtaatcac attctctaga	2312
accatttagt ttgtgttaac tatgaaccaa gcagtgtggt ggccactggt gacttgaaaa	2372
tatagagaaa aaaaaaacct gctctatata tgaaagagct cttgggaaga cagagaaaca	2432

taaagaggaa attacagcac agtgtggtgg gtgttacggg aagtccaacc ccagcattat	2492
gggagttcag ggggaaggggc atagcccagc ctggaaggag aggggtgagtg ggggatggct	2552
ttctgaaaag ggtggtctaa aggatgccta tgggtcaatag ggaaaagagg ggaagaagca	2612
tottaagaag aggaaacagc agagaactgg ctggatgacc tgtgactctg gagcactggg	2672
ttgtctccat tgtcattatg ggcagatgtg tgccatcccc agcogacgcc actcactgcc	2732
tccttctctc tgggtgttgc acttctgggt gagattaagg tgcagggcct gggggcagga	2792
ggacataagg tatagccata aatcataacc cagggaccac actcaaccct agggaaattg	2852
tcttctgat cagttgatta ccatctgagg tcaagaaatg agatagtggg agcaaattgg	2912
tcacaaatag ctgagctgtg ggctcagaaa ctgctaggta aaagaattcc agaaggaggc	2972
cagggcataa gttggatgac ctatgaactt tagtctaaag aattgagact accgtaattg	3032
agactactgt agtgacatct gagaaatggg atggaagagt gaccatgttt tattttcttg	3092
ttcttgtcac tattggattt tattttgcat aatcatgccc ttcactgaca gtctccttaa	3152
catcatctgt ttactctgct cagtggaaac tacaatgctc tgtcatctcc ctactgggtc	3212
tcctgggagg agggg	3227

<210> 104
 <211> 7827
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (121)..(7497)

<400> 104	
ccattcccaa gctggctagc gtatagattt ccgtttggta ccgagctcgg atccactagt	60
ccagtgtggt ggaattcgag acatgtgact ttaccctctt cccctcgaag caacactcca	120
atg gga gac aag gat gat gat gac gat gat gat gca gat gag aaa atg	168
Met Gly Asp Lys Asp Asp Asp Asp Asp Ala Asp Glu Lys Met	
1 5 10 15	
cag tca tca ggg atc ccg aat ggt ggt cac atc cgt cag gaa agc cag	216
Gln Ser Ser Gly Ile Pro Asn Gly Gly His Ile Arg Gln Glu Ser Gln	
17 22 27 32	
gaa cag agt gag gtg gac cat gga gat ttt gag atg gtg tct gag tcg	264
Glu Gln Ser Glu Val Asp His Gly Asp Phe Glu Met Val Ser Glu Ser	
33 38 43 48	

atg gtc ctg gag aca gct gaa aat gtc aac aat ggc aac ccc tct ccc	312
Met Val Leu Glu Thr Ala Glu Asn Val Asn Asn Gly Asn Pro Ser Pro	
49 54 59 64	
ctg gag gcc ctg ctg gca ggc gca gag ggc ttc ccc ccc atg ctg gac	360
Leu Glu Ala Leu Leu Ala Gly Ala Glu Gly Phe Pro Pro Met Leu Asp	
65 70 75 80	
atc cca cct gat gca gat gac gag acc atg gtt gaa cta gcc att gcc	408
Ile Pro Pro Asp Ala Asp Asp Glu Thr Met Val Glu Leu Ala Ile Ala	
81 86 91 96	
ctg agc ctg cag cag gac caa caa ggc agc agc agc agt gcc ctg ggc	456
Leu Ser Leu Gln Gln Asp Gln Gln Gly Ser Ser Ser Ser Ala Leu Gly	
97 102 107 112	
ctg cag agc ctg gga ctg tcc ggc cag gca ccc agc tct tcc tct ctg	504
Leu Gln Ser Leu Gly Leu Ser Gly Gln Ala Pro Ser Ser Ser Ser Leu	
113 118 123 128	
gac gca gga acc ctc tct gac acc aca gca tca gct cca gcc tca gac	552
Asp Ala Gly Thr Leu Ser Asp Thr Thr Ala Ser Ala Pro Ala Ser Asp	
129 134 139 144	
gac gag ggc agt aca gca gcg aca gat ggt tct acc ctt cgg acc tct	600
Asp Glu Gly Ser Thr Ala Ala Thr Asp Gly Ser Thr Leu Arg Thr Ser	
145 150 155 160	
cct gct gac cac ggt ggt agt gtg ggc tcg gag agc ggg ggc agt gca	648
Pro Ala Asp His Gly Gly Ser Val Gly Ser Glu Ser Gly Gly Ser Ala	
161 166 171 176	
gtg gac tca gtg gct ggc gag cac agt gta tct ggc cgg agc agt gct	696
Val Asp Ser Val Ala Gly Glu His Ser Val Ser Gly Arg Ser Ser Ala	
177 182 187 192	
tat ggc gat gct aca gct gag ggg cat ccg gct gga cca gga agt gtc	744
Tyr Gly Asp Ala Thr Ala Glu Gly His Pro Ala Gly Pro Gly Ser Val	
193 198 203 208	
agc tca agc act gga gcc atc agc acc acc act ggg cac cag gag gga	792
Ser Ser Ser Thr Gly Ala Ile Ser Thr Thr Thr Gly His Gln Glu Gly	
209 214 219 224	
gat ggc tcc gag gga gaa gga gaa gga gaa act gaa gga gat gtc cac	840
Asp Gly Ser Glu Gly Glu Gly Glu Gly Glu Thr Glu Gly Asp Val His	
225 230 235 240	
act agc aac agg ctg cac atg gtc cgt cta atg ctg ttg gag aga tta	888
Thr Ser Asn Arg Leu His Met Val Arg Leu Met Leu Leu Glu Arg Leu	
241 246 251 256	
ctg cag acc ctg cct caa tta cga aac gtt ggc ggt gtc cgg gcc atc	936
Leu Gln Thr Leu Pro Gln Leu Arg Asn Val Gly Gly Val Arg Ala Ile	
257 262 267 272	

cca tac atg cag gtc att cta atg ctc act aca gat ctg gat gga gaa	984
Pro Tyr Met Gln Val Ile Leu Met Leu Thr Thr Asp Leu Asp Gly Glu	
273 278 283 288	
gat gag aaa gac aag ggg gcc cta gac aac ctg ctc tcc cag ctt att	1032
Asp Glu Lys Asp Lys Gly Ala Leu Asp Asn Leu Leu Ser Gln Leu Ile	
289 294 299 304	
gct gag ttg ggt atg gat aaa aag gat gtc tcc aag aag aat gag cgc	1080
Ala Glu Leu Gly Met Asp Lys Lys Asp Val Ser Lys Lys Asn Glu Arg	
305 310 315 320	
agc gcc ctg aat gaa gtc cat ctg gta gta atg aga ctc ctg agt gtc	1128
Ser Ala Leu Asn Glu Val His Leu Val Val Met Arg Leu Leu Ser Val	
321 326 331 336	
ttc atg tcc cgc acc aaa tct gga tcc aag tct tcc ata tgt gag tca	1176
Phe Met Ser Arg Thr Lys Ser Gly Ser Lys Ser Ser Ile Cys Glu Ser	
337 342 347 352	
tct tcc ctc atc tcc agt gcc aca gca gca gct cta ctg agc tct ggg	1224
Ser Ser Leu Ile Ser Ser Ala Thr Ala Ala Ala Leu Leu Ser Ser Gly	
353 358 363 368	
gct gtg gac tac tgc ctg cac gtg ctc aaa tca ctg ctg gaa tat tgg	1272
Ala Val Asp Tyr Cys Leu His Val Leu Lys Ser Leu Leu Glu Tyr Trp	
369 374 379 384	
aag agc caa cag aat gac gag gag cct gtg gct acc agc cag ttg ctg	1320
Lys Ser Gln Gln Asn Asp Glu Glu Pro Val Ala Thr Ser Gln Leu Leu	
385 390 395 400	
aaa cca cat act acc tcc tcc cca cct gac atg agc cca ttc ttt ctc	1368
Lys Pro His Thr Thr Ser Ser Pro Pro Asp Met Ser Pro Phe Phe Leu	
401 406 411 416	
cgc cag tat gtg aag ggt cat gct gct gat gtg ttt gag gcc tat act	1416
Arg Gln Tyr Val Lys Gly His Ala Ala Asp Val Phe Glu Ala Tyr Thr	
417 422 427 432	
cag ctt cta aca gaa atg gta ctg agg ctt cct tac caa atc aaa aag	1464
Gln Leu Leu Thr Glu Met Val Leu Arg Leu Pro Tyr Gln Ile Lys Lys	
433 438 443 448	
att act gac acc aat tct cga atc cca cct cct gtc ttt gac cac tcg	1512
Ile Thr Asp Thr Asn Ser Arg Ile Pro Pro Pro Val Phe Asp His Ser	
449 454 459 464	
tgg ttt tac ttt ctc tcc gag tac ctc atg atc cag cag act cca ttt	1560
Trp Phe Tyr Phe Leu Ser Glu Tyr Leu Met Ile Gln Gln Thr Pro Phe	
465 470 475 480	
gtg cgc cgt caa gtc cgc aaa ctt ctg ctc ttc atc tgt gga tcc aaa	1608
Val Arg Arg Gln Val Arg Lys Leu Leu Leu Phe Ile Cys Gly Ser Lys	
481 486 491 496	
gag aag tac cgc cag ctc cgg gat ttg cac acc ctg gac tct cac gtg	1656

Glu Lys Tyr Arg Gln Leu Arg Asp Leu His Thr Leu Asp Ser His Val	
497 502 507 512	
cgt ggg atc aag aag ctg cta gaa gag cag ggg ata ttc ctc cgg gca	1704
Arg Gly Ile Lys Lys Leu Leu Glu Glu Gln Gly Ile Phe Leu Arg Ala	
513 518 523 528	
agt gtg gtt aca gcc agc tca ggc tcc gcc ttg caa tat gac aca ctc	1752
Ser Val Val Thr Ala Ser Ser Gly Ser Ala Leu Gln Tyr Asp Thr Leu	
529 534 539 544	
atc agc ctg atg gag cac ctg aaa gcc tgt gca gag att gcc gcc cag	1800
Ile Ser Leu Met Glu His Leu Lys Ala Cys Ala Glu Ile Ala Ala Gln	
545 550 555 560	
cga acc atc aac tgg cag aaa ttc tgc atc aaa gat gac tcc gtc ctg	1848
Arg Thr Ile Asn Trp Gln Lys Phe Cys Ile Lys Asp Asp Ser Val Leu	
561 566 571 576	
tac ttc ctc ctc caa gtc agt ttc ctt gtg gat gag ggc gtg tcc cca	1896
Tyr Phe Leu Leu Gln Val Ser Phe Leu Val Asp Glu Gly Val Ser Pro	
577 582 587 592	
gtg ctg ctg caa ctg ctc tcc tgt gct ctg tgc ggc agc aag gtg ctc	1944
Val Leu Leu Gln Leu Leu Ser Cys Ala Leu Cys Gly Ser Lys Val Leu	
593 598 603 608	
gct gca ctg gca gcc tct tcg gga tcc tcc agt gct tct tcc tcc tca	1992
Ala Ala Leu Ala Ala Ser Ser Gly Ser Ser Ser Ala Ser Ser Ser Ser	
609 614 619 624	
gcc cct gtg gct gcc agt tct gga caa gcc aca aca cag tcc aag tct	2040
Ala Pro Val Ala Ala Ser Ser Gly Gln Ala Thr Thr Gln Ser Lys Ser	
625 630 635 640	
tcc act aaa aag agc aag aaa gaa gaa aaa aaa aag gag aaa gat ggt	2088
Ser Thr Lys Lys Ser Lys Lys Glu Glu Lys Lys Lys Glu Lys Asp Gly	
641 646 651 656	
gag acc tct ggc agc cag gag gac cag ctg tgc aca gct ctg gtg aac	2136
Glu Thr Ser Gly Ser Gln Glu Asp Gln Leu Cys Thr Ala Leu Val Asn	
657 662 667 672	
cag ctg aac aaa ttt gcc gat aag gaa acc ctg atc cag ttc ctg cgt	2184
Gln Leu Asn Lys Phe Ala Asp Lys Glu Thr Leu Ile Gln Phe Leu Arg	
673 678 683 688	
tgt ttc ctg tta gag tcc aat tct tcc tcg gtg cgc tgg cag gcc cac	2232
Cys Phe Leu Leu Glu Ser Asn Ser Ser Ser Val Arg Trp Gln Ala His	
689 694 699 704	
tgt ctg aca ctg cac atc tac aga aat tcc agc aaa tct caa cag gag	2280
Cys Leu Thr Leu His Ile Tyr Arg Asn Ser Ser Lys Ser Gln Gln Glu	
705 710 715 720	
ctc ctg cta gat ctg atg tgg tcc atc tgg cca gaa ctc cca gcc tat	2328
Leu Leu Leu Asp Leu Met Trp Ser Ile Trp Pro Glu Leu Pro Ala Tyr	

721	726	731	736	
ggt cgt aag gct gcc	cag ttt gtg gac cta	cta gga tat ttc tcc ctg		2376
Gly Arg Lys Ala Ala	Gln Phe Val Asp Leu	Leu Gly Tyr Phe Ser Leu		
737	742	747	752	
aaa act cca caa aca	gag aag aag ttg aag	gag tat tca cag aag gct		2424
Lys Thr Pro Gln Thr	Glu Lys Lys Leu Lys	Glu Tyr Ser Gln Lys Ala		
753	758	763	768	
gtg gag att ctg cgg	act caa aac cat att	ctt acc aac cac ccc aac		2472
Val Glu Ile Leu Arg	Thr Gln Asn His Ile	Leu Thr Asn His Pro Asn		
769	774	779	784	
tcg aac att tat aac	act ttg tct ggc tta	gtg gag ttt gat ggc tat		2520
Ser Asn Ile Tyr Asn	Thr Leu Ser Gly Leu	Val Glu Phe Asp Gly Tyr		
785	790	795	800	
tac ctg gag agc gat	ccc tgc ctg gtg tgt	aat aac ccg gaa gta ccg		2568
Tyr Leu Glu Ser Asp	Pro Cys Leu Val Cys	Asn Asn Pro Glu Val Pro		
801	806	811	816	
ttc tgt tat atc aag	ctg tct tcc att aaa	gtg gac acg cgg tac acc		2616
Phe Cys Tyr Ile Lys	Leu Ser Ser Ile Lys	Val Asp Thr Arg Tyr Thr		
817	822	827	832	
acc acc cag cag gtt	gtg aag ctc att ggc	agt cac acc atc agc aaa		2664
Thr Thr Gln Gln Val	Val Lys Leu Ile Gly	Ser His Thr Ile Ser Lys		
833	838	843	848	
gtg aca gtg aaa atc	ggg gat ctg aaa cgg	acc aag atg gtg cgg acc		2712
Val Thr Val Lys Ile	Gly Asp Leu Lys Arg	Thr Lys Met Val Arg Thr		
849	854	859	864	
atc aac ctg tat tat	aac aac cga acc gtg	cag gcc atc gtg gag ttg		2760
Ile Asn Leu Tyr Tyr	Asn Asn Arg Thr Val	Gln Ala Ile Val Glu Leu		
865	870	875	880	
aaa aac aag cca gct	cgc tgg cac aaa gcc	aag aag gtt cag ctg acc		2808
Lys Asn Lys Pro Ala	Arg Trp His Lys Ala	Lys Lys Val Gln Leu Thr		
881	886	891	896	
cct gga cag aca gag	gtg aag att gac ctg	ccg ttg ccc att gtg gcc		2856
Pro Gly Gln Thr Glu	Val Lys Ile Asp Leu	Pro Leu Pro Ile Val Ala		
897	902	907	912	
tcc aat ctg atg att	gag ttt gca gac ttc	tat gaa aac tac cag gcc		2904
Ser Asn Leu Met Ile	Glu Phe Ala Asp Phe	Tyr Glu Asn Tyr Gln Ala		
913	918	923	928	
tcc aca gag acc ctg	cag tgc cct cgc tgt	agt gcc tcg gtc cct gcc		2952
Ser Thr Glu Thr Leu	Gln Cys Pro Arg Cys	Ser Ala Ser Val Pro Ala		
929	934	939	944	
aac cca gga gtc tgt	ggc aac tgt gga gag	aat gtg tac cag tgt cac		3000
Asn Pro Gly Val Cys	Gly Asn Cys Gly Glu	Asn Val Tyr Gln Cys His		
945	950	955	960	

aaa tgc aga tcc atc aac tac gat gaa aag gat ccc ttc ctc tgc aat	3048
Lys Cys Arg Ser Ile Asn Tyr Asp Glu Lys Asp Pro Phe Leu Cys Asn	
961 966 971 976	
gcc tgt ggc ttc tgt aaa tat gcc cgc ttc gac ttc atg ctc tat gcc	3096
Ala Cys Gly Phe Cys Lys Tyr Ala Arg Phe Asp Phe Met Leu Tyr Ala	
977 982 987 992	
aag cct tgc tgt gca gtg gat ccc att gag aat gaa gaa gac cgg aag	3144
Lys Pro Cys Cys Ala Val Asp Pro Ile Glu Asn Glu Glu Asp Arg Lys	
993 998 1003 1008	
aag gct gta tcc aac atc aat aca ctt ttg gac aaa gct gat cga gtg	3192
Lys Ala Val Ser Asn Ile Asn Thr Leu Leu Asp Lys Ala Asp Arg Val	
1009 1014 1019 1024	
tat cat cag ctg atg gga cac cgg cca cag ctg gag aac ctg ctc tgc	3240
Tyr His Gln Leu Met Gly His Arg Pro Gln Leu Glu Asn Leu Leu Cys	
1025 1030 1035 1040	
aaa gtg aat gag gca gct cca gaa aag cca cag gat gac tca gga aca	3288
Lys Val Asn Glu Ala Ala Pro Glu Lys Pro Gln Asp Asp Ser Gly Thr	
1041 1046 1051 1056	
gca ggg ggc atc agc tcc act tct gcc agt gtg aat cgt tac atc ctg	3336
Ala Gly Gly Ile Ser Ser Thr Ser Ala Ser Val Asn Arg Tyr Ile Leu	
1057 1062 1067 1072	
cag ttg gct cag gag tat tgt gga gac tgc aag aac tct ttt gat gaa	3384
Gln Leu Ala Gln Glu Tyr Cys Gly Asp Cys Lys Asn Ser Phe Asp Glu	
1073 1078 1083 1088	
ctc tcc aaa atc atc cag aaa gtc ttt gct tgc cgc aaa gag ttg ttg	3432
Leu Ser Lys Ile Ile Gln Lys Val Phe Ala Ser Arg Lys Glu Leu Leu	
1089 1094 1099 1104	
gaa tat gac cta cag cag agg gaa gca gcc act aaa tca tcc cgg acc	3480
Glu Tyr Asp Leu Gln Gln Arg Glu Ala Ala Thr Lys Ser Ser Arg Thr	
1105 1110 1115 1120	
tcc gtg cag ccc aca ttc act gcc agc cag tac cgt gcc tta tcc gtc	3528
Ser Val Gln Pro Thr Phe Thr Ala Ser Gln Tyr Arg Ala Leu Ser Val	
1121 1126 1131 1136	
ctg ggc tgt ggc cac aca tcc tcc acc aag tgc tat ggc tgc gcc tgc	3576
Leu Gly Cys Gly His Thr Ser Ser Thr Lys Cys Tyr Gly Cys Ala Ser	
1137 1142 1147 1152	
gct gtc aca gaa cat tgt atc aca cta ctt cgg gcc ctg gcc acc aac	3624
Ala Val Thr Glu His Cys Ile Thr Leu Leu Arg Ala Leu Ala Thr Asn	
1153 1158 1163 1168	
cca gcc ttg agg cac atc ctt gtc tcc cag ggc ctt atc cgg gag ctc	3672
Pro Ala Leu Arg His Ile Leu Val Ser Gln Gly Leu Ile Arg Glu Leu	
1169 1174 1179 1184	

ttt gat tat aat ctt cgc cga ggg gct gcg gcc atg cgg gag gag gtc	3720
Phe Asp Tyr Asn Leu Arg Arg Gly Ala Ala Met Arg Glu Glu Val	
1185 1190 1195 1200	
cgc cag ctc atg tgc ctc cta act cga gac aac cca gaa gcc acc caa	3768
Arg Gln Leu Met Cys Leu Leu Thr Arg Asp Asn Pro Glu Ala Thr Gln	
1201 1206 1211 1216	
cag atg aat gac ctg att att ggc aag gtc tcc aca gcc ctg aag ggc	3816
Gln Met Asn Asp Leu Ile Ile Gly Lys Val Ser Thr Ala Leu Lys Gly	
1217 1222 1227 1232	
cac tgg gcc aac ccc gat ctg gca agt agc ctg cag tat gaa atg ctg	3864
His Trp Ala Asn Pro Asp Leu Ala Ser Ser Leu Gln Tyr Glu Met Leu	
1233 1238 1243 1248	
ctg ctg acg gat tct atc tcc aag gag gac agc tgc tgg gag ctc cgg	3912
Leu Leu Thr Asp Ser Ile Ser Lys Glu Asp Ser Cys Trp Glu Leu Arg	
1249 1254 1259 1264	
tta cgc tgt gct ctc agc ctt ttc ctc atg gct gtg aac att aag act	3960
Leu Arg Cys Ala Leu Ser Leu Phe Leu Met Ala Val Asn Ile Lys Thr	
1265 1270 1275 1280	
cct gtg gtg gtt gaa aac att acc ctc atg tgc ctg agg atc ttg cag	4008
Pro Val Val Val Glu Asn Ile Thr Leu Met Cys Leu Arg Ile Leu Gln	
1281 1286 1291 1296	
aag ctg ata aaa cca cct gct ccc act agc aag aag aac aag gat gtc	4056
Lys Leu Ile Lys Pro Pro Ala Pro Thr Ser Lys Lys Asn Lys Asp Val	
1297 1302 1307 1312	
ccc gtt gag gcc ctc acc acg gtg aag cca tac tgc aat gag atc cat	4104
Pro Val Glu Ala Leu Thr Thr Val Lys Pro Tyr Cys Asn Glu Ile His	
1313 1318 1323 1328	
gcc cag gct caa ctg tgg ctc aag aga gac ccc aag gca tcc tat gat	4152
Ala Gln Ala Gln Leu Trp Leu Lys Arg Asp Pro Lys Ala Ser Tyr Asp	
1329 1334 1339 1344	
gcc tgg aag aag tgt ctt cct atc aga ggg ata gat ggc aat ggg aaa	4200
Ala Trp Lys Lys Cys Leu Pro Ile Arg Gly Ile Asp Gly Asn Gly Lys	
1345 1350 1355 1360	
gcc ccc agc aaa tca gag ctc cgc cat ctc tat ttg act gag aag tat	4248
Ala Pro Ser Lys Ser Glu Leu Arg His Leu Tyr Leu Thr Glu Lys Tyr	
1361 1366 1371 1376	
gtg tgg agg tgg aaa cag ttc ctg agt cgt cgg ggg aag agg acc tcc	4296
Val Trp Arg Trp Lys Gln Phe Leu Ser Arg Arg Gly Lys Arg Thr Ser	
1377 1382 1387 1392	
ccc ttg gat ctc aaa ctg ggg cat aac aac tgg ctg cga caa gtg ctt	4344
Pro Leu Asp Leu Lys Leu Gly His Asn Asn Trp Leu Arg Gln Val Leu	
1393 1398 1403 1408	
ttc act cca gca acg cag gcc gca cgg cag gca gcc tgt acc att gtg	4392

1633	1638	1643	1648	
agc aat gag cca ggc atc ggg ccg ctg atg agg gat ata aag aac aag				5112
Ser Asn Glu Pro Gly Ile Gly Pro Leu Met Arg Asp Ile Lys Asn Lys				
1649	1654	1659	1664	
att tgc cag gac tgt gac tta gtg gcc ctc ctg gaa gat gac agt ggc				5160
Ile Cys Gln Asp Cys Asp Leu Val Ala Leu Leu Glu Asp Asp Ser Gly				
1665	1670	1675	1680	
atg gag ctt cta gtg aac aat aaa atc att agt ttg gac ctt cct gtg				5208
Met Glu Leu Leu Val Asn Asn Lys Ile Ile Ser Leu Asp Leu Pro Val				
1681	1686	1691	1696	
gct gaa gtt tac aag aaa gtc tgg tgt acc acg aat gag gga gag ccc				5256
Ala Glu Val Tyr Lys Lys Val Trp Cys Thr Thr Asn Glu Gly Glu Pro				
1697	1702	1707	1712	
atg agg att gtt tat cgt atg cgg ggg ctg ctg ggc gat gcc aca gag				5304
Met Arg Ile Val Tyr Arg Met Arg Gly Leu Leu Gly Asp Ala Thr Glu				
1713	1718	1723	1728	
gag ttc att gag tcc ctg gac tct act aca gat gaa gaa gaa gat gaa				5352
Glu Phe Ile Glu Ser Leu Asp Ser Thr Thr Asp Glu Glu Glu Asp Glu				
1729	1734	1739	1744	
gaa gaa gtg tat aaa atg gct ggt gtg atg gcc cag tgt ggg ggc ctg				5400
Glu Glu Val Tyr Lys Met Ala Gly Val Met Ala Gln Cys Gly Gly Leu				
1745	1750	1755	1760	
gaa tgc atg ctt aac aga ctc gca ggg atc aga gat ttc aag cag gga				5448
Glu Cys Met Leu Asn Arg Leu Ala Gly Ile Arg Asp Phe Lys Gln Gly				
1761	1766	1771	1776	
cgc cac ctt cta aca gtg cta ctg aaa ttg ttc agt tac tgc gtg aag				5496
Arg His Leu Leu Thr Val Leu Leu Lys Leu Phe Ser Tyr Cys Val Lys				
1777	1782	1787	1792	
gtg aaa gtc aac cgg cag caa ctg gtc aaa ctg gaa atg aac acc ttg				5544
Val Lys Val Asn Arg Gln Gln Leu Val Lys Leu Glu Met Asn Thr Leu				
1793	1798	1803	1808	
aac gtc atg ctg ggg acc cta aac ctg gcc ctt gta gct gaa caa gaa				5592
Asn Val Met Leu Gly Thr Leu Asn Leu Ala Leu Val Ala Glu Gln Glu				
1809	1814	1819	1824	
agc aag gac agt ggg ggt gca gct gtg gct gag cag gtg ctt agc atc				5640
Ser Lys Asp Ser Gly Gly Ala Ala Val Ala Glu Gln Val Leu Ser Ile				
1825	1830	1835	1840	
atg gag atc att cta gat gag tcc aat gct gag ccc ctg agt gag gac				5688
Met Glu Ile Ile Leu Asp Glu Ser Asn Ala Glu Pro Leu Ser Glu Asp				
1841	1846	1851	1856	
aag ggc aac ctc ctc ctg aca ggt gac aag gat caa ctg gtg atg ctc				5736
Lys Gly Asn Leu Leu Leu Thr Gly Asp Lys Asp Gln Leu Val Met Leu				
1857	1862	1867	1872	

ttg gac cag atc aac agc acc ttt gtt cgc tcc aac ccc agt gtg ctc Leu Asp Gln Ile Asn Ser Thr Phe Val Arg Ser Asn Pro Ser Val Leu 1873 1878 1883 1888	5784
cag ggc ctg ctt cgc atc atc ccg tac ctt tcc ttt gga gag gtg gag Gln Gly Leu Leu Arg Ile Ile Pro Tyr Leu Ser Phe Gly Glu Val Glu 1889 1894 1899 1904	5832
aaa atg cag atc ttg gtg gag cga ttc aaa cca tac tgc aac ttt gat Lys Met Gln Ile Leu Val Glu Arg Phe Lys Pro Tyr Cys Asn Phe Asp 1905 1910 1915 1920	5880
aaa tat gat gaa gat cac agt ggt gat gat aaa gtc ttc ctg gac tgc Lys Tyr Asp Glu Asp His Ser Gly Asp Asp Lys Val Phe Leu Asp Cys 1921 1926 1931 1936	5928
ttc tgt aaa ata gct gct ggc atc aag aac aac agc aat ggg cac cag Phe Cys Lys Ile Ala Ala Gly Ile Lys Asn Asn Ser Asn Gly His Gln 1937 1942 1947 1952	5976
ctg aag gat ctg att ctc cag aag ggg atc acc cag aat gca ctt gac Leu Lys Asp Leu Ile Leu Gln Lys Gly Ile Thr Gln Asn Ala Leu Asp 1953 1958 1963 1968	6024
tac atg aaa aag cac atc cct agc gcc aag aat ttg gat gcc gac atc Tyr Met Lys Lys His Ile Pro Ser Ala Lys Asn Leu Asp Ala Asp Ile 1969 1974 1979 1984	6072
tgg aaa aag ttt ttg tct cgc cca gcc ttg cca ttt atc cta agg ctg Trp Lys Lys Phe Leu Ser Arg Pro Ala Leu Pro Phe Ile Leu Arg Leu 1985 1990 1995 2000	6120
ctt cgg ggc ctg gcc atc cag cac cct ggc acc cag gtt ctg att gga Leu Arg Gly Leu Ala Ile Gln His Pro Gly Thr Gln Val Leu Ile Gly 2001 2006 2011 2016	6168
act gat tcc atc ccg aac ctg cat aag ctg gag cag gtg tcc agt gat Thr Asp Ser Ile Pro Asn Leu His Lys Leu Glu Gln Val Ser Ser Asp 2017 2022 2027 2032	6216
gag ggc att ggg acc ttg gca gag aac ctg ctg gaa gcc ctg cgg gaa Glu Gly Ile Gly Thr Leu Ala Glu Asn Leu Leu Glu Ala Leu Arg Glu 2033 2038 2043 2048	6264
cac cct gac gta aac aag aag att gac gca gcc cgc agg gag acc cgg His Pro Asp Val Asn Lys Lys Ile Asp Ala Ala Arg Arg Glu Thr Arg 2049 2054 2059 2064	6312
gca gag aag aaa cgc atg gcc atg gca atg agg cag aag gcc ctg ggc Ala Glu Lys Lys Arg Met Ala Met Ala Met Arg Gln Lys Ala Leu Gly 2065 2070 2075 2080	6360
acc ctg ggc atg acg aca aat gaa aag ggc cag gtc gtg acc aag aca Thr Leu Gly Met Thr Thr Asn Glu Lys Gly Gln Val Val Thr Lys Thr 2081 2086 2091 2096	6408

gca ctc ctg aag cag atg gaa gag ctg atc gag gag cct ggc ctc acg	6456
Ala Leu Leu Lys Gln Met Glu Glu Leu Ile Glu Glu Pro Gly Leu Thr	
2097 2102 2107 2112	
tgc tgc atc tgc agg gag gga tac aag ttc cag ccc aca aag gtc ctg	6504
Cys Cys Ile Cys Arg Glu Gly Tyr Lys Phe Gln Pro Thr Lys Val Leu	
2113 2118 2123 2128	
ggc att tat acc ttc acg aag cgg gta gcc ttg gag gag ttg gag aat	6552
Gly Ile Tyr Thr Phe Thr Lys Arg Val Ala Leu Glu Glu Leu Glu Asn	
2129 2134 2139 2144	
aag ccc cgg aaa cag cag ggc tac agc acc gtg tcc cac ttc aac att	6600
Lys Pro Arg Lys Gln Gln Gly Tyr Ser Thr Val Ser His Phe Asn Ile	
2145 2150 2155 2160	
gtg cac tac gac tgc cat ctg gct gcc gtc agg ttg gct cga ggc cgg	6648
Val His Tyr Asp Cys His Leu Ala Ala Val Arg Leu Ala Arg Gly Arg	
2161 2166 2171 2176	
gaa gag tgg gag agt gcc gcc ctg cag aat gcc aac acc aag tgc aac	6696
Glu Glu Trp Glu Ser Ala Ala Leu Gln Asn Ala Asn Thr Lys Cys Asn	
2177 2182 2187 2192	
ggg ctc ctt ccg gtc tgg gga cct cat gtc cct gaa tca gct ttt gcc	6744
Gly Leu Leu Pro Val Trp Gly Pro His Val Pro Glu Ser Ala Phe Ala	
2193 2198 2203 2208	
act tgc ttg gca aga cac aac act tac ctc cag gaa tgt aca ggc cag	6792
Thr Cys Leu Ala Arg His Asn Thr Tyr Leu Gln Glu Cys Thr Gly Gln	
2209 2214 2219 2224	
cgg gag ccc acg tat cag ctc aac atc cat gac atc aaa ctg ctc ttc	6840
Arg Glu Pro Thr Tyr Gln Leu Asn Ile His Asp Ile Lys Leu Leu Phe	
2225 2230 2235 2240	
ctg cgc ttc gcc atg gag cag tcg ttc agc gca gac act ggc ggg gcc	6888
Leu Arg Phe Ala Met Glu Gln Ser Phe Ser Ala Asp Thr Gly Gly Gly	
2241 2246 2251 2256	
ggc cgg gag agc aac atc cac ctg atc ccg tac atc att cac act gtg	6936
Gly Arg Glu Ser Asn Ile His Leu Ile Pro Tyr Ile Ile His Thr Val	
2257 2262 2267 2272	
ctt tac gtc ctg aac aca acc cga gca act tcc cga gaa gag aag aac	6984
Leu Tyr Val Leu Asn Thr Thr Arg Ala Thr Ser Arg Glu Glu Lys Asn	
2273 2278 2283 2288	
ctc caa ggc ttt ctg gaa cag ccc aag gag aag tgg gtg gag agt gcc	7032
Leu Gln Gly Phe Leu Glu Gln Pro Lys Glu Lys Trp Val Glu Ser Ala	
2289 2294 2299 2304	
ttt gaa gtg gac ggg ccc tac tat ttc aca gtc ttg gcc ctt cac atc	7080
Phe Glu Val Asp Gly Pro Tyr Tyr Phe Thr Val Leu Ala Leu His Ile	
2305 2310 2315 2320	
ctg ccc cct gag cag tgg aga gcc aca cgt gtg gaa atc ttg cgg agg	7128

<222> (55) .. (2406)

<400> 105

cttcctctcc acgcggttga gaagaccggt cggcctgggc aacctgcgct gaag atg	57
Met	
1	
ccg gga aaa ctc cgt agt gac gct ggt ttg gaa tca gac acc gca atg	105
Pro Gly Lys Leu Arg Ser Asp Ala Gly Leu Glu Ser Asp Thr Ala Met	
2 7 12 17	
aaa aaa ggg gag aca ctg cga aag caa acc gag gag aaa gag aaa aaa	153
Lys Lys Gly Glu Thr Leu Arg Lys Gln Thr Glu Glu Lys Glu Lys Lys	
18 23 28 33	
gag aag cca aaa tct gat aag act gaa gag ata gca gaa gag gaa gaa	201
Glu Lys Pro Lys Ser Asp Lys Thr Glu Glu Ile Ala Glu Glu Glu Glu	
34 39 44 49	
act gtt ttc ccc aaa gct aaa caa gtt aaa aag aaa gca gag cct tct	249
Thr Val Phe Pro Lys Ala Lys Gln Val Lys Lys Lys Ala Glu Pro Ser	
50 55 60 65	
gaa gtt gac atg aat tct cct aaa tcc aaa aag gca aaa aag aaa gag	297
Glu Val Asp Met Asn Ser Pro Lys Ser Lys Lys Ala Lys Lys Lys Glu	
66 71 76 81	
gag cca tct caa aat gac att tct cct aaa acc aaa agt ttg aga aag	345
Glu Pro Ser Gln Asn Asp Ile Ser Pro Lys Thr Lys Ser Leu Arg Lys	
82 87 92 97	
aaa aag gag ccc att gaa aag aaa gtg gtt tct tct aaa acc aaa aaa	393
Lys Lys Glu Pro Ile Glu Lys Lys Val Val Ser Ser Lys Thr Lys Lys	
98 103 108 113	
gtg aca aaa aat gag gag cct tct gag gaa gaa ata gat gct cct aag	441
Val Thr Lys Asn Glu Glu Pro Ser Glu Glu Glu Ile Asp Ala Pro Lys	
114 119 124 129	
ccc aag aag atg aag aaa gaa aag gaa atg aat gga gaa act aga gag	489
Pro Lys Lys Met Lys Lys Glu Lys Glu Met Asn Gly Glu Thr Arg Glu	
130 135 140 145	
aaa agc ccc aaa ctg aag aat gga ttt cct cat cct gaa ccg gac tgt	537
Lys Ser Pro Lys Leu Lys Asn Gly Phe Pro His Pro Glu Pro Asp Cys	
146 151 156 161	
aac ccc agt gaa gct gcc agt gaa gaa agt aac agt gag ata gag cag	585
Asn Pro Ser Glu Ala Ala Ser Glu Glu Ser Asn Ser Glu Ile Glu Gln	
162 167 172 177	
gaa ata cct gtg gaa caa aaa gaa ggc gct ttc tct aat ttt ccc ata	633
Glu Ile Pro Val Glu Gln Lys Glu Gly Ala Phe Ser Asn Phe Pro Ile	
178 183 188 193	
tct gaa gaa act att aaa ctt ctc aaa ggc cga gga gtg acc ttc cta	681
Ser Glu Glu Thr Ile Lys Leu Leu Lys Gly Arg Gly Val Thr Phe Leu	

194	199	204	209	
ttt cct ata caa gca aag aca ttc cat cat gtt tac agc ggg aag gac				729
Phe Pro Ile Gln Ala Lys Thr Phe His His Val Tyr Ser Gly Lys Asp				
210	215	220	225	
tta att gca cag gca cgg aca gga act ggg aag aca ttc tcc ttt gcc				777
Leu Ile Ala Gln Ala Arg Thr Gly Thr Gly Lys Thr Phe Ser Phe Ala				
226	231	236	241	
atc cct ttg att gag aaa ctt cat ggg gaa ctg caa gac agg aag aga				825
Ile Pro Leu Ile Glu Lys Leu His Gly Glu Leu Gln Asp Arg Lys Arg				
242	247	252	257	
ggc cgt gcc cct cag gta ctg gtt ctt gca cct aca aga gag ttg gca				873
Gly Arg Ala Pro Gln Val Leu Val Leu Ala Pro Thr Arg Glu Leu Ala				
258	263	268	273	
aat caa gta agc aaa gac ttc agt gac atc aca aaa aag ctg tca gtg				921
Asn Gln Val Ser Lys Asp Phe Ser Asp Ile Thr Lys Lys Leu Ser Val				
274	279	284	289	
gct tgt ttt tat ggt gga act ccc tat gga ggt caa ttt gaa cgc atg				969
Ala Cys Phe Tyr Gly Gly Thr Pro Tyr Gly Gly Gln Phe Glu Arg Met				
290	295	300	305	
agg aat ggg att gat atc ctg gtt gga aca cca ggt cgt atc aaa gac				1017
Arg Asn Gly Ile Asp Ile Leu Val Gly Thr Pro Gly Arg Ile Lys Asp				
306	311	316	321	
cac ata cag aat ggc aaa cta gat ctc acc aaa ctt aag cat gtt gtc				1065
His Ile Gln Asn Gly Lys Leu Asp Leu Thr Lys Leu Lys His Val Val				
322	327	332	337	
ctg gat gaa gtg gac cag atg ttg gat atg gga ttt gct gat caa gtg				1113
Leu Asp Glu Val Asp Gln Met Leu Asp Met Gly Phe Ala Asp Gln Val				
338	343	348	353	
gaa gag att tta agt gtg gca tac aag aaa gat tct gaa gac aat ccc				1161
Glu Glu Ile Leu Ser Val Ala Tyr Lys Lys Asp Ser Glu Asp Asn Pro				
354	359	364	369	
caa aca ttg ctt ttt tct gca act tgc cct cat tgg gta ttt aat gtt				1209
Gln Thr Leu Leu Phe Ser Ala Thr Cys Pro His Trp Val Phe Asn Val				
370	375	380	385	
gcc aag aaa tac atg aaa tct aca tat gaa cag gtg gac ctg att ggt				1257
Ala Lys Lys Tyr Met Lys Ser Thr Tyr Glu Gln Val Asp Leu Ile Gly				
386	391	396	401	
aaa aag act cag aaa acg gca ata act gtg gag cat ctg gct att aag				1305
Lys Lys Thr Gln Lys Thr Ala Ile Thr Val Glu His Leu Ala Ile Lys				
402	407	412	417	
tgc cac tgg act cag agg gca gca gtt att ggg gat gtc atc cga gta				1353
Cys His Trp Thr Gln Arg Ala Ala Val Ile Gly Asp Val Ile Arg Val				
418	423	428	433	

tat agt ggt cat caa gga cgc act atc atc ttt tgt gaa acc aag aaa	1401
Tyr Ser Gly His Gln Gly Arg Thr Ile Ile Phe Cys Glu Thr Lys Lys	
434 439 444 449	
gaa gcc cag gag ctg tcc cag aat tca gct ata aag cag gat gct cag	1449
Glu Ala Gln Glu Leu Ser Gln Asn Ser Ala Ile Lys Gln Asp Ala Gln	
450 455 460 465	
tcc ttg cat gga gac att cca cag aag caa agg gaa atc acc ctg aaa	1497
Ser Leu His Gly Asp Ile Pro Gln Lys Gln Arg Glu Ile Thr Leu Lys	
466 471 476 481	
ggg ttt aga aat ggt agt ttt gga gtt ttg gtg gca acc aat gtt gct	1545
Gly Phe Arg Asn Gly Ser Phe Gly Val Leu Val Ala Thr Asn Val Ala	
482 487 492 497	
gca cgt ggg tta gac atc cct gag gtt gat ttg gtt ata caa agc tct	1593
Ala Arg Gly Leu Asp Ile Pro Glu Val Asp Leu Val Ile Gln Ser Ser	
498 503 508 513	
cca cca aag gat gta gag tcc tac att cat cga tcc ggg cgg aca ggc	1641
Pro Pro Lys Asp Val Glu Ser Tyr Ile His Arg Ser Gly Arg Thr Gly	
514 519 524 529	
aga gct gga agg acg ggg gtg tgc atc tgc ttt tat cag cac aag gaa	1689
Arg Ala Gly Arg Thr Gly Val Cys Ile Cys Phe Tyr Gln His Lys Glu	
530 535 540 545	
gaa tat cag tta gta caa gtg gag caa aaa gcg gga att aag ttc aaa	1737
Glu Tyr Gln Leu Val Gln Val Glu Gln Lys Ala Gly Ile Lys Phe Lys	
546 551 556 561	
cga ata ggt gtt cct tct gca aca gaa ata ata aaa gct tcc agc aaa	1785
Arg Ile Gly Val Pro Ser Ala Thr Glu Ile Ile Lys Ala Ser Ser Lys	
562 567 572 577	
gat gcc atc agg ctt ttg gat tcc gtg cct ccc act gcc att agt cac	1833
Asp Ala Ile Arg Leu Leu Asp Ser Val Pro Pro Thr Ala Ile Ser His	
578 583 588 593	
ttc aaa caa tca gct gag aag ctg ata gag gag aag gga gct gtg gaa	1881
Phe Lys Gln Ser Ala Glu Lys Leu Ile Glu Glu Lys Gly Ala Val Glu	
594 599 604 609	
gct ctg gca gca gca ctg gcc cat att tca ggt gcc acg tcc gta gac	1929
Ala Leu Ala Ala Ala Leu Ala His Ile Ser Gly Ala Thr Ser Val Asp	
610 615 620 625	
cag cgc tcc ttg atc aac tca aat gtg ggt ttt gtg acc atg atc ttg	1977
Gln Arg Ser Leu Ile Asn Ser Asn Val Gly Phe Val Thr Met Ile Leu	
626 631 636 641	
cag tgc tca att gaa atg cca aat att agt tat gct tgg aaa gaa ctt	2025
Gln Cys Ser Ile Glu Met Pro Asn Ile Ser Tyr Ala Trp Lys Glu Leu	
642 647 652 657	

aaa gag cag ctg ggc gag gag att gat tcc aaa gtg aag gga atg gtt	2073
Lys Glu Gln Leu Gly Glu Glu Ile Asp Ser Lys Val Lys Gly Met Val	
658 663 668 673	
ttt ctc aaa gga aag ctg ggt gtt tgc ttt gat gta cct acc gca tca	2121
Phe Leu Lys Gly Lys Leu Gly Val Cys Phe Asp Val Pro Thr Ala Ser	
674 679 684 689	
gta aca gaa ata cag gag aaa tgg cat gat tca cga cgc tgg cag ctc	2169
Val Thr Glu Ile Gln Glu Lys Trp His Asp Ser Arg Arg Trp Gln Leu	
690 695 700 705	
tct gtg gcc aca gag caa cca gaa ctg gaa gga cca cgg gaa gga tat	2217
Ser Val Ala Thr Glu Gln Pro Glu Leu Glu Gly Pro Arg Glu Gly Tyr	
706 711 716 721	
gga ggc ttc agg gga cag cgg gaa ggc agt cga ggc ttc agg gga cag	2265
Gly Gly Phe Arg Gly Gln Arg Glu Gly Ser Arg Gly Phe Arg Gly Gln	
722 727 732 737	
cgg gac gga aac aga aga ttc aga gga cag cgg gaa ggc agt aga ggc	2313
Arg Asp Gly Asn Arg Arg Phe Arg Gly Gln Arg Glu Gly Ser Arg Gly	
738 743 748 753	
ccg aga gga cag cga tca gga ggt ggc aac aaa agt aac aga tcc caa	2361
Pro Arg Gly Gln Arg Ser Gly Gly Gly Asn Lys Ser Asn Arg Ser Gln	
754 759 764 769	
aac aaa ggc cag aag cgg agt ttc agt aaa gca ttt ggt caa taa tta	2409
Asn Lys Gly Gln Lys Arg Ser Phe Ser Lys Ala Phe Gly Gln *	
770 775 780	
gaaatagaag atttatatag caaaaagaga atgatgtttg gcaatataga actgaacatt	2469
atttttcatg caaagttaaa agcacattgt gcttcctttt gaccacttgc caagtcctg	2529
tctctttcag acacagacaa gcttcattta aattatttca tctgatcatt atcatttata	2589
actttattgt tacttcttca tcagtttttc cttttgaaag gtgtatgaat tcattacatt	2649
tttattctaa tgtattatct gtagattaga agataaaatc aagcatgtat ctgcctatac	2709
tttgtgagtt cacctgtctt tataactcaaa agtgtccctt aatagtgtcc ttccctgaaa	2769
taaataccta agggagtgtgta acagtctctg gaggaccact ttgagccttt ggaagttaag	2829
gtttcctcag ccacctgccg aacagtttct catgtgggtcc tattatttgt ctactgagac	2889
ttaatactga gcaatgtttt gaaacaagat ttcaaaactaa tctgggttgt aatacagttt	2949
ataccagtgt atgctctaga cttggaagat gtagtatgtt tgatgtggat tacctatact	3009
tatgttcggt ttgatacatt tttagcttct cattataagg tgattcatgc tttagtgaat	3069
tcttcataga tagtatatat aaaagtacat tttaatagaa agccagggtt ttaaggaatt	3129
tcacatgtat aagggtggctc catagcttta tttgtaagta ggctggataa atgggtgctta	3189

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

```
<220>
<221> CDS
<222> (83)..(2284)
```

365

Glu Glu Glu Glu Lys	Glu Glu Asn Glu Ser His Lys Trp Ser Thr Gly	
139	144 149 154	
gaa gaa tac atc gct gtt gga gat ttt act gct cag caa gtt gga gat		592
Glu Glu Tyr Ile Ala Val Gly Asp Phe Thr Ala Gln Gln Val Gly Asp		
155	160 165 170	
ctt aca ttt aag aaa ggg gaa att ctc ctt gta att gaa aaa aaa cct		640
Leu Thr Phe Lys Lys Gly Glu Ile Leu Leu Val Ile Glu Lys Lys Pro		
171	176 181 186	
gat ggt tgg tgg ata gct aag gat gcc aaa gga aat gaa ggt ctt gtt		688
Asp Gly Trp Trp Ile Ala Lys Asp Ala Lys Gly Asn Glu Gly Leu Val		
187	192 197 202	
ccc aga acc tac cta gag cct tat agt gaa gaa gaa gaa ggc caa gaa		736
Pro Arg Thr Tyr Leu Glu Pro Tyr Ser Glu Glu Glu Glu Gly Gln Glu		
203	208 213 218	
tca agt gaa gag ggc agt gaa gaa gat gta gag gcg gtg gat gaa aca		784
Ser Ser Glu Glu Gly Ser Glu Glu Asp Val Glu Ala Val Asp Glu Thr		
219	224 229 234	
gca gat gga gca gaa gtt aag caa aga act gat ccc cac tgg agt gct		832
Ala Asp Gly Ala Glu Val Lys Gln Arg Thr Asp Pro His Trp Ser Ala		
235	240 245 250	
gtt cag aaa gcg att tca gag gcg ggc atc ttc tgt ctt gtt aat cat		880
Val Gln Lys Ala Ile Ser Glu Ala Gly Ile Phe Cys Leu Val Asn His		
251	256 261 266	
gtc tcg ttt tgc tac cta ata gtt ctg atg cga aat agg atg gag act		928
Val Ser Phe Cys Tyr Leu Ile Val Leu Met Arg Asn Arg Met Glu Thr		
267	272 277 282	
gtg gaa gac acc aat gga tct gaa aca ggg ttc agg gca tgg aat gta		976
Val Glu Asp Thr Asn Gly Ser Glu Thr Gly Phe Arg Ala Trp Asn Val		
283	288 293 298	
cag agc aga gga cgt ata ttt ctg gtt tct aag cct gtg ctc cag cag		1024
Gln Ser Arg Gly Arg Ile Phe Leu Val Ser Lys Pro Val Leu Gln Gln		
299	304 309 314	
ata aac act gtt gat gtg tta act acg atg gga gct att cct gca ggg		1072
Ile Asn Thr Val Asp Val Leu Thr Thr Met Gly Ala Ile Pro Ala Gly		
315	320 325 330	
ttc agg cct tcc acg ctc tca cag ctt ctg gag gaa ggg aat caa ttt		1120
Phe Arg Pro Ser Thr Leu Ser Gln Leu Leu Glu Glu Gly Asn Gln Phe		
331	336 341 346	
cga gca aat tac ttc tta caa cca gag ctc atg cct tca caa ctg gcc		1168
Arg Ala Asn Tyr Phe Leu Gln Pro Glu Leu Met Pro Ser Gln Leu Ala		
347	352 357 362	
ttc aga gat ctg atg tgg gat gct aca gaa ggc act att agg tcg aga		1216
Phe Arg Asp Leu Met Trp Asp Ala Thr Glu Gly Thr Ile Arg Ser Arg		

363	368	373	378	
cca agt cgt att tca ttg att ctg aca tta tgg agc tgt aaa atg att				1264
Pro Ser Arg Ile Ser Leu Ile Leu Thr Leu Trp Ser Cys Lys Met Ile				
379	384	389	394	
cct ctt cca gga atg agc ata cag gtt ctg agc aga cat gta cgc ctg				1312
Pro Leu Pro Gly Met Ser Ile Gln Val Leu Ser Arg His Val Arg Leu				
395	400	405	410	
tgt cta ttt gat ggt aat aag gtt ctg agc aac att cat aca gtc aga				1360
Cys Leu Phe Asp Gly Asn Lys Val Leu Ser Asn Ile His Thr Val Arg				
411	416	421	426	
gcc aca tgg caa cct aaa aag ccc aaa aca tgg acc ttt tct ccc cag				1408
Ala Thr Trp Gln Pro Lys Lys Pro Lys Thr Trp Thr Phe Ser Pro Gln				
427	432	437	442	
gtt act cgc atc tta cca tgt ttg ctt gat ggt gat tgc ttt atc agg				1456
Val Thr Arg Ile Leu Pro Cys Leu Leu Asp Gly Asp Cys Phe Ile Arg				
443	448	453	458	
tct aat tct gca tct cca gat ctt gga ata tta ttt gaa ctt gga att				1504
Ser Asn Ser Ala Ser Pro Asp Leu Gly Ile Leu Phe Glu Leu Gly Ile				
459	464	469	474	
tct tat att cgc aat tca act ggt gaa aga gga gag tta agc tgt ggc				1552
Ser Tyr Ile Arg Asn Ser Thr Gly Glu Arg Gly Glu Leu Ser Cys Gly				
475	480	485	490	
tgg gtg ttt ctt aaa ctt ttt gat gcc agt gga gtt cct att cca gca				1600
Trp Val Phe Leu Lys Leu Phe Asp Ala Ser Gly Val Pro Ile Pro Ala				
491	496	501	506	
aaa act tat gag ctt ttc ttg aat ggt ggt act cct tat gaa aaa ggt				1648
Lys Thr Tyr Glu Leu Phe Leu Asn Gly Gly Thr Pro Tyr Glu Lys Gly				
507	512	517	522	
att gaa gtg gac cct tca ata tcc aga aga gca cac ggc agt gtt ttc				1696
Ile Glu Val Asp Pro Ser Ile Ser Arg Arg Ala His Gly Ser Val Phe				
523	528	533	538	
tac cag att atg aca atg aga agg cag cct caa ctt cta gtg aaa ctg				1744
Tyr Gln Ile Met Thr Met Arg Arg Gln Pro Gln Leu Leu Val Lys Leu				
539	544	549	554	
aga tcc ttg aac aga aga tca aga aat gta cta agt cta ctg cca gaa				1792
Arg Ser Leu Asn Arg Arg Ser Arg Asn Val Leu Ser Leu Leu Pro Glu				
555	560	565	570	
aca tta att gga aat atg tgt tct att cac ttg ttg ata ttt tat cga				1840
Thr Leu Ile Gly Asn Met Cys Ser Ile His Leu Leu Ile Phe Tyr Arg				
571	576	581	586	
caa att ctt gga gat gtg ctg ctg aaa gac agg atg agc ttg caa agt				1888
Gln Ile Leu Gly Asp Val Leu Leu Lys Asp Arg Met Ser Leu Gln Ser				
587	592	597	602	

act gat tta att agc cat ccc atg ctg gcc acc ttc ccc atg ctc ttg	1936
Thr Asp Leu Ile Ser His Pro Met Leu Ala Thr Phe Pro Met Leu Leu	
603 608 613 618	
gag cag cct gat gtg atg gat gct ctc agg agt tgc tgg gct gga aaa	1984
Glu Gln Pro Asp Val Met Asp Ala Leu Arg Ser Ser Trp Ala Gly Lys	
619 624 629 634	
gaa agc aca tta aaa aga tca gag aag aga gac aaa gag ttc ctg aag	2032
Glu Ser Thr Leu Lys Arg Ser Glu Lys Arg Asp Lys Glu Phe Leu Lys	
635 640 645 650	
tcc acg ttt ctc ctg gtt tac cat gac tgc gtg ctc cca ctt ctc cac	2080
Ser Thr Phe Leu Leu Val Tyr His Asp Cys Val Leu Pro Leu Leu His	
651 656 661 666	
tcc aca cgc cta ccc cca ttc agg tgg gca gaa gaa gag act gag act	2128
Ser Thr Arg Leu Pro Pro Phe Arg Trp Ala Glu Glu Glu Thr Glu Thr	
667 672 677 682	
gca cgg tgg aaa gtt atc act gac ttc ctt aag caa aac caa gaa aac	2176
Ala Arg Trp Lys Val Ile Thr Asp Phe Leu Lys Gln Asn Gln Glu Asn	
683 688 693 698	
cag ggc gcc ctc caa gct ctg ctg tca cca gac gga gtt cat gaa cct	2224
Gln Gly Ala Leu Gln Ala Leu Leu Ser Pro Asp Gly Val His Glu Pro	
699 704 709 714	
ttt gac ctt tca gag cag acc tat gac ttc ttg ggt gaa atg aga aag	2272
Phe Asp Leu Ser Glu Gln Thr Tyr Asp Phe Leu Gly Glu Met Arg Lys	
715 720 725 730	
aat gca gtg tga cag tggcagcctc tagcctcag ctccccaagg aatcagatgg	2327
Asn Ala Val *	
731	
atcctccacg attacgtgaa taaaatgatg gaaccaaaaa tcaactgtcac ttacaaactt	2387
aggttttact cttttctttc tacagaccat attttttaaag aaatgtttat acaataattt	2447
aaatattttt taaaaccata aaataaattt ttataaggaa tactgttata tctaaattta	2507
aacagtattt atttttttcaa aaacagctac ttaagttaat ggtatagatt tctataaaag	2567
caagatttttg tcaaaaaacta aatttatgat tattcaagaa agtgaaaaaa acaacctaca	2627
gaatgggaaa acatattttgc aaatcatcta actgataaag gtctagtatc caaaatattt	2687
aaatttatga gtgttaataa aatttatctt gttcaatgaa gaggaagtta aagtgatoca	2747
tttgagaaag ttgtatcaact taattcagtc tgatacttga atgtgattta cccctaatta	2807
agtacaaaaa cagagtcgct tttgcctttt caaatcaaga aaataagtgc tctgtcaaaa	2867
gcacaaaaag aaactttcag gcactggaga gtggagtcga ctcacccttt caggccttgt	2927

tgcattctcag ataaacctgt gactgctggt aaaataatgt cccaagcctt tccttttagt 2987
 gataaacagt agcagcctgc gtttaattgag cacctactgt gtgtctgagc atttctcatt 3047
 agcccagtta atcctcacac ctactgtagg agataggtac tgttggtttt tattacogcc 3107
 gaagaaacag gccagataag tgaagtaatt tgcctaaggt cacagctaata aagtggcaca 3167
 gctaatatct ccagtaaaga taccatgtat aattttctac aacctaagat gttctgcctt 3227
 atcgggggcga accttttagg attccatgtg aaaataaaat atgaggaaaa gtttaacctt 3287
 aataattaga atcccattag aggtactttt ttttgatggc atgctgcctt aaaagagcca 3347
 tttattttta gagatctgtc atattatgaa agttctgggc tatcttagct aacttatcct 3407
 aaacccttaa cctaaattta acttgagccc cagtctcaga aattaacatg gtatgaaagt 3467
 gtttccaggc caggcgcggt ggctcacgcc tgtaatccca acactttggg aggccgaggt 3527
 ggggtggatca cctgaggtca ggagtttgag accagcctgg ccaacactat ctgtactaaa 3587
 aacacaaaat tagctgggtg tggtagtgcg tgcctgtgat ccagctact tgggaggctg 3647
 aggtagaaga attgtttgaa cctgggaggt ggaggttgca gtgagccaag atcgtgccat 3707
 tgcactccag cctaggcaac aagagtgaaa ctccatctca aaaaaaaaaa 3757

<210> 107
 <211> 2783
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (84)..(1448)

<400> 107
 atctcagagt ggcggaattc gccgggacca gccgctcggg gccgggctga tacagccgct 60
 tcaccgtgcc cctgcccgcg acc atg gcc tcc tcc gag gtg gcg cgg cac 110
 Met Ala Ser Ser Glu Val Ala Arg His
 1 5
 ctg ctc ttt cag tct cac atg gca acg aaa aca act tgt atg tct tca 158
 Leu Leu Phe Gln Ser His Met Ala Thr Lys Thr Thr Cys Met Ser Ser
 10 15 20 25
 caa gga tca gat gat gaa cag ata aaa aga gaa aac att cgt tcg ttg 206
 Gln Gly Ser Asp Asp Glu Gln Ile Lys Arg Glu Asn Ile Arg Ser Leu
 26 31 36 41
 act atg tct ggc cat gtt ggt ttt gag agt ttg cct gat cag ctg gtg 254
 Thr Met Ser Gly His Val Gly Phe Glu Ser Leu Pro Asp Gln Leu Val

42	47	52	57	
aac aga tcc att cag	caa ggg ttc tgc ttt	aat att ctc tgt gtg ggg		302
Asn Arg Ser Ile Gln	Gln Gly Phe Cys Phe	Asn Ile Leu Cys Val Gly		
58	63	68	73	
gaa act gga att gga	aaa tca aca ctg att	gac aca ttg ttt aat act		350
Glu Thr Gly Ile Gly	Lys Ser Thr Leu Ile	Asp Thr Leu Phe Asn Thr		
74	79	84	89	
aat ttt gaa gac tat	gaa tcc tca cat ttt	tgc cca aat gtt aaa ctt		398
Asn Phe Glu Asp Tyr	Glu Ser Ser His Phe	Cys Pro Asn Val Lys Leu		
90	95	100	105	
aaa gct cag aca tat	gaa ctc cag gaa agt	aat gtt caa ttg aaa ttg		446
Lys Ala Gln Thr Tyr	Glu Leu Gln Glu Ser	Asn Val Gln Leu Lys Leu		
106	111	116	121	
acc att gtg aat aca	gtg gga ttt ggt gac	caa ata aat aaa gaa gag		494
Thr Ile Val Asn Thr	Val Gly Phe Gly Asp	Gln Ile Asn Lys Glu Glu		
122	127	132	137	
agc tac caa cca ata	gtt gac tac ata gat	gct cag ttt gag gcc tat		542
Ser Tyr Gln Pro Ile	Val Asp Tyr Ile Asp	Ala Gln Phe Glu Ala Tyr		
138	143	148	153	
ctc caa gaa gaa ctg	aag att aag cgt tct	ctc ttt acc tac cat gat		590
Leu Gln Glu Glu Leu	Lys Ile Lys Arg Ser	Leu Phe Thr Tyr His Asp		
154	159	164	169	
tct cgc atc cat gtg	tgt ctc tac ttc att	tca ccg aca ggc cac tct		638
Ser Arg Ile His Val	Cys Leu Tyr Phe Ile	Ser Pro Thr Gly His Ser		
170	175	180	185	
ctg aag aca ctt gat	ctc tta acc atg aag	aac ctt gac agc aag gta		686
Leu Lys Thr Leu Asp	Leu Leu Thr Met Lys	Asn Leu Asp Ser Lys Val		
186	191	196	201	
aac att ata cca gtg	att gcc aaa gca gat	acg gtt tct aaa act gaa		734
Asn Ile Ile Pro Val	Ile Ala Lys Ala Asp	Thr Val Ser Lys Thr Glu		
202	207	212	217	
tta cag aag ttt aag	atc aag ctc atg agt	gaa ttg gtc agc aat ggc		782
Leu Gln Lys Phe Lys	Ile Lys Leu Met Ser	Glu Leu Val Ser Asn Gly		
218	223	228	233	
gtc cag ata tac cag	ttc cca acg gat gat	gac act att gct aag gtc		830
Val Gln Ile Tyr Gln	Phe Pro Thr Asp Asp	Asp Thr Ile Ala Lys Val		
234	239	244	249	
aac gct gca atg aat	gga cag ttg ccg ttt	gct gtt gtg gga agt atg		878
Asn Ala Ala Met Asn	Gly Gln Leu Pro Phe	Ala Val Val Gly Ser Met		
250	255	260	265	
gat gag gta aaa gtc	gga aac aag atg gtc	aaa gct cgc cag tac cct		926
Asp Glu Val Lys Val	Gly Asn Lys Met Val	Lys Ala Arg Gln Tyr Pro		
266	271	276	281	

tgg ggt gtt gta caa gtg gaa aat gaa aac cac tgt gac ttt gta aag	974
Trp Gly Val Val Gln Val Glu Asn Glu Asn His Cys Asp Phe Val Lys	
282 287 292 297	
ctg cgg gaa atg ctc att tgt aca aat atg gag gac ctg cga gag cag	1022
Leu Arg Glu Met Leu Ile Cys Thr Asn Met Glu Asp Leu Arg Glu Gln	
298 303 308 313	
acc cat acc agg cac tat gag ctt tac agg cgc tgc aaa ctg gag gaa	1070
Thr His Thr Arg His Tyr Glu Leu Tyr Arg Arg Cys Lys Leu Glu Glu	
314 319 324 329	
atg ggc ttt aca gat gtg ggc cca gaa aac aag cca gtc agt gtt caa	1118
Met Gly Phe Thr Asp Val Gly Pro Glu Asn Lys Pro Val Ser Val Gln	
330 335 340 345	
gag acc tat gaa gcc aaa aga cat gag ttc cat ggt gaa cgt cag agg	1166
Glu Thr Tyr Glu Ala Lys Arg His Glu Phe His Gly Glu Arg Gln Arg	
346 351 356 361	
aag gaa gaa gaa atg aaa cag atg ttt gtg cag cga gta aag gag aaa	1214
Lys Glu Glu Glu Met Lys Gln Met Phe Val Gln Arg Val Lys Glu Lys	
362 367 372 377	
gaa gcc ata ttg aaa gaa gct gag aga gag cta cag gcc aaa ttt gag	1262
Glu Ala Ile Leu Lys Glu Ala Glu Arg Glu Leu Gln Ala Lys Phe Glu	
378 383 388 393	
cac ctt aag aga ctt cac caa gaa gag aga atg aag ctt gaa gaa aag	1310
His Leu Lys Arg Leu His Gln Glu Glu Arg Met Lys Leu Glu Glu Lys	
394 399 404 409	
aga aga ctt ttg gaa gaa gaa ata att gct ttc tct aaa aag aaa gct	1358
Arg Arg Leu Leu Glu Glu Glu Ile Ile Ala Phe Ser Lys Lys Lys Ala	
410 415 420 425	
acc tcc gag ata ttt cac agc cag tcc ttt ctg gca aca ggc agc aac	1406
Thr Ser Glu Ile Phe His Ser Gln Ser Phe Leu Ala Thr Gly Ser Asn	
426 431 436 441	
ctg agg aag gac aag gac cgt aag aac tcc aat ttt ttg taa aacagaa	1455
Leu Arg Lys Asp Lys Asp Arg Lys Asn Ser Asn Phe Leu *	
442 447 452	
gttccagagc acagaaggct atcatcacaa gcaaacttta ttaaaaaaaaa actagaagtg	1515
tgctttgatt ttgctgttat ttgttttatc acttctatat ttggtgaaca gccacagtta	1575
ctgatattta tggaaaagta ctttcaagta caagggtcaat acataagcca gagtgaatga	1635
tactacaagt tgagcatctc taattcaaaa atctgaaatc cagaagcttc aaaatctgaa	1695
tctttttgag cactgacttg accccacaag tggaaaattc cccacccgac acctttgctt	1755
tctgatgggt cagtttaaac agattttgtt tcttgcacaa aatttttgta taaattactt	1815

tcaggctata tgtataaggt ggatgtgaaa catgaattat gtaattagag tcgggtcccg	1875
ttgtgtatat gcagatattc caaacctgaa atccaaaaca cttctggtcc ctagcatttt	1935
ggataagggg tactcagctt gtacctatat attcatatat attcactgtt gttagaaatg	1995
tttaagttgc tgttctgtga tgaatctaaa tcttttctct tgctaccaag ctattgtcac	2055
tgcagtgcac tataccaaaag agcgaagtca gtgccactga aaatacagaa cccattaata	2115
tcgtaggtat ctgattacat ttatattcca agatgaacct tttttatata tgctaaaaat	2175
tttggggaat atgttttggg atgtattatg gagctaaaac tctaacctct taatagtttt	2235
atagaactta aaaatttttt atacaattac ccaattgggtg atatgatctt aagcttttgt	2295
gtcagattat ttaatatgat gacttcatgc tttattatgc cttattatgg ctgacgtatt	2355
actgtggtga aacaaaaatat ctttaaaagt taaaacatcc agatatataa gctatttttt	2415
cctaaggata aagtaccttt gagcatgagt gtatcacagc tttcattagg aaaacttttc	2475
attacatact tgtttaaact ctgtcttcca gggtaaaaat aataagggtg aatcatttta	2535
ttaaaaatac tttttaagaa aataactatg aacatctgaa tattaaagat ataaaaatgc	2595
acataattca tatttcaggt ggtatttgca ttcagtgcct tactgggtatt ctcagaacat	2655
tttaatgatt tctaacattt cttaacagtc atagatatat acattttcat tttttgtact	2715
tgaatattct aaataaaaact gacatttact cttgacaaat aaaacatata tttactaaaa	2775
aaaaaaaa	2783

<210> 108
 <211> 2265
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (79)..(1614)

<400> 108	
taagcttgcg accgcagctc cttcaccagc ttggtggtgg gcgtgttcgt ggtctacgtg	60
gtgcacacct gctgggctc atg tac ggc atc gtc tac acc cgc ccg tgc tcc	111
Met Tyr Gly Ile Val Tyr Thr Arg Pro Cys Ser	
1 5	
ggc gac gcc aac tgc atc cag ccc tac ctg gcg cgg cgg ccc aag ctg	159
Gly Asp Ala Asn Cys Ile Gln Pro Tyr Leu Ala Arg Arg Pro Lys Leu	
12 17 22 27	

cag ctg agc gtg tac acc acg acg agg tcc cac ctg ggt gct gag aac	207
Gln Leu Ser Val Tyr Thr Thr Thr Arg Ser His Leu Gly Ala Glu Asn	
28 33 38 43	
aac atc gac ctg gtc ttg aat gtg gaa gac ttt gat gtg gag tcc aaa	255
Asn Ile Asp Leu Val Leu Asn Val Glu Asp Phe Asp Val Glu Ser Lys	
44 49 54 59	
ttt gaa agg aca gtt aat gtt tct gta cca aag aaa acg aga aac aat	303
Phe Glu Arg Thr Val Asn Val Ser Val Pro Lys Lys Thr Arg Asn Asn	
60 65 70 75	
ggg acg ctg tat gcc tac atc ttc ctc cat cac gct ggg gtc ctg ccg	351
Gly Thr Leu Tyr Ala Tyr Ile Phe Leu His His Ala Gly Val Leu Pro	
76 81 86 91	
tgg cac gac ggg aag cag gtg cac ctg gtc agt cct ctg acc acc tac	399
Trp His Asp Gly Lys Gln Val His Leu Val Ser Pro Leu Thr Thr Tyr	
92 97 102 107	
atg gtc ccc aag cca gaa gaa atc aac ctg ctc acc ggg gag tct gat	447
Met Val Pro Lys Pro Glu Glu Ile Asn Leu Leu Thr Gly Glu Ser Asp	
108 113 118 123	
aca cag atc gag gcg gag aag aag ccg acg agt gcc ctg gat gag cca	495
Thr Gln Ile Glu Ala Glu Lys Lys Pro Thr Ser Ala Leu Asp Glu Pro	
124 129 134 139	
gtg tcc cac tgg cga ccg cgg ctg gcg ctg aac gtg atg gcg gac aac	543
Val Ser His Trp Arg Pro Arg Leu Ala Leu Asn Val Met Ala Asp Asn	
140 145 150 155	
ttt gtc ttt gac ggg tcc tcc ctg cct gcc gat gtg cat cgg tac atg	591
Phe Val Phe Asp Gly Ser Ser Leu Pro Ala Asp Val His Arg Tyr Met	
156 161 166 171	
aag atg atc cag ctg ggg aaa acc gtg cat tac ctg ccc atc ctg ttc	639
Lys Met Ile Gln Leu Gly Lys Thr Val His Tyr Leu Pro Ile Leu Phe	
172 177 182 187	
atc gac cag ctc agc aac cgc gtg aag gac ctg atg gtc ata aac cgc	687
Ile Asp Gln Leu Ser Asn Arg Val Lys Asp Leu Met Val Ile Asn Arg	
188 193 198 203	
tcc acc acc gag ctg ccc ctc acc gtg tcc tac gac aag gtc tca ctg	735
Ser Thr Thr Glu Leu Pro Leu Thr Val Ser Tyr Asp Lys Val Ser Leu	
204 209 214 219	
ggg cgg ctg cgc ttc tgg atc cac atg cag gac gcc gtg tac tcc ctg	783
Gly Arg Leu Arg Phe Trp Ile His Met Gln Asp Ala Val Tyr Ser Leu	
220 225 230 235	
cag cag ttc ggg ttt tca gag aaa gat gct gat gag gtg aaa gga att	831
Gln Gln Phe Gly Phe Ser Glu Lys Asp Ala Asp Glu Val Lys Gly Ile	
236 241 246 251	
ttt gta gat acc aac tta tac ttc ctg gcg ctg acc ttc ttt gtc gca	879

Phe Val Asp Thr Asn Leu Tyr Phe Leu Ala Leu Thr Phe Phe Val Ala	
252 257 262 267	
gcg ttc cat ctt ctc ttt gat ttc ctg gcc ttt aaa aat gac atc agt	927
Ala Phe His Leu Leu Phe Asp Phe Leu Ala Phe Lys Asn Asp Ile Ser	
268 273 278 283	
ttc tgg aag aag aag aag agc atg atc ggc atg tcc acc aag gca gtg	975
Phe Trp Lys Lys Lys Lys Ser Met Ile Gly Met Ser Thr Lys Ala Val	
284 289 294 299	
ctc tgg cgc tgc ttc agc acc gtg gtc atc ttt ctg ttc ctg ctg gac	1023
Leu Trp Arg Cys Phe Ser Thr Val Val Ile Phe Leu Phe Leu Leu Asp	
300 305 310 315	
gag cag acg agc ctg ctg gtg ctg gtc ccg gcg ggt gtt gga gcc gcc	1071
Glu Gln Thr Ser Leu Leu Val Leu Val Pro Ala Gly Val Gly Ala Ala	
316 321 326 331	
att gag ctg tgg aaa gtg aag aag gca ttg aag atg act att ttt tgg	1119
Ile Glu Leu Trp Lys Val Lys Lys Ala Leu Lys Met Thr Ile Phe Trp	
332 337 342 347	
aga ggc ctg atg ccc gaa ttt cag ttt ggc act tac agc gaa tct gag	1167
Arg Gly Leu Met Pro Glu Phe Gln Phe Gly Thr Tyr Ser Glu Ser Glu	
348 353 358 363	
agg aaa acc gag gag tac gat act cag gcc atg aag tac ttg tca tac	1215
Arg Lys Thr Glu Glu Tyr Asp Thr Gln Ala Met Lys Tyr Leu Ser Tyr	
364 369 374 379	
ctg ctg tac cct ctc tgt gtc ggg ggt got gtc tat tca ctc ctg aat	1263
Leu Leu Tyr Pro Leu Cys Val Gly Gly Ala Val Tyr Ser Leu Leu Asn	
380 385 390 395	
atc aaa tat aag agc tgg tac tcc tgg tta atc aac agc ttc gtc aac	1311
Ile Lys Tyr Lys Ser Trp Tyr Ser Trp Leu Ile Asn Ser Phe Val Asn	
396 401 406 411	
ggg gtc tat gcc ttt ggt ttc ctc ttc atg ctg ccc cag ctc ttt gtg	1359
Gly Val Tyr Ala Phe Gly Phe Leu Phe Met Leu Pro Gln Leu Phe Val	
412 417 422 427	
aac tac aag ttg aag tca gtg gca cat ctg ccc tgg aag gcc ttc acc	1407
Asn Tyr Lys Leu Lys Ser Val Ala His Leu Pro Trp Lys Ala Phe Thr	
428 433 438 443	
tac aag gct ttc aac acc ttc att gat gac gtc ttt gcc ttc atc atc	1455
Tyr Lys Ala Phe Asn Thr Phe Ile Asp Asp Val Phe Ala Phe Ile Ile	
444 449 454 459	
acc atg ccc acg tct cac cgg ctg gcc tgc ttc cgg gac gac gtg gtg	1503
Thr Met Pro Thr Ser His Arg Leu Ala Cys Phe Arg Asp Asp Val Val	
460 465 470 475	
ttt ctg gtc tac ctg tac cag cgg tgg ctt tat cct gtg gat aaa cgc	1551
Phe Leu Val Tyr Leu Tyr Gln Arg Trp Leu Tyr Pro Val Asp Lys Arg	

476	481	486	491	
aga gtg aac gag ttt	ggg gag tcc tac	gag gag aag gcc acg	cgg gcg	1599
Arg Val Asn Glu Phe	Gly Glu Ser Tyr	Glu Glu Lys Ala Thr	Arg Ala	
492	497	502	507	
ccc cac acg gac tga	aggccgccccg	ggctgccgcc	agccaagtgc	aacttgaatt
Pro His Thr Asp *				1654
508				
gtcaatgagt	atTTTTTggaa	gcatttggag	gaattcctag	acattgcgtt
				ttctgtgttg
1714				
ccaaaatccc	ttcggacatt	tctcagacat	ctcccaagtt	cccatcacgt
				cagatttggg
1774				
gctggttagcg	cttacgatgc	ccccacgtgt	gaacatctgt	cttggtcaca
				gagctgggtg
1834				
ctgccggtca	ccttgagctg	tggtggctcc	cggcacacga	gtgtccgggg
				ttcggccatg
1894				
tcctcacgcg	ggcaggggtg	ggagccctca	caggcaaggg	ggctggttga
				tttccatttc
1954				
aggtggtttt	ctaagtgtc	cttatgtgaa	tttcaaacac	gtatggaatt
				cattccgcat
2014				
ggactctggg	atcaaaggct	ctttcctctt	ttgtttgaga	gttggttgtt
				ttaaagctta
2074				
atgtatgttt	ctatTTTTaaa	ataaattttt	ctggctgtgg	caaaaaaaaaa
				aaaaaaaaaag
2134				
ggcggccgct	ctagagtatc	cctcgagggg	cccaagctta	cgcgtaacca
				gctttcttgt
2194				
acaaagtggg	ccctatagtg	agtcgtatat	aagctaggca	gtttcatcca
				gcagtcaacc
2254				
ctcatccttg	g			
				2265

<210> 109
 <211> 2349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (79)..(1698)

<400> 109	
taagcttgcg accgcagctc	cttcaccagc
ttgggtgggtg	gcgtgttcgt
ggctctacgtg	
60	
gtgcacacct	gctgggtc
atg tac ggc atc	gtc tac acc
cgc cgg tgc tcc	
111	
Met Tyr Gly Ile Val	Tyr Thr Arg Pro Cys Ser
1	5
ggc gac gcc aac tgc	atc cag ccc
tac ctg gcg cgg	cgg ccc
aag ctg	
159	
Gly Asp Ala Asn Cys	Ile Gln Pro Tyr
Leu Ala Arg Arg	Pro Lys Leu
12	17
22	27
cag ctg agc gtg	tac acc acg
acg agg tcc	cac ctg
ggt gct	gag aac
207	
Gln Leu Ser Val	Tyr Thr Thr Arg
Ser His Leu	Gly Ala Glu Asn

28	33	38	43	
aac atc gac ctg gtc ttg aat gtg gaa gac ttt gat gtg gag tcc aaa				255
Asn Ile Asp Leu Val Leu Asn Val Glu Asp Phe Asp Val Glu Ser Lys				
44	49	54	59	
ttt gaa agg aca gtt aat gtt tct gta cca aag aaa acg aga aac aat				303
Phe Glu Arg Thr Val Asn Val Ser Val Pro Lys Lys Thr Arg Asn Asn				
60	65	70	75	
ggg acg ctg tat gcc tac atc ttc ctc cat cac gct ggg gtc ctg ccg				351
Gly Thr Leu Tyr Ala Tyr Ile Phe Leu His His Ala Gly Val Leu Pro				
76	81	86	91	
tgg cac gac ggg aag cag gtg cac ctg gtc agt cct ctg acc acc tac				399
Trp His Asp Gly Lys Gln Val His Leu Val Ser Pro Leu Thr Thr Tyr				
92	97	102	107	
atg gtc ccc aag cca gaa gaa atc aac ctg ctc acc ggg gag tct gat				447
Met Val Pro Lys Pro Glu Glu Ile Asn Leu Leu Thr Gly Glu Ser Asp				
108	113	118	123	
aca cag atc gag gcg gag aag aag ccg acg agt gcc ctg gat gag cca				495
Thr Gln Ile Glu Ala Glu Lys Lys Pro Thr Ser Ala Leu Asp Glu Pro				
124	129	134	139	
gtg tcc cac tgg cga ccg cgg ctg gcg ctg aac gtg atg gcg gac aac				543
Val Ser His Trp Arg Pro Arg Leu Ala Leu Asn Val Met Ala Asp Asn				
140	145	150	155	
ttt gtc ttt gac ggg tcc tcc ctg cct gcc gat gtg cat cgg tac atg				591
Phe Val Phe Asp Gly Ser Ser Leu Pro Ala Asp Val His Arg Tyr Met				
156	161	166	171	
aag atg atc cag ctg ggg aaa acc gtg cat tac ctg ccc atc ctg ttc				639
Lys Met Ile Gln Leu Gly Lys Thr Val His Tyr Leu Pro Ile Leu Phe				
172	177	182	187	
atc gac cag ctc agc aac cgc gtg aag gac ctg atg gtc ata aac cgc				687
Ile Asp Gln Leu Ser Asn Arg Val Lys Asp Leu Met Val Ile Asn Arg				
188	193	198	203	
tcc acc acc gag ctg ccc ctc acc gtg tcc tac gac aag gtc tca ctg				735
Ser Thr Thr Glu Leu Pro Leu Thr Val Ser Tyr Asp Lys Val Ser Leu				
204	209	214	219	
ggg cgg ctg cgc ttc tgg atc cac atg cag gac gcc gtg tac tcc ctg				783
Gly Arg Leu Arg Phe Trp Ile His Met Gln Asp Ala Val Tyr Ser Leu				
220	225	230	235	
cag cag ttc ggg ttt tca gag aaa gat gct gat gag gtg aaa gga att				831
Gln Gln Phe Gly Phe Ser Glu Lys Asp Ala Asp Glu Val Lys Gly Ile				
236	241	246	251	
ttt gta gat acc aac tta tac ttc ctg gcg ctg acc ttc ttt gtc gca				879
Phe Val Asp Thr Asn Leu Tyr Phe Leu Ala Leu Thr Phe Phe Val Ala				
252	257	262	267	

gcg ttc cat ctt ctc ttt gat ttc ctg gcc ttt aaa aat gac atc agt	927
Ala Phe His Leu Leu Phe Asp Phe Leu Ala Phe Lys Asn Asp Ile Ser	
268 273 278 283	
ttc tgg aag aag aag aag agc atg atc ggc atg tcc acc aag gca gtg	975
Phe Trp Lys Lys Lys Lys Ser Met Ile Gly Met Ser Thr Lys Ala Val	
284 289 294 299	
ctc tgg cgc tgc ttc agc acc gtg gtc atc ttt ctg ttc ctg ctg gac	1023
Leu Trp Arg Cys Phe Ser Thr Val Val Ile Phe Leu Phe Leu Leu Asp	
300 305 310 315	
gag cag acg agc ctg ctg gtg ctg gtc ccg gcg ggt gtt gga gcc gcc	1071
Glu Gln Thr Ser Leu Leu Val Leu Val Pro Ala Gly Val Gly Ala Ala	
316 321 326 331	
att gag ctg tgg aaa gtg aag aag gca ttg aag atg act att ttt tgg	1119
Ile Glu Leu Trp Lys Val Lys Lys Ala Leu Lys Met Thr Ile Phe Trp	
332 337 342 347	
aga ggc ctg atg ccc gaa ttt cag ttt ggc act tac agc gaa tct gag	1167
Arg Gly Leu Met Pro Glu Phe Gln Phe Gly Thr Tyr Ser Glu Ser Glu	
348 353 358 363	
agg aaa acc gag gag tac gat act cag gcc atg aag tac ttg tca tac	1215
Arg Lys Thr Glu Glu Tyr Asp Thr Gln Ala Met Lys Tyr Leu Ser Tyr	
364 369 374 379	
ctg ctg tac cct ctc tgt gtc ggg ggt gct gtc tat tca ctc ctg aat	1263
Leu Leu Tyr Pro Leu Cys Val Gly Gly Ala Val Tyr Ser Leu Leu Asn	
380 385 390 395	
atc aaa tat aag agc tgg tac tcc tgg tta atc aac agc ttc gtc aac	1311
Ile Lys Tyr Lys Ser Trp Tyr Ser Trp Leu Ile Asn Ser Phe Val Asn	
396 401 406 411	
ggg gtc tat gcc ttt ggt ttc ctc ttc atg ctg ccc cag ctc ttt gtg	1359
Gly Val Tyr Ala Phe Gly Phe Leu Phe Met Leu Pro Gln Leu Phe Val	
412 417 422 427	
aac tac aag gta aga cgg tgt gtg ctg ccc gcg gcc cgg ccc ccg tct	1407
Asn Tyr Lys Val Arg Arg Cys Val Leu Pro Ala Ala Arg Pro Pro Ser	
428 433 438 443	
cct gtg ctg ccc aca gct gac ctg ggc ctg tct ctc ctg ttt cag ttg	1455
Pro Val Leu Pro Thr Ala Asp Leu Gly Leu Ser Leu Leu Phe Gln Leu	
444 449 454 459	
aag tca gtg gca cat ctg ccc tgg aag gcc ttc acc tac aag gct ttc	1503
Lys Ser Val Ala His Leu Pro Trp Lys Ala Phe Thr Tyr Lys Ala Phe	
460 465 470 475	
aac acc ttc att gat gac gtc ttt gcc ttc atc atc acc atg ccc acg	1551
Asn Thr Phe Ile Asp Asp Val Phe Ala Phe Ile Ile Thr Met Pro Thr	
476 481 486 491	

tct cac cgg ctg gcc tgc ttc cgg gac gac gtg gtg ttt ctg gtc tac	1599
Ser His Arg Leu Ala Cys Phe Arg Asp Asp Val Val Phe Leu Val Tyr	
492 497 502 507	

ctg tac cag cgg tgg ctt tat cct gtg gat aaa cgc aga gtg aac gag	1647
Leu Tyr Gln Arg Trp Leu Tyr Pro Val Asp Lys Arg Arg Val Asn Glu	
508 513 518 523	

ttt ggg gag tcc tac gag gag aag gcc acg cgg gcg ccc cac acg gac	1695
Phe Gly Glu Ser Tyr Glu Glu Lys Ala Thr Arg Ala Pro His Thr Asp	
524 529 534 539	

tga aggc cgcccgggct gccgccagcc aagtgcact tgaattgtca atgagtattt	1752
* 540	

ttggaagcat ttggaggaat tcctagacat tgcgttttct gtgttgccaa aatcccttcg	1812
---	------

gacattttctc agacatctcc caagttccca tcacgtcaga tttggagctg gtagcgctta	1872
--	------

cgatgcccc acgtgtgaac atctgtcttg gtcacagagc tgggtgctgc cggtcacctt	1932
--	------

gagctgtggt ggctcccggc acacgagtgt ccgggggttcg gccatgtcct cacgcgggca	1992
--	------

gggggtgggag ccctcacagg caagggggct gttggatttc catttcagggt ggttttctaa	2052
---	------

gtgctcctta tgtgaatttc aaacacgtat ggaattcatt ccgcatggac totgggatca	2112
---	------

aaggctcttt cctcttttgt ttgagagttg gttgttttaa agcttaatgt atgtttctat	2172
---	------

tttaaaataa atttttctgg ctgtggcaaa aaaaaaaaaa aaaaagggcg gccgctctag	2232
---	------

agtatccctc gaggggcca agcttaacgcg taccagctt tottgtaaa agtggctcct	2292
---	------

atagtgagtc gtatataagc taggcagttt catccagcag tcaaccctca tccttgg	2349
--	------

<210> 110
 <211> 6674
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1312)..(6330)

<220>
 <221> misc_feature
 <222> (1)...(6674)
 <223> n = a,t,c or g

<400> 110	
ccactttgta caagaaagct gggtacgcgt aagcttgggc ccctcgaggg atactctaga	60

gcggccgccc ttcttttttt tttttcccaa aggtcctgtg octataacaa ttccagggtg	120
---	-----

gccaggagga cctgcttcac ccttttctcc ctgcggggccc tggcggccta tgagtcctgg 180
 gtaccogggt tcaccaggaa aaccgggact ccotttttcc cctttgtcac catctttttcc 240
 gggtttgctt ctgggtcctg gttttccggg ttcacctttc tctccgaccc ctggcatccc 300
 ctgaaatcca ggttcacctt tttggccctt ttctcccttg gtggcgaagt ctcctttttc 360
 ttgaacttga gcttgtcctg gtactcctgg aggcccaactg accccttggg cacccttgct 420
 acottttggg ccttgaaaac ttaagcccat ttgtcccttt tcacctggag ggccngggagg 480
 gcctggggga cctgtgtggt cggtaaatcc tggaggccca acaggacctt gaagccctgg 540
 cagtcctggg gggcctggag tccttgggat tccgggaaat cctctttcac ctttcaacag 600
 catcccgggc acatggccaa gtatctcacc tggatcacc ttaccatcat caggcttcac 660
 catctcacct tggaagcgtt caatcttttg gtcaatattt ctgcaccaca gcatccaggt 720
 gcacgtcttg tgggatccct gccgttggg ggctgacct acagaccctt tgctgaagga 780
 ccottttgctg aaggctcctg gcctgtggcc atcacggac agaccctttg ctgaaggctc 840
 ctggcctgtg gccaccactg tcatcacagg ctgttccttg ggctggaggg agagcttttg 900
 ccacctcatc tcccatccgc caagacgtc tgggcgagga accccacggg cactgtcccc 960
 agcagcagcc accgccgtag ggcaggggcg gccaccgcgc gctggtctct ccccatgctg 1020
 gcggttcgtc cactctgggc ccgggtcagt ccacttagc ctcgggctcg gcttcagggg 1080
 ctgctgcccc aacgcattgg ccttccaga agcaccgcgc ggcggcacac cggcagggcg 1140
 gccggccttg ctgggtctc tgggcgcggg ccccgggggc tcgggcggcc cctttcggtc 1200
 ctcgcccggg gacggtgctg agcgtggaa gtccggcctt ccgagagcta gctgtccgcc 1260
 gcggcccccg cacgccgggc agcgtccct cgccgcctcg ggcgcgccac c atg ggg 1317
 Met Gly
 1
 ccc cgg ctc agc gtc tgg ctg ctg ctg ctg ccc gcc gcc ctt ctg ctc 1365
 Pro Arg Leu Ser Val Trp Leu Leu Leu Leu Pro Ala Ala Leu Leu Leu
 3 8 13 18
 cac gag gag cac agc cgg gcc gct gcg aag ggt ggc tgt gct ggc tct 1413
 His Glu Glu His Ser Arg Ala Ala Ala Lys Gly Gly Cys Ala Gly Ser
 19 24 29 34
 ggc tgt ggc aaa tgt gac tgc cat gga gtg aag gga caa aag ggt gaa 1461
 Gly Cys Gly Lys Cys Asp Cys His Gly Val Lys Gly Gln Lys Gly Glu
 35 40 45 50
 aga ggc ctc ccg ggg tta caa ggt gtc att ggg ttt cct gga atg caa 1509
 Arg Gly Leu Pro Gly Leu Gln Gly Val Ile Gly Phe Pro Gly Met Gln

51	56	61	66	
gga cct gag ggg cca cag gga cca cca gga caa aag ggt gat act gga				1557
Gly Pro Glu Gly Pro Gln Gly Pro Pro Gly Gln Lys Gly Asp Thr Gly				
67	72	77	82	
gaa cca gga cta cct gga aca aaa ggg aca aga gga cct ccg gga gca				1605
Glu Pro Gly Leu Pro Gly Thr Lys Gly Thr Arg Gly Pro Pro Gly Ala				
83	88	93	98	
tct ggc tac cct gga aac cca gga ctt ccc gga att cct ggc caa gac				1653
Ser Gly Tyr Pro Gly Asn Pro Gly Leu Pro Gly Ile Pro Gly Gln Asp				
99	104	109	114	
ggc ccg cca ggc ccc cca ggt att cca gga tgc aat ggc aca aag ggg				1701
Gly Pro Pro Gly Pro Pro Gly Ile Pro Gly Cys Asn Gly Thr Lys Gly				
115	120	125	130	
gag aga ggg ccg ctc ggg cct cct ggc ttg cct ggt ttc gca gga aat				1749
Glu Arg Gly Pro Leu Gly Pro Pro Gly Leu Pro Gly Phe Ala Gly Asn				
131	136	141	146	
ccc gga cca cca ggc tta cca ggg atg aag ggt gat cca ggt gag ata				1797
Pro Gly Pro Pro Gly Leu Pro Gly Met Lys Gly Asp Pro Gly Glu Ile				
147	152	157	162	
ctt ggc cat gtg ccc ggg atg ctg ttg aaa ggt gaa aga gga ttt ccc				1845
Leu Gly His Val Pro Gly Met Leu Leu Lys Gly Glu Arg Gly Phe Pro				
163	168	173	178	
gga atc cca ggg act cca ggc cca cca gga ctg cca ggg ctt caa ggt				1893
Gly Ile Pro Gly Thr Pro Gly Pro Pro Gly Leu Pro Gly Leu Gln Gly				
179	184	189	194	
cct gtt ggg cct cca gga ttt acc gga cca cca ggt ccc cca ggc cct				1941
Pro Val Gly Pro Pro Gly Phe Thr Gly Pro Pro Gly Pro Pro Gly Pro				
195	200	205	210	
ccc ggc cct cca ggt gaa aag gga caa atg ggc tta agt ttt caa gga				1989
Pro Gly Pro Pro Gly Glu Lys Gly Gln Met Gly Leu Ser Phe Gln Gly				
211	216	221	226	
cca aaa ggt gac aag ggt gac caa ggg gtc agt ggg cct cca gga gta				2037
Pro Lys Gly Asp Lys Gly Asp Gln Gly Val Ser Gly Pro Pro Gly Val				
227	232	237	242	
cca gga caa gct caa gtt caa gaa aaa gga gac ttc gcc acc aag gga				2085
Pro Gly Gln Ala Gln Val Gln Glu Lys Gly Asp Phe Ala Thr Lys Gly				
243	248	253	258	
gaa aag ggc caa aaa ggt gaa cct gga ttt cag ggg atg cca ggg gtc				2133
Glu Lys Gly Gln Lys Gly Glu Pro Gly Phe Gln Gly Met Pro Gly Val				
259	264	269	274	
gga gag aaa ggt gaa ccc gga aaa cca gga ccc aga ggc aaa ccc gga				2181
Gly Glu Lys Gly Glu Pro Gly Lys Pro Gly Pro Arg Gly Lys Pro Gly				
275	280	285	290	

aaa gat ggt gac aaa ggg gaa aaa ggg agt ccc ggt ttt cct ggt gaa Lys Asp Gly Asp Lys Gly Glu Lys Gly Ser Pro Gly Phe Pro Gly Glu 291 296 301 306	2229
ccc ggg tac cca gga ctc ata ggc cgc cag ggc ccg cag gga gaa aag Pro Gly Tyr Pro Gly Leu Ile Gly Arg Gln Gly Pro Gln Gly Glu Lys 307 312 317 322	2277
ggt gaa gca ggt cct cct ggc cca cct gga att gtt ata ggc aca gga Gly Glu Ala Gly Pro Pro Gly Pro Pro Gly Ile Val Ile Gly Thr Gly 323 328 333 338	2325
cct ttg gga gaa aaa gga gag agg ggc tac cct gga act ccg ggg cca Pro Leu Gly Glu Lys Gly Glu Arg Gly Tyr Pro Gly Thr Pro Gly Pro 339 344 349 354	2373
aga gga gag cca ggc cca aaa ggt ttc cca gga cta cca ggc caa ccc Arg Gly Glu Pro Gly Pro Lys Gly Phe Pro Gly Leu Pro Gly Gln Pro 355 360 365 370	2421
gga cct cca ggc ctc cct gta cct ggg cag gct ggt gcc cct ggc ttc Gly Pro Pro Gly Leu Pro Val Pro Gly Gln Ala Gly Ala Pro Gly Phe 371 376 381 386	2469
cct ggt gaa aga gga gaa aaa ggt gac cga gga ttt cct ggt aca tct Pro Gly Glu Arg Gly Glu Lys Gly Asp Arg Gly Phe Pro Gly Thr Ser 387 392 397 402	2517
ctg cca gga cca agt gga aga gat ggg ctc ccg ggt cct cct ggt tcc Leu Pro Gly Pro Ser Gly Arg Asp Gly Leu Pro Gly Pro Pro Gly Ser 403 408 413 418	2565
cct ggg ccc cct ggg cag cct ggc tac aca aat gga att gtg gaa tgt Pro Gly Pro Pro Gly Gln Pro Gly Tyr Thr Asn Gly Ile Val Glu Cys 419 424 429 434	2613
cag ccc gga cct cca ggt gac cag ggt cct cct gga att aca ggg cag Gln Pro Gly Pro Pro Gly Asp Gln Gly Pro Pro Gly Ile Thr Gly Gln 435 440 445 450	2661
cca gga ttt ata ggc gaa att gga gag aaa gga caa aaa gga gag agt Pro Gly Phe Ile Gly Glu Ile Gly Glu Lys Gly Gln Lys Gly Glu Ser 451 456 461 466	2709
tgc ctc atc tgt gat ata gac gga tat cgg ggg cct ccc ggg cca cag Cys Leu Ile Cys Asp Ile Asp Gly Tyr Arg Gly Pro Pro Gly Pro Gln 467 472 477 482	2757
gga ccc ccg gga gaa ata ggt ttc cca ggg cag cca ggg gcc aag ggc Gly Pro Pro Gly Glu Ile Gly Phe Pro Gly Gln Pro Gly Ala Lys Gly 483 488 493 498	2805
gac aga ggt ttg cct ggc aga gat ggt gtt gca gga gtg cca ggc cgt Asp Arg Gly Leu Pro Gly Arg Asp Gly Val Ala Gly Val Pro Gly Arg 499 504 509 514	2853

caa ggt aca cca ggg ctg ata ggc cag cca gga gcc aag ggg gag cct	2901
Gln Gly Thr Pro Gly Leu Ile Gly Gln Pro Gly Ala Lys Gly Glu Pro	
515 520 525 530	
ggt gag ttt tat ttc gac ttg cgg ctc aaa ggt gac aaa gga gac cca	2949
Gly Glu Phe Tyr Phe Asp Leu Arg Leu Lys Gly Asp Lys Gly Asp Pro	
531 536 541 546	
ggc ttt cca gga cag ccc ggc atg cca ggg aga gcg ggt tct cct gga	2997
Gly Phe Pro Gly Gln Pro Gly Met Pro Gly Arg Ala Gly Ser Pro Gly	
547 552 557 562	
aga gat ggc cat ccg ggt ctt cct ggc ccc aag ggc tcg ccg ggt tct	3045
Arg Asp Gly His Pro Gly Leu Pro Gly Pro Lys Gly Ser Pro Gly Ser	
563 568 573 578	
gta gga ttg aaa gga gag cgt ggc ccc cct gga gga gtt gga ttc cca	3093
Val Gly Leu Lys Gly Glu Arg Gly Pro Pro Gly Gly Val Gly Phe Pro	
579 584 589 594	
ggc agt cgt ggt gac acc ggc ccc cct ggg cct cca gga tat ggt cct	3141
Gly Ser Arg Gly Asp Thr Gly Pro Pro Gly Pro Pro Gly Tyr Gly Pro	
595 600 605 610	
gct ggt ccc att ggt gac aaa gga caa gca ggc ttt cct gga ggc cct	3189
Ala Gly Pro Ile Gly Asp Lys Gly Gln Ala Gly Phe Pro Gly Gly Pro	
611 616 621 626	
gga tcc cca ggc ctg cca ggt cca aag ggc tcg ccg ggt tct gta gga	3237
Gly Ser Pro Gly Leu Pro Gly Pro Lys Gly Ser Pro Gly Ser Val Gly	
627 632 637 642	
aaa att gtt cct tta cca ggc ccc cct gga gca gaa gga ctg ccg ggg	3285
Lys Ile Val Pro Leu Pro Gly Pro Pro Gly Ala Glu Gly Leu Pro Gly	
643 648 653 658	
tcc cca ggc ttc cca ggt ccc caa gga gac cga ggc ttt ccc gga acc	3333
Ser Pro Gly Phe Pro Gly Pro Gln Gly Asp Arg Gly Phe Pro Gly Thr	
659 664 669 674	
gca gga ggg cca ggc ctg cca gga gag aag ggc gct gtg ggc cag cca	3381
Ala Gly Gly Pro Gly Leu Pro Gly Glu Lys Gly Ala Val Gly Gln Pro	
675 680 685 690	
ggc att gga ttt cca ggg ccc ccc ggc ccc aaa ggt gtt gac ggc tta	3429
Gly Ile Gly Phe Pro Gly Pro Pro Gly Pro Lys Gly Val Asp Gly Leu	
691 696 701 706	
cct gga gac atg ggg cca ccg ggg act cca ggt cgc ccg gga ttt aat	3477
Pro Gly Asp Met Gly Pro Pro Gly Thr Pro Gly Arg Pro Gly Phe Asn	
707 712 717 722	
ggc tta cct ggg aac cca ggt gtg cag ggc cag aag gga gag cct gga	3525
Gly Leu Pro Gly Asn Pro Gly Val Gln Gly Gln Lys Gly Glu Pro Gly	
723 728 733 738	
ggt ggt cta ccg gga ctc aaa ggt ttg cca ggt ctt ccc ggc att cct	3573

Val Gly Leu Pro Gly Leu Lys Gly Leu Pro Gly Leu Pro Gly Ile Pro	
739 744 749 754	
ggc aca ccc ggg gag aag ggg agc att ggg gta cca ggc gtt cct gga	3621
Gly Thr Pro Gly Glu Lys Gly Ser Ile Gly Val Pro Gly Val Pro Gly	
755 760 765 770	
gaa cat gga gcg atc gga ccc cct ggg ctt cag ggg atc aga ggt gaa	3669
Glu His Gly Ala Ile Gly Pro Pro Gly Leu Gln Gly Ile Arg Gly Glu	
771 776 781 786	
ccg gga cct cct gga ttg cca ggc tcc gtg ggg tct cca gga gtt cca	3717
Pro Gly Pro Pro Gly Leu Pro Gly Ser Val Gly Ser Pro Gly Val Pro	
787 792 797 802	
gga ata ggc ccc cct gga gct agg ggt ccc cct gga gga cag gga cca	3765
Gly Ile Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly Gly Gln Gly Pro	
803 808 813 818	
ccg ggg ttg tca ggc cct cct gga ata aaa gga gag aag ggt ttc ccc	3813
Pro Gly Leu Ser Gly Pro Pro Gly Ile Lys Gly Glu Lys Gly Phe Pro	
819 824 829 834	
gga ttc cct gga ctg gac atg ccg ggc cct aaa gga gat aaa ggg gct	3861
Gly Phe Pro Gly Leu Asp Met Pro Gly Pro Lys Gly Asp Lys Gly Ala	
835 840 845 850	
caa gga ctc cct ggc ata acg gga cag tcg ggg ctc cct ggc ctt cct	3909
Gln Gly Leu Pro Gly Ile Thr Gly Gln Ser Gly Leu Pro Gly Leu Pro	
851 856 861 866	
gga cag cag ggg gct cct ggg att cct ggg ttt cca ggt tcc aag gga	3957
Gly Gln Gln Gly Ala Pro Gly Ile Pro Gly Phe Pro Gly Ser Lys Gly	
867 872 877 882	
gaa atg ggc gtc atg ggg acc ccc ggg cag ccg ggc tca cca gga cca	4005
Glu Met Gly Val Met Gly Thr Pro Gly Gln Pro Gly Ser Pro Gly Pro	
883 888 893 898	
gtg ggt gct cct gga tta ccg ggt gaa aaa ggg gac cat ggc ttt ccg	4053
Val Gly Ala Pro Gly Leu Pro Gly Glu Lys Gly Asp His Gly Phe Pro	
899 904 909 914	
ggc tcc tca gga ccc agg gga gac cct ggc ttg aaa ggt gat aag ggg	4101
Gly Ser Ser Gly Pro Arg Gly Asp Pro Gly Leu Lys Gly Asp Lys Gly	
915 920 925 930	
gat gtc ggt ctc cct ggc aag cct ggc tcc atg gat aag gtg gac atg	4149
Asp Val Gly Leu Pro Gly Lys Pro Gly Ser Met Asp Lys Val Asp Met	
931 936 941 946	
ggc agc atg aag ggc cag aaa gga gac caa gga gag aaa gga caa att	4197
Gly Ser Met Lys Gly Gln Lys Gly Asp Gln Gly Glu Lys Gly Gln Ile	
947 952 957 962	
gga cca att ggt gag aag gga tcc cga gga gac cct ggg acc cca gga	4245
Gly Pro Ile Gly Glu Lys Gly Ser Arg Gly Asp Pro Gly Thr Pro Gly	

963	968	973	978
gtg cct gga aag gac ggg cag gca gga cag cct ggg cag cca gga cct Val Pro Gly Lys Asp Gly Gln Ala Gly Gln Pro Gly Gln Pro Gly Pro 979 984 989 994			4293
aaa ggt gat cca ggt ata agt gga acc cca ggt gct cca gga ctt ccg Lys Gly Asp Pro Gly Ile Ser Gly Thr Pro Gly Ala Pro Gly Leu Pro 995 1000 1005 1010			4341
gga cca aaa gga tct gtt ggt gga atg ggc ttg cca gga aca cct gga Gly Pro Lys Gly Ser Val Gly Gly Met Gly Leu Pro Gly Thr Pro Gly 1011 1016 1021 1026			4389
gag aaa ggt gtg cct ggc atc cct ggc cca caa ggt tca cct ggc tta Glu Lys Gly Val Pro Gly Ile Pro Gly Pro Gln Gly Ser Pro Gly Leu 1027 1032 1037 1042			4437
cct gga gac aaa ggt gca aaa gga gag aaa ggg cag gca ggc cca cct Pro Gly Asp Lys Gly Ala Lys Gly Glu Lys Gly Gln Ala Gly Pro Pro 1043 1048 1053 1058			4485
ggc ata ggc atc cca gga ctg cgt ggt gaa aag gga gat caa ggg ata Gly Ile Gly Ile Pro Gly Leu Arg Gly Glu Lys Gly Asp Gln Gly Ile 1059 1064 1069 1074			4533
gcg ggt ttc cca gga agc cct gga gag aag gga gaa aaa gga agc att Ala Gly Phe Pro Gly Ser Pro Gly Glu Lys Gly Glu Lys Gly Ser Ile 1075 1080 1085 1090			4581
ggg atc cca gga atg cca ggg tcc cca ggc ctt aaa ggg tct ccc ggg Gly Ile Pro Gly Met Pro Gly Ser Pro Gly Leu Lys Gly Ser Pro Gly 1091 1096 1101 1106			4629
agt gtt ggc tat cca gga agt cct ggg cta cct gga gaa aaa ggt gac Ser Val Gly Tyr Pro Gly Ser Pro Gly Leu Pro Gly Glu Lys Gly Asp 1107 1112 1117 1122			4677
aaa ggc ctc cca gga ttg gat ggc atc cct ggt gtc aaa gga gaa gca Lys Gly Leu Pro Gly Leu Asp Gly Ile Pro Gly Val Lys Gly Glu Ala 1123 1128 1133 1138			4725
ggt ctt cct ggg act cct ggc ccc aca ggc cca gct ggc cag aaa ggg Gly Leu Pro Gly Thr Pro Gly Pro Thr Gly Pro Ala Gly Gln Lys Gly 1139 1144 1149 1154			4773
gag cca ggc agt gat gga atc ccg ggg tca gca gga gag aag ggt gaa Glu Pro Gly Ser Asp Gly Ile Pro Gly Ser Ala Gly Glu Lys Gly Glu 1155 1160 1165 1170			4821
cca ggt cta cca gga aga gga ttc cca ggg ttt cca ggg gcc aaa gga Pro Gly Leu Pro Gly Arg Gly Phe Pro Gly Phe Pro Gly Ala Lys Gly 1171 1176 1181 1186			4869
gac aaa ggt tca aag ggt gag gtg ggt ttc cca gga tta gcc ggg agc Asp Lys Gly Ser Lys Gly Glu Val Gly Phe Pro Gly Leu Ala Gly Ser 1187 1192 1197 1202			4917

cca gga att cct gga tcc aaa gga gag caa gga ttc atg ggt cct ccg Pro Gly Ile Pro Gly Ser Lys Gly Glu Gln Gly Phe Met Gly Pro Pro	4965
1203 1208 1213 1218	
ggg ccc cag gga cag ccg ggg tta ccg gga tcc cca ggc cat gcc acg Gly Pro Gln Gly Gln Pro Gly Leu Pro Gly Ser Pro Gly His Ala Thr	5013
1219 1224 1229 1234	
gag ggg ccc aaa gga gac cgc gga cct cag ggc cag cct ggc ctg cca Glu Gly Pro Lys Gly Asp Arg Gly Pro Gln Gly Gln Pro Gly Leu Pro	5061
1235 1240 1245 1250	
gga ctt ccg gga ccc atg ggg cct cca ggg ctt cct ggg att gat gga Gly Leu Pro Gly Pro Met Gly Pro Pro Gly Leu Pro Gly Ile Asp Gly	5109
1251 1256 1261 1266	
gtt aaa ggt gac aaa gga aat cca ggc tgg cca gga gca ccc ggt gtc Val Lys Gly Asp Lys Gly Asn Pro Gly Trp Pro Gly Ala Pro Gly Val	5157
1267 1272 1277 1282	
cca ggg ccc aag gga gac cct gga ttc cag ggc atg cct ggt att ggt Pro Gly Pro Lys Gly Asp Pro Gly Phe Gln Gly Met Pro Gly Ile Gly	5205
1283 1288 1293 1298	
ggc tct cca gga atc aca ggc tct aag ggt gat atg ggg cct cca gga Gly Ser Pro Gly Ile Thr Gly Ser Lys Gly Asp Met Gly Pro Pro Gly	5253
1299 1304 1309 1314	
gtt cca gga ttt caa ggt cca aaa ggt ctt cct ggc ctc cag gga att Val Pro Gly Phe Gln Gly Pro Lys Gly Leu Pro Gly Leu Gln Gly Ile	5301
1315 1320 1325 1330	
aaa ggt gat caa ggc gat caa ggc gtc ccg gga gct aaa ggt ctc ccg Lys Gly Asp Gln Gly Asp Gln Gly Val Pro Gly Ala Lys Gly Leu Pro	5349
1331 1336 1341 1346	
ggg cct cct ggc ccc cca ggt cct tac gac atc atc aaa ggg gag ccc Gly Pro Pro Gly Pro Pro Gly Pro Tyr Asp Ile Ile Lys Gly Glu Pro	5397
1347 1352 1357 1362	
ggg ctc cct ggt cct gag ggc ccc cca ggg ctg aaa ggg ctt cag gga Gly Leu Pro Gly Pro Gly Glu Gly Pro Pro Gly Leu Lys Gly Leu Gln Gly	5445
1363 1368 1373 1378	
ctg cca ggc ccg aaa ggc cag caa ggt gtt aca gga ttg gtg ggt ata Leu Pro Gly Pro Lys Gly Gln Gln Gly Val Thr Gly Leu Val Gly Ile	5493
1379 1384 1389 1394	
cct gga cct cca ggt att cct ggg ttt gac ggt gcc cct ggc cag aaa Pro Gly Pro Pro Gly Ile Pro Gly Phe Asp Gly Ala Pro Gly Gln Lys	5541
1395 1400 1405 1410	
gga gag atg gga cct gcc ggg cct act ggt cca aga gga ttt cca ggt Gly Glu Met Gly Pro Ala Gly Pro Thr Gly Pro Arg Gly Phe Pro Gly	5589
1411 1416 1421 1426	

cca cca ggc ccc gat ggg ttg cca gga tcc atg ggg ccc cca ggc acc	5637
Pro Pro Gly Pro Asp Gly Leu Pro Gly Ser Met Gly Pro Pro Gly Thr	
1427 1432 1437 1442	
cca tct gtt gat cac ggc ttc ctt gtg acc agg cat agt caa aca ata	5685
Pro Ser Val Asp His Gly Phe Leu Val Thr Arg His Ser Gln Thr Ile	
1443 1448 1453 1458	
gat gac cca cag tgt cct tct ggg acc aaa att ctt tac cac ggg tac	5733
Asp Asp Pro Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr	
1459 1464 1469 1474	
tct ttg ctc tac gtg caa ggc aat gaa cgg gcc cat ggc cag gac ttg	5781
Ser Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu	
1475 1480 1485 1490	
ggc acg gcc ggc agc tgc ctg cgc aag ttc agc aca atg ccc ttc ctg	5829
Gly Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu	
1491 1496 1501 1506	
ttc tgc aat att aac aac gtg tgc aac ttt gca tca cga aat gac tac	5877
Phe Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr	
1507 1512 1517 1522	
tcg tac tgg ctg tcc acc cct gag ccc atg ccc atg tca atg gca ccc	5925
Ser Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro	
1523 1528 1533 1538	
atc acg ggg gaa aac ata aga cca ttt att agt agg tgt gct gtg tgt	5973
Ile Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys	
1539 1544 1549 1554	
gag gcg cct gcc atg gtg atg gcc gtg cac agc cag acc att cag atc	6021
Glu Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile	
1555 1560 1565 1570	
cca ccg tgc ccc agc ggg tgg tcc tcg ctg tgg atc ggc tac tct ttt	6069
Pro Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe	
1571 1576 1581 1586	
gtg atg cac acc agc gct ggt gca gaa ggc tct ggc caa gcc ctg gcg	6117
Val Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala	
1587 1592 1597 1602	
tcc ccc ggc tcc tgc ctg gag gag ttt aga agt gcg cca ttc atc gag	6165
Ser Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu	
1603 1608 1613 1618	
tgt cac ggc cgt ggg acc tgc aat tac tac gca aac gct tac agc ttt	6213
Cys His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe	
1619 1624 1629 1634	
tgg ctc gcc acc ata gag agg agc gag atg ttc aag aag cct acg ccg	6261
Trp Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro	
1635 1640 1645 1650	
tcc acc ttg aag gca ggg gag ctg cgc acg cac gtc agc cgc tgc caa	6309

Ser Thr Leu Lys Ala Gly Glu Leu Arg Thr His Val Ser Arg Cys Gln
1651 1656 1661 1666

gtc tgt atg aga aga aca taa tg aagcctgact cagctaattgt cacaacatgg 6362
Val Cys Met Arg Arg Thr *

1667 1672

tgctacttct tcttcttttt gttacagca acgaacccta gaaatatatc ctgtgtacct 6422

cactgtocaa tatgaaaacc gtaaagtgcc ttataggaat ttgcgtaact aacacaccct 6482

gcttcattga cctctacttg ctgaaggaga aaaagacagc gataagcttt caatagtggc 6542

ataccaaatg gcacttttga tgaaataaaa tatcaatatt ttctgcaaaa aaaaaaaaaa 6602

aagggcggcc gctctagagt atccctcgag gggcccaagc ttacgcgtac ccagctttct 6662

tgtacaaagt gg 6674

<210> 111
<211> 1421
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (217)..(1230)

<400> 111
ataaattaga acgctgtgg taccgctccg gaattcccgg gtcgaccac gcgtccggag 60

ggagtggaga acgcataagc aagctggttt gaccagaaac agaactgcct gtgacagatt 120

aagagacaag caaggcttgg aatctgagag caagcaaaga gagtggaaat ttacagctgc 180

cctatcattc catattggaa gaagagattt ctacac atg aaa aaa atg cct ttg 234
Met Lys Lys Met Pro Leu
1

ttt agt aaa tca cac aaa aat cca gca gaa att gtg aaa atc ctg aaa 282
Phe Ser Lys Ser His Lys Asn Pro Ala Glu Ile Val Lys Ile Leu Lys
7 12 17 22

gac aat ttg gcc att ttg gaa aag caa gac aaa aag aca gac aag gct 330
Asp Asn Leu Ala Ile Leu Glu Lys Gln Asp Lys Lys Thr Asp Lys Ala
23 28 33 38

tca gaa gaa gtg tct aaa tca ctg caa gca atg aaa gaa att ctg tgt 378
Ser Glu Glu Val Ser Lys Ser Leu Gln Ala Met Lys Glu Ile Leu Cys
39 44 49 54

ggc aca aac gag aaa gaa ccc cca aca gaa gca gtg gct cag cta gca 426
Gly Thr Asn Glu Lys Glu Pro Pro Thr Glu Ala Val Ala Gln Leu Ala
55 60 65 70

caa gaa ctc tac agc agt ggc ctg cta gtg aca ctg ata gct gac ctg	474
Gln Glu Leu Tyr Ser Ser Gly Leu Leu Val Thr Leu Ile Ala Asp Leu	
71 76 81 86	
cag ctg ata gac ttt gag gga aaa aaa gat gtg acc cag ata ttt aac	522
Gln Leu Ile Asp Phe Glu Gly Lys Lys Asp Val Thr Gln Ile Phe Asn	
87 92 97 102	
aac atc ttg aga aga cag ata ggc act cgg agt cct act gtg gag tat	570
Asn Ile Leu Arg Arg Gln Ile Gly Thr Arg Ser Pro Thr Val Glu Tyr	
103 108 113 118	
att agt gct cat cct cat atc ctg ttt atg ctc ctc aaa gga tat gaa	618
Ile Ser Ala His Pro His Ile Leu Phe Met Leu Leu Lys Gly Tyr Glu	
119 124 129 134	
gcc cca cag att gcc tta cgt tgt ggg att atg ctg aga gaa tgt att	666
Ala Pro Gln Ile Ala Leu Arg Cys Gly Ile Met Leu Arg Glu Cys Ile	
135 140 145 150	
cga cat gaa cca ctt gcc aaa atc atc ctc ttt tct aat caa ttc aga	714
Arg His Glu Pro Leu Ala Lys Ile Ile Leu Phe Ser Asn Gln Phe Arg	
151 156 161 166	
gat ttc ttt aag tac gtg gag ttg tca aca ttt gat att gct tca gat	762
Asp Phe Phe Lys Tyr Val Glu Leu Ser Thr Phe Asp Ile Ala Ser Asp	
167 172 177 182	
gcc ttt gct act ttc aag gat tta cta acc aga cat aaa gtg ttg gta	810
Ala Phe Ala Thr Phe Lys Asp Leu Leu Thr Arg His Lys Val Leu Val	
183 188 193 198	
gca gac ttc tta gaa caa aat tac gac act att ttt gaa gac tat gag	858
Ala Asp Phe Leu Glu Gln Asn Tyr Asp Thr Ile Phe Glu Asp Tyr Glu	
199 204 209 214	
aaa ttg ctt cag tct gag aat tat gtt act aag aga cag tct tta aag	906
Lys Leu Leu Gln Ser Glu Asn Tyr Val Thr Lys Arg Gln Ser Leu Lys	
215 220 225 230	
ctg cta ggg gag ctg atc ctg gac cgt cac aac ttt gcc atc atg aca	954
Leu Leu Gly Glu Leu Ile Leu Asp Arg His Asn Phe Ala Ile Met Thr	
231 236 241 246	
aag tat atc agc aag ccg gag aac ctg aaa ctc atg atg aac ctc ctt	1002
Lys Tyr Ile Ser Lys Pro Glu Asn Leu Lys Leu Met Met Asn Leu Leu	
247 252 257 262	
cgg gat aaa agt ccc aac atc cag ttt gaa gcc ttt cat gtt ttt aag	1050
Arg Asp Lys Ser Pro Asn Ile Gln Phe Glu Ala Phe His Val Phe Lys	
263 268 273 278	
gtg ttt gtg gcc agt cct cac aaa aca cag cct att gtg gag atc ctg	1098
Val Phe Val Ala Ser Pro His Lys Thr Gln Pro Ile Val Glu Ile Leu	
279 284 289 294	

Ala Leu Arg Val Ala Glu Val Trp Met Asp Asp Tyr Lys Ser His Val	
97 102 107 112	
tac ata gcg tgg aac ctg ccg ctg gag aat ccg gga att gac atc ggt	442
Tyr Ile Ala Trp Asn Leu Pro Leu Glu Asn Pro Gly Ile Asp Ile Gly	
113 118 123 128	
gat gtc tcc gaa aga aga gca tta agg aaa agt tta aag tgt aag aat	490
Asp Val Ser Glu Arg Arg Ala Leu Arg Lys Ser Leu Lys Cys Lys Asn	
129 134 139 144	
ttc cag tgg tac ctg gac cat gtt tac cca gaa atg aga aga tac aat	538
Phe Gln Trp Tyr Leu Asp His Val Tyr Pro Glu Met Arg Arg Tyr Asn	
145 150 155 160	
aat acc gtt gct tac ggg gag ctt cgc aac aac aag gca aaa gac gtc	586
Asn Thr Val Ala Tyr Gly Glu Leu Arg Asn Asn Lys Ala Lys Asp Val	
161 166 171 176	
tgc ttg gac cag ggg ccg ctg gag aac cac aca gca ata ttg tat ccg	634
Cys Leu Asp Gln Gly Pro Leu Glu Asn His Thr Ala Ile Leu Tyr Pro	
177 182 187 192	
tgc cat ggc tgg gga cca cag ctt gcc cgc tac acc aag gaa ggc ttc	682
Cys His Gly Trp Gly Pro Gln Leu Ala Arg Tyr Thr Lys Glu Gly Phe	
193 198 203 208	
ctg cac ttg ggt gcc ctg ggg acc acc aca ctc ctc cct gac acc cgc	730
Leu His Leu Gly Ala Leu Gly Thr Thr Thr Leu Leu Pro Asp Thr Arg	
209 214 219 224	
tgc ctg gtg gac aac tcc aag agt cgg ctg ccc cag ctc ctg gac tgc	778
Cys Leu Val Asp Asn Ser Lys Ser Arg Leu Pro Gln Leu Leu Asp Cys	
225 230 235 240	
gac aag gtc aag agc agc ctg tac aag cgc tgg aac ttc atc cag aat	826
Asp Lys Val Lys Ser Ser Leu Tyr Lys Arg Trp Asn Phe Ile Gln Asn	
241 246 251 256	
gga gcc atc atg aac aag ggc acg gga cgc tgc ctg gag gtg gag aac	874
Gly Ala Ile Met Asn Lys Gly Thr Gly Arg Cys Leu Glu Val Glu Asn	
257 262 267 272	
cgg ggc ctg gct ggc atc gac ctc atc ctc cgc agc tgc aca ggt cag	922
Arg Gly Leu Ala Gly Ile Asp Leu Ile Leu Arg Ser Cys Thr Gly Gln	
273 278 283 288	
agg tgg acc att aag aac tcc atc aag tag a gggagggagc tggggcactg	973
Arg Trp Thr Ile Lys Asn Ser Ile Lys *	
289 294	
gagcctggcc cccaggacat ggctgctccc cccaacatct ggaccagctg ccctggcgga	1033
gagacagcaa ggggcccggca ggtgctcgat gggcccccca gggcttctcc agggcagcac	1093
agggaccccc gatgaagact ctgtccccc tcaggcattc agctgcccac aagtttctg	1153

caccctggaa aagccccca cccttctct gggaaactga cagctgtctt ccacagcctc	1213
tgatgtggac ctggtactga ggagcaagac tgtccagttc tcctccacat ctcccatccc	1273
agaatcagga tctgggactg gcagggtccc ctctgtgtc tcatctcttg cagcagcagc	1333
tgctgaactc cagccatcaa cacgggtggga ggcagcgggg gcttcagcca tgtcctagct	1393
ccccgcccta aaaggaggca gtgaggacca ggcactatct cctccgaggt tacttctacc	1453
cagatgacac ctgcctgttc acgccccaa ggcagctactg cccctaacc ttcccaccag	1513
ggtagctttg ggcactgcag ctctggactt ttctggcccc tcctgagatg acctgatgga	1573
gctgatgctt tctctcctaa tccctgggca ctaggtctct atcagtgtgc ttggggccagc	1633
tctcctgcct gtgtctagag gaagccagag acagaaatag gctaagcctg cagtaggata	1693
tcagccacaa gggccccgca ggatggagct gggcaagga ccaggagacc ctgactccca	1753
gaggctgcca ccggggagaa gcagcgggtc tccatccaga acctaaagggc tgaagcaaag	1813
gctgccagga ccttgaaga tgcttttggc tcacctatt tcacccacg ctctgctggc	1873
tggcagagga gaaggcagtc gtttcctctc tgaagagtat ttttttcgat tggcctctgg	1933
ttagggtgca catataaatc agagttaata tatgaacgcg tgtgcatgca caagtgtgtg	1993
tgtgcctgog tgctgtgcgt ggcagggtgt gtgtgtgtgt gtctggctgt gcgttccgga	2053
gtgtgtgacg atgctgacct agctgtgtgg ccttgggctt gctgcttcat tactcaoctg	2113
gatggggacg agggatgaga aggggtgtggg tttggcccca tgtcactggc cggaaggatg	2173
tgtctcagcc ctgccctgtg ggggtgcccc gatgggaggc tgtcccatct cccagtcccc	2233
atctcttttt cccacactg tccctggcca agcctgccc agagctgaac cctgtagctg	2293
cccccttgcc ctgtgtggga ttgcagtggt ctcatctgtg gacgtcttac tggatgatcat	2353
ctctcaccac catctccac cttgtggaat aaatacatgt tagcacttcc caaaaaaaaa	2413
aaa	2416

<210> 113
 <211> 1007
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (58) .. (786)

<400> 113

atttggccct cgaggccaag aattcggcac gagcaagttg aaaaccagct gctaaaa	57
atg aag gtg gaa tcg tcc caa gaa gcc aat gct gag gtg atg cga gag	105
Met Lys Val Glu Ser Ser Gln Glu Ala Asn Ala Glu Val Met Arg Glu	
1 5 10 15	
atg acc aag aag ctg tac agc cag tat gag gag aag ctg cag gaa gaa	153
Met Thr Lys Lys Leu Tyr Ser Gln Tyr Glu Glu Lys Leu Gln Glu Glu	
17 22 27 32	
cag agg aag cac agt gct gag aag gag gct ctt ttg gaa gaa acc aat	201
Gln Arg Lys His Ser Ala Glu Lys Glu Ala Leu Leu Glu Glu Thr Asn	
33 38 43 48	
agt ttt ctg aaa gcg att gaa gaa gcc aat aaa aag atg caa gca gca	249
Ser Phe Leu Lys Ala Ile Glu Glu Ala Asn Lys Lys Met Gln Ala Ala	
49 54 59 64	
gag atc agc cta gag gag aaa gac cag agg atc ggg gag ctg gac agg	297
Glu Ile Ser Leu Glu Glu Lys Asp Gln Arg Ile Gly Glu Leu Asp Arg	
65 70 75 80	
ctg att gag cgc atg gaa aag gaa cgt cat caa ctg caa ctt caa ctc	345
Leu Ile Glu Arg Met Glu Lys Glu Arg His Gln Leu Gln Leu Gln Leu	
81 86 91 96	
cta gaa cat gaa aca gaa atg tct ggg gag tta act gat tct gac aag	393
Leu Glu His Glu Thr Glu Met Ser Gly Glu Leu Thr Asp Ser Asp Lys	
97 102 107 112	
gaa agg tat cag cag ttg gag gag gca tca gcc agc ctc cgt gag cgg	441
Glu Arg Tyr Gln Gln Leu Glu Glu Ala Ser Ala Ser Leu Arg Glu Arg	
113 118 123 128	
atc aga cac cta gat gac atg gtg cat tgc cag cag aag aaa gtc aag	489
Ile Arg His Leu Asp Asp Met Val His Cys Gln Gln Lys Lys Val Lys	
129 134 139 144	
cag atg gtc gag gag att gaa tca tta aag aaa aag ttg caa cag aaa	537
Gln Met Val Glu Glu Ile Glu Ser Leu Lys Lys Lys Leu Gln Gln Lys	
145 150 155 160	
cag ctc tta ata ctg cag ctt tta gaa aag ata tct ttc tta gaa gga	585
Gln Leu Leu Ile Leu Gln Leu Leu Glu Lys Ile Ser Phe Leu Glu Gly	
161 166 171 176	
gag aat aat gaa cta caa agc agg ttg gac tat tta aca gaa acc cag	633
Glu Asn Asn Glu Leu Gln Ser Arg Leu Asp Tyr Leu Thr Glu Thr Gln	
177 182 187 192	
gcc aag acc gaa gtg gaa acc aga gag ata gga gtg ggc tgt gat ctt	681
Ala Lys Thr Glu Val Glu Thr Arg Glu Ile Gly Val Gly Cys Asp Leu	
193 198 203 208	
cta ccc agc caa aca ggc agg act cgt gaa att gtg atg cct tct agg	729
Leu Pro Ser Gln Thr Gly Arg Thr Arg Glu Ile Val Met Pro Ser Arg	
209 214 219 224	

aac tac acc cca tac aca aga gtc ctg gag tta acc atg aag aaa act 777
 Asn Tyr Thr Pro Tyr Thr Arg Val Leu Glu Leu Thr Met Lys Lys Thr
 225 230 235 240

ctg act tag gcactca gaggcataca ctttttacag atggacaaaa gctctggaac 833
 Leu Thr *
 241

cctgtggcctt caaatccttt gggaaggggtg actgttggtt cccctacaca cagtgtgaagc 893

cggaatggga atcgctgagg ctctgatcca cttctaagac aggaaggaaa gtgaaggcag 953

agtgagcagg taagagaggg atatacaagg tcacatttca gaaccccact cggg 1007

<210> 114
 <211> 3074
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (366)..(2213)

<400> 114
 ccggaattcc cgggtcgacg atttcgtgga cacctggcaa gtctgacct gcctgtcccc 60

caaccttggg cggcccgccc ggcacgggt ggctcccta ggccacattc ttgcacaaag 120

ttcgagaggg tgtgggaaaa gcaacctga accggccaag ggccggcgaa gctgatccccg 180

caatggcatt ttgttttgaa cagttgctgg ggttgacgtt tcctcataag aggggtactg 240

gacaccagcg cagagtgcag actgaatggg gaaaggagat gcagagaaaa tctggcaaca 300

tacctattct tcacatccta ctctggggg agggctgcta gtggccctct gcaccaaccc 360

aaaga atg tct tcc aag caa gcc acc tct cca ttt gcc tgt gca gct 407
 Met Ser Ser Lys Gln Ala Thr Ser Pro Phe Ala Cys Ala Ala
 1 5 10

gat gga gag gat gca atg acc cag gat tta acc tca agg gaa aag gaa 455
 Asp Gly Glu Asp Ala Met Thr Gln Asp Leu Thr Ser Arg Glu Lys Glu
 15 20 25 30

gag ggc agt gat caa cat gtg gcc tcc cat ctg cct ctg cac ccc ata 503
 Glu Gly Ser Asp Gln His Val Ala Ser His Leu Pro Leu His Pro Ile
 31 36 41 46

atg cac aac aaa cct cac tct gag gag cta cca aca ctt gtc agt acc 551
 Met His Asn Lys Pro His Ser Glu Glu Leu Pro Thr Leu Val Ser Thr
 47 52 57 62

att caa caa gat gct gac tgg gac agc gtt ctg tca tct cag caa aga 599
 Ile Gln Gln Asp Ala Asp Trp Asp Ser Val Leu Ser Ser Gln Gln Arg

63	68	73	78	
atg gaa tca gag aat aat aag tta tgt tcc cta tat tcc ttc cga aat				647
Met Glu Ser Glu Asn Asn Lys Leu Cys Ser Leu Tyr Ser Phe Arg Asn				
79	84	89	94	
acc tct acc tca cca cat aag cct gac gaa ggg agt cgg gac cgt gag				695
Thr Ser Thr Ser Pro His Lys Pro Asp Glu Gly Ser Arg Asp Arg Glu				
95	100	105	110	
ata atg acc agt gtt act ttt gga acc cca gag cgc cgc aaa ggg agt				743
Ile Met Thr Ser Val Thr Phe Gly Thr Pro Glu Arg Arg Lys Gly Ser				
111	116	121	126	
ctt gcc gat gtg gtg gac aca ctg aaa cag aag aag ctt gag gaa atg				791
Leu Ala Asp Val Val Asp Thr Leu Lys Gln Lys Lys Leu Glu Glu Met				
127	132	137	142	
act cgg act gaa caa gag gat tcc tcc tgc atg gaa aaa cta ctt tca				839
Thr Arg Thr Glu Gln Glu Asp Ser Ser Cys Met Glu Lys Leu Leu Ser				
143	148	153	158	
aaa gat tgg aag gaa aaa atg gaa aga cta aat acc agt gaa ctt ctt				887
Lys Asp Trp Lys Glu Lys Met Glu Arg Leu Asn Thr Ser Glu Leu Leu				
159	164	169	174	
gga gaa att aaa ggt aca cct gag agc ctg gca gaa aaa gaa cgg cag				935
Gly Glu Ile Lys Gly Thr Pro Glu Ser Leu Ala Glu Lys Glu Arg Gln				
175	180	185	190	
ctc tcc acc atg att acc cag ctg atc agt tta cgg gag cag cta ctg				983
Leu Ser Thr Met Ile Thr Gln Leu Ile Ser Leu Arg Glu Gln Leu Leu				
191	196	201	206	
gca gcg cat gat gaa cag aaa aaa ctg gca gcg tca caa att gag aaa				1031
Ala Ala His Asp Glu Gln Lys Lys Leu Ala Ala Ser Gln Ile Glu Lys				
207	212	217	222	
caa cgg cag caa atg gac ctt gct cgc caa cag caa gaa cag att gcg				1079
Gln Arg Gln Gln Met Asp Leu Ala Arg Gln Gln Gln Glu Gln Ile Ala				
223	228	233	238	
aga caa cag cag caa ctt ctg caa cag cag cac aaa att aat ctc ctg				1127
Arg Gln Gln Gln Gln Leu Leu Gln Gln Gln His Lys Ile Asn Leu Leu				
239	244	249	254	
cag caa cag atc cag cag gtt cag ggt cac atg cct ccg ctc atg atc				1175
Gln Gln Gln Ile Gln Gln Val Gln Gly His Met Pro Pro Leu Met Ile				
255	260	265	270	
cca att ttt cca cat gac cag cgg act ctg gca gca gct gct gct gcc				1223
Pro Ile Phe Pro His Asp Gln Arg Thr Leu Ala Ala Ala Ala Ala Ala				
271	276	281	286	
caa cag gga ttc ctc ttc ccc cct gga ata aca tac aaa cca ggt gat				1271
Gln Gln Gly Phe Leu Phe Pro Pro Gly Ile Thr Tyr Lys Pro Gly Asp				
287	292	297	302	

aac tac ccc gta cag ttc att cca tca aca atg gca gct gct gct gct	1319
Asn Tyr Pro Val Gln Phe Ile Pro Ser Thr Met Ala Ala Ala Ala	
303 308 313 318	
tct gga ctc agc cct tta cag ctc cag aag ggt cat gtc tcc cac cca	1367
Ser Gly Leu Ser Pro Leu Gln Leu Gln Lys Gly His Val Ser His Pro	
319 324 329 334	
caa att aac caa agg cta aag ggc cta agt gac cgt ttt ggc agg aat	1415
Gln Ile Asn Gln Arg Leu Lys Gly Leu Ser Asp Arg Phe Gly Arg Asn	
335 340 345 350	
ttg gac acc ttt gaa cat ggt ggt ggc cac tct tac aac cac aaa cag	1463
Leu Asp Thr Phe Glu His Gly Gly Gly His Ser Tyr Asn His Lys Gln	
351 356 361 366	
att gag cag ctc tat gcc gct cag ctg gcc agc atg cag gtg tca cct	1511
Ile Glu Gln Leu Tyr Ala Ala Gln Leu Ala Ser Met Gln Val Ser Pro	
367 372 377 382	
gga gca aag atg cca tca act cca cag cca cca aac aca gca ggg acg	1559
Gly Ala Lys Met Pro Ser Thr Pro Gln Pro Pro Asn Thr Ala Gly Thr	
383 388 393 398	
gtc tca cct act ggg ata aaa aat gaa aag aga ggg acc agc cct gta	1607
Val Ser Pro Thr Gly Ile Lys Asn Glu Lys Arg Gly Thr Ser Pro Val	
399 404 409 414	
act caa gtt aag gat gaa gca gca gca cag cct ctg aat ctc tca tcc	1655
Thr Gln Val Lys Asp Glu Ala Ala Ala Gln Pro Leu Asn Leu Ser Ser	
415 420 425 430	
cga ccc aag aca gca gag cct gta aag tcc cca acg tct ccc acc cag	1703
Arg Pro Lys Thr Ala Glu Pro Val Lys Ser Pro Thr Ser Pro Thr Gln	
431 436 441 446	
aac ctc ttc cca gcc agc aaa acc agc cct gtc aat ctg cca aac aaa	1751
Asn Leu Phe Pro Ala Ser Lys Thr Ser Pro Val Asn Leu Pro Asn Lys	
447 452 457 462	
agc agc atc cct agc ccc att gga gga agc ctg gga aga gga tcc tct	1799
Ser Ser Ile Pro Ser Pro Ile Gly Gly Ser Leu Gly Arg Gly Ser Ser	
463 468 473 478	
tta gat atc cta tct agt ctc aac tcc cct gcc ctt ttt ggg gat cag	1847
Leu Asp Ile Leu Ser Ser Leu Asn Ser Pro Ala Leu Phe Gly Asp Gln	
479 484 489 494	
gat aca gtg atg aaa gcc att cag gag gcg cgg aag atg cga gag cag	1895
Asp Thr Val Met Lys Ala Ile Gln Glu Ala Arg Lys Met Arg Glu Gln	
495 500 505 510	
atc cag cgg gag caa cag cag caa cag cca cat ggt gtt gac ggg aaa	1943
Ile Gln Arg Glu Gln Gln Gln Gln Gln Pro His Gly Val Asp Gly Lys	
511 516 521 526	

ctg tcc tcc ata aat aat atg ggg ctg aat agc tgc agg aat gaa aag	1991
Leu Ser Ser Ile Asn Asn Met Gly Leu Asn Ser Cys Arg Asn Glu Lys	
527 532 537 542	
gaa aga acg cgc ttt gag aat ttg ggg ccc cag tta acg gga aag tca	2039
Glu Arg Thr Arg Phe Glu Asn Leu Gly Pro Gln Leu Thr Gly Lys Ser	
543 548 553 558	
aat gaa gat gga aaa ctg ggc cca ggt gtc atc gac ctt act cgg cca	2087
Asn Glu Asp Gly Lys Leu Gly Pro Gly Val Ile Asp Leu Thr Arg Pro	
559 564 569 574	
gaa gat gca gag gga ggt gcc act gtg gct gaa gca cga gtc tac agg	2135
Glu Asp Ala Glu Gly Gly Ala Thr Val Ala Glu Ala Arg Val Tyr Arg	
575 580 585 590	
gac gcc cgc ggc ctg cca gca gcg agc cac aca tta agc gac cat atg	2183
Asp Ala Arg Gly Leu Pro Ala Ala Ser His Thr Leu Ser Asp His Met	
591 596 601 606	
aat gca ttc ata ggt ttg ggc aaa gga tga g aggagaaaaa tccttcaggc	2234
Asn Ala Phe Ile Gly Leu Gly Lys Gly *	
607 612	
cttccccgac atgcataact ccaacattag caaaatctta ggatctcgct ggaaatcaat	2294
gtccaaccag gagaagcaac cttattatga agagcaggcc cggctaagca agatccactt	2354
agagaagtac ccaaactata aatacaaaacc cggaccgaaa cgcacctgca ttgttgatgg	2414
caaaaagctt cggattgggg agtataagca actgatgagg tctcggagac aggagatgag	2474
gcagttcttt actgtggggc aacagcctca gattccaatc accacaggaa cagggtgttg	2534
gtatcctggt gctatcacta tggcaactac cacaccatcg cctcagatga catctgactg	2594
ctctagcacc tcggccagcc cggagcccag cctcccggtc atccagagca cttatggtat	2654
gaagacagat ggcggaagcc tagctggaaa tgaaatgatc aatggagagg atgaaatgga	2714
aatgtatgat gactatgaag atgaccccaa atcagactat agcagtgaaa atgaagcccc	2774
ggaggctgtc agtgccaact gaggagtgtt tgtttgctga attaaagtac tctgacattt	2834
cacccccctc cccaacaaag agttattaaa gagcccgcat gcatttgtgg ctccacaatt	2894
acatcagcag aatggtctta attgtttcgt aaagtgtgag acagattaag ttttccctga	2954
tttttcatga acttgagttt tttgttggtt ttgttattgt tgttggtgtt gtttttttaa	3014
tttaggtgaa gacatattaa atatgagaca ccaggacttg aaacttaaaa aaaaaaaaaa	3074

<210> 115
<211> 3442

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (145)..(3078)

<400> 115

```

gctaccgggtc cggaattccc gggtcgacga tttcgtctcg gctccttggc gctgcctggg      60
gtccttttcg cccgggtcccc gcttgccagc ccccgctgct ctgtgccctg tccggccagg      120
cctggagccg acaccaccgc catc      atg ccg gcc gtg tcc aag ggc gat ggg      171
                               Met Pro Ala Val Ser Lys Gly Asp Gly
                               1               5

atg cgg ggg ctc gcg gtg ttc atc tcc gac atc cgg aac tgt aag agc      219
Met Arg Gly Leu Ala Val Phe Ile Ser Asp Ile Arg Asn Cys Lys Ser
 10               15               20               25

aaa gag gcg gaa att aag aga atc aac aag gaa ctg gcc aac atc cgc      267
Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala Asn Ile Arg
 26               31               36               41

tcc aag ttc aaa gga gac aaa gcc ttg gat ggc tac agt aag aaa aaa      315
Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser Lys Lys Lys
 42               47               52               57

tat gtg tgt aaa ctg ctt ttc atc ttc ctg ctt ggc cat gac att gac      363
Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His Asp Ile Asp
 58               63               68               73

ttt ggg cac atg gag gct gtg aat ctg ttg agt tcc aat aaa tac aca      411
Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn Lys Tyr Thr
 74               79               84               89

gag aag caa ata ggt tac ctg ttc att tct gtg ctg gtg aac tcg aac      459
Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn
 90               95               100              105

tcg gag ctg atc cgc ctc atc aac aac gcc atc aag aat gac ctg gcc      507
Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala
106              111              116              121

agc cgc aac ccc acc ttc atg tgc ctg gcc ctg cac tgc atc gcc aac      555
Ser Arg Asn Pro Thr Phe Met Cys Leu Ala Leu His Cys Ile Ala Asn
122              127              132              137

gtg ggc agc cgg gag atg ggc gag gcc ttt gcc gct gac atc ccc cgc      603
Val Gly Ser Arg Glu Met Gly Glu Ala Phe Ala Ala Asp Ile Pro Arg
138              143              148              153

atc ctg gtg gcc ggg gac agc atg gac agt gtc aag cag agt gcg gcc      651
Ile Leu Val Ala Gly Asp Ser Met Asp Ser Val Lys Gln Ser Ala Ala
154              159              164              169

ctg tgc ctc ctt cga ctg tac aag gcc tcg cct gac ctg gtg ccc atg      699

```

Leu Cys Leu Leu Arg Leu Tyr Lys Ala Ser Pro Asp Leu Val Pro Met	
170 175 180 185	
ggc gag tgg acg gcg cgt gtg gta cac ctg ctc aat gac cag cac atg	747
Gly Glu Trp Thr Ala Arg Val Val His Leu Leu Asn Asp Gln His Met	
186 191 196 201	
ggt gtg gtc acg gcc gcc gtc agc ctc atc acc tgt ctc tgc aag aag	795
Gly Val Val Thr Ala Ala Val Ser Leu Ile Thr Cys Leu Cys Lys Lys	
202 207 212 217	
aac cca gat gac ttc aag acg tgc gtc tct ctg gct gtg tcg cgc ctg	843
Asn Pro Asp Asp Phe Lys Thr Cys Val Ser Leu Ala Val Ser Arg Leu	
218 223 228 233	
agc cgg atc gtc tcc tct gcc tcc acc gac ctc cag gac tac acc tac	891
Ser Arg Ile Val Ser Ser Ala Ser Thr Asp Leu Gln Asp Tyr Thr Tyr	
234 239 244 249	
tac ttc gtc cca gca ccc tgg ctc tcg gtg aag ctc ctg cgg ctg ctg	939
Tyr Phe Val Pro Ala Pro Trp Leu Ser Val Lys Leu Leu Arg Leu Leu	
250 255 260 265	
cag tgc tac ccg cct cca gag gat gcg gct gtg aag ggg cgg ctg gtg	987
Gln Cys Tyr Pro Pro Pro Glu Asp Ala Ala Val Lys Gly Arg Leu Val	
266 271 276 281	
gaa tgt ctg gag act gtg ctc aac aag gcc cag gag ccc ccc aaa tcc	1035
Glu Cys Leu Glu Thr Val Leu Asn Lys Ala Gln Glu Pro Pro Lys Ser	
282 287 292 297	
aag aag gtg cag cat tcc aac gcc aag aac gcc atc ctc ttc gag acc	1083
Lys Lys Val Gln His Ser Asn Ala Lys Asn Ala Ile Leu Phe Glu Thr	
298 303 308 313	
atc agc ctc atc atc cac tat gac agt gag ccc aac ctc ctg gtt cgg	1131
Ile Ser Leu Ile Ile His Tyr Asp Ser Glu Pro Asn Leu Leu Val Arg	
314 319 324 329	
gcc tgc aac cag ctg gcc cag ttc ctg cag cac cgg gag acc aac ctg	1179
Ala Cys Asn Gln Leu Glu Gln Phe Leu Gln His Arg Glu Thr Asn Leu	
330 335 340 345	
cgc tac ctg gcc ctg gag agc atg tgc acg ctg gcc agc tcc gag ttc	1227
Arg Tyr Leu Ala Leu Glu Ser Met Cys Thr Leu Ala Ser Ser Glu Phe	
346 351 356 361	
tcc cat gaa gcc gtc aag acg cac att gac acc gtc atc aat gcc ctc	1275
Ser His Glu Ala Val Lys Thr His Ile Asp Thr Val Ile Asn Ala Leu	
362 367 372 377	
aag acg gag cgg gac gtc agc gtg cgg cag cgg gcg gct gac ctc ctc	1323
Lys Thr Glu Arg Asp Val Ser Val Arg Gln Arg Ala Ala Asp Leu Leu	
378 383 388 393	
tac gcc atg tgt gac cgg agc aat gcc aag cag atc gtg tcg gag atg	1371
Tyr Ala Met Cys Asp Arg Ser Asn Ala Lys Gln Ile Val Ser Glu Met	

394	399	404	409	
ctg cgg tac ctg gag acg gca gac tac gcc atc cgc gag gag atc gtc				1419
Leu Arg Tyr Leu Glu Thr Ala Asp Tyr Ala Ile Arg Glu Glu Ile Val				
410	415	420	425	
ctg aag gtg gcc atc ctg gcc gag aag tac gcc gtg gac tac agc tgg				1467
Leu Lys Val Ala Ile Leu Ala Glu Lys Tyr Ala Val Asp Tyr Ser Trp				
426	431	436	441	
tac gtg gac acc atc ctc aac ctc atc cgc att gcg ggc gac tac gtg				1515
Tyr Val Asp Thr Ile Leu Asn Leu Ile Arg Ile Ala Gly Asp Tyr Val				
442	447	452	457	
agt gag gag gtg tgg tac cgt gtg cta cag atc gtc acc aac cgt gat				1563
Ser Glu Glu Val Trp Tyr Arg Val Leu Gln Ile Val Thr Asn Arg Asp				
458	463	468	473	
gac gtc cag ggc tat gcc gcc aag acc gtc ttt gag gcg ctc cag gcc				1611
Asp Val Gln Gly Tyr Ala Ala Lys Thr Val Phe Glu Ala Leu Gln Ala				
474	479	484	489	
cct gcc tgt cac gag aac atg gtg aag gtt ggc ggc tac atc ctt ggg				1659
Pro Ala Cys His Glu Asn Met Val Lys Val Gly Gly Tyr Ile Leu Gly				
490	495	500	505	
gag ttt ggg aac ctg att gct ggg gac ccc cgc tcc agc ccc cca gtg				1707
Glu Phe Gly Asn Leu Ile Ala Gly Asp Pro Arg Ser Ser Pro Pro Val				
506	511	516	521	
cag ttc tcc ctg ctc cac tcc aag ttc cat ctg tgc agc gtg gcc acg				1755
Gln Phe Ser Leu Leu His Ser Lys Phe His Leu Cys Ser Val Ala Thr				
522	527	532	537	
cgg gcg ctg ctg ctg tcc acc tac atc aag ttc atc aac ctc tcc ccc				1803
Arg Ala Leu Leu Leu Ser Thr Tyr Ile Lys Phe Ile Asn Leu Ser Pro				
538	543	548	553	
gag acc aag gcc acc atc cag gcc gtc ctg cgg gcc ggc tcc cag ctg				1851
Glu Thr Lys Ala Thr Ile Gln Gly Val Leu Arg Ala Gly Ser Gln Leu				
554	559	564	569	
cgc aat gct gac gtg gag ctg cag cag cga gcc gtg gag tac ctc acc				1899
Arg Asn Ala Asp Val Glu Leu Gln Gln Arg Ala Val Glu Tyr Leu Thr				
570	575	580	585	
ctc agc tca gtg gcc agc acc gac gtc ctg gcc acg gtg ctg gag gag				1947
Leu Ser Ser Val Ala Ser Thr Asp Val Leu Ala Thr Val Leu Glu Glu				
586	591	596	601	
atg ccg ccc ttc ccc gag cgc gag tcg tcc atc ctg gcc aag ctg aaa				1995
Met Pro Pro Phe Pro Glu Arg Glu Ser Ser Ile Leu Ala Lys Leu Lys				
602	607	612	617	
cgc aag aag ggg cca ggg gcc gcc agc gcc ctg gac gat ggc cgg agg				2043
Arg Lys Lys Gly Pro Gly Ala Gly Ser Ala Leu Asp Asp Gly Arg Arg				
618	623	628	633	

gac ccc agc agc aac gac atc aac ggg ggc atg gag ccc acc ccc agc Asp Pro Ser Ser Asn Asp Ile Asn Gly Gly Met Glu Pro Thr Pro Ser 634 639 644 649	2091
act gtg tcg acg ccc tcg ccc tcc gcc gac ctc ctg ggg ctg cgg gca Thr Val Ser Thr Pro Ser Pro Ser Ala Asp Leu Leu Gly Leu Arg Ala 650 655 660 665	2139
gcc cct ccc ccg gca gca ccc ccg gct tct gca gga gca ggg aac ctt Ala Pro Pro Pro Ala Ala Pro Pro Ala Ser Ala Gly Ala Gly Asn Leu 666 671 676 681	2187
ctg gtg gac gtc ttc gat ggc ccg gcc gcc cag ccc agc ctg ggg ccc Leu Val Asp Val Phe Asp Gly Pro Ala Ala Gln Pro Ser Leu Gly Pro 682 687 692 697	2235
acc ccc gag gag gcc ttc ctc agc gag ctg gag ccg cct gcc ccc gag Thr Pro Glu Glu Ala Phe Leu Ser Glu Leu Glu Pro Pro Ala Pro Glu 698 703 708 713	2283
agc ccc atg gct ttg ctg gct gac cca gct cca gct gct gac cca ggt Ser Pro Met Ala Leu Leu Ala Asp Pro Ala Pro Ala Ala Asp Pro Gly 714 719 724 729	2331
cct gag gac atc ggc cct ccc att ccg gaa gcc gat gag ttg ctg aat Pro Glu Asp Ile Gly Pro Pro Ile Pro Glu Ala Asp Glu Leu Leu Asn 730 735 740 745	2379
aag ttt gtg tgt aag aac aac ggg gtc ctg ttc gag aac cag ctg ctg Lys Phe Val Cys Lys Asn Asn Gly Val Leu Phe Glu Asn Gln Leu Leu 746 751 756 761	2427
cag atc gga gtc aag tca gag ttc cga cag aac ctg ggc cgc atg tat Gln Ile Gly Val Lys Ser Glu Phe Arg Gln Asn Leu Gly Arg Met Tyr 762 767 772 777	2475
ctc ttc tat ggc aac aag acc tcg gtg cag ttc cag aat ttc tca ccc Leu Phe Tyr Gly Asn Lys Thr Ser Val Gln Phe Gln Asn Phe Ser Pro 778 783 788 793	2523
act gtg gtt cac ccg gga gac ctc cag act cag ctg gct gtg cag acc Thr Val Val His Pro Gly Asp Leu Gln Thr Gln Leu Ala Val Gln Thr 794 799 804 809	2571
aag cgc gtg gcg gcg cag gtg gac ggc ggc gcg cag gtg cag cag gtg Lys Arg Val Ala Ala Gln Val Asp Gly Gly Ala Gln Val Gln Gln Val 810 815 820 825	2619
ctc aat atc gag tgc ctg cgg gac ttc ctg acg ccc ccg ctg ctg tcc Leu Asn Ile Glu Cys Leu Arg Asp Phe Leu Thr Pro Pro Leu Leu Ser 826 831 836 841	2667
gtg cgc ttc cgg tac ggt ggc gcc ccc cag gcc ctc acc ctg aag ctc Val Arg Phe Arg Tyr Gly Gly Ala Pro Gln Ala Leu Thr Leu Lys Leu 842 847 852 857	2715

cca gtg acc atc aac aag ttc ttc cag ccc acc gag atg gcg gcc cag	2763
Pro Val Thr Ile Asn Lys Phe Phe Gln Pro Thr Glu Met Ala Ala Gln	
858 863 868 873	
gat ttc ttc cag cgc tgg aag cag ctg agc ctc cct caa cag gag gcg	2811
Asp Phe Phe Gln Arg Trp Lys Gln Leu Ser Leu Pro Gln Gln Glu Ala	
874 879 884 889	
cag aaa atc ttc aaa gcc aac cac ccc atg gac gca gaa gtt act aag	2859
Gln Lys Ile Phe Lys Ala Asn His Pro Met Asp Ala Glu Val Thr Lys	
890 895 900 905	
gcc aag ctt ctg ggg ttt ggc tct gct ctc ctg gag aat gtg gac ccc	2907
Ala Lys Leu Leu Gly Phe Gly Ser Ala Leu Leu Asp Asn Val Asp Pro	
906 911 916 921	
aac cct gag aac ttc gtg ggg gcg ggg atc atc cag act aaa gcc ctg	2955
Asn Pro Glu Asn Phe Val Gly Ala Gly Ile Ile Gln Thr Lys Ala Leu	
922 927 932 937	
cag gtg ggc tgt ctg ctt cgg ctg gag ccc aat gcc cag gcc cag atg	3003
Gln Val Gly Cys Leu Leu Arg Leu Glu Pro Asn Ala Gln Ala Gln Met	
938 943 948 953	
tac cgg ctg acc ctg cgc acc agc aag gag ccc gtc tcc cgt cac ctg	3051
Tyr Arg Leu Thr Leu Arg Thr Ser Lys Glu Pro Val Ser Arg His Leu	
954 959 964 969	
tgt gag ctg ctg gca cag cag ttc tga gccct ggactctgcc ccgggggatg	3103
Cys Glu Leu Leu Ala Gln Gln Phe *	
970 975	
tggccggcac tgggcagccc cttggactga ggcagttttg gtggatgggg gacctccact	3163
ggtgacagag aagacaccag ggtttggggg atgcctggga ctttcctccg gccttttgta	3223
tttttatttt tgttcactctg ctgctgttta cattctgggg ggttaggggg agtccccctc	3283
cctccctttc ccccccaagc acagagggga gaggggccag ggaagtggat gtctcctccc	3343
ctcccacccc accctgttgt agccctcct acccctccc catccagggg ctgtgtatta	3403
ttgtgagcga ataaacagag agacgctaaa aaaaaaaaaa	3442

<210> 116
 <211> 3376
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (145)..(3012)

 <400> 116

gctaccggtc cggaattccc gggtcgacga tttcgtctcg gctccttggc gctgcctggg 60

gtccttttccg cccgggtcccc gcttgccagc ccccgtgct ctgtgccctg tccggccagg 120

cctggagccg acaccaccgc catc atg ccg gcc gtg tcc aag ggc gat ggg 171
Met Pro Ala Val Ser Lys Gly Asp Gly
1 5

atg cgg ggg ctc gcg gtg ttc atc tcc gac atc cgg aac tgt aag agc 219
Met Arg Gly Leu Ala Val Phe Ile Ser Asp Ile Arg Asn Cys Lys Ser
10 15 20 25

aaa gag gcg gaa att aag aga atc aac aag gaa ctg gcc aac atc cgc 267
Lys Glu Ala Glu Ile Lys Arg Ile Asn Lys Glu Leu Ala Asn Ile Arg
26 31 36 41

tcc aag ttc aaa gga gac aaa gcc ttg gat ggc tac agt aag aaa aaa 315
Ser Lys Phe Lys Gly Asp Lys Ala Leu Asp Gly Tyr Ser Lys Lys Lys
42 47 52 57

tat gtg tgt aaa ctg ctt ttc atc ttc ctg ctt ggc cat gac att gac 363
Tyr Val Cys Lys Leu Leu Phe Ile Phe Leu Leu Gly His Asp Ile Asp
58 63 68 73

ttt ggg cac atg gag gct gtg aat ctg ttg agt tcc aat aaa tac aca 411
Phe Gly His Met Glu Ala Val Asn Leu Leu Ser Ser Asn Lys Tyr Thr
74 79 84 89

gag aag caa ata ggt tac ctg ttc att tct gtg ctg gtg aac tcg aac 459
Glu Lys Gln Ile Gly Tyr Leu Phe Ile Ser Val Leu Val Asn Ser Asn
90 95 100 105

tcg gag ctg atc cgc ctc atc aac aac gcc atc aag aat gac ctg gcc 507
Ser Glu Leu Ile Arg Leu Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala
106 111 116 121

agc cgc aac ccc acc ttc atg tgc ctg gcc ctg cac tgc atc gcc aac 555
Ser Arg Asn Pro Thr Phe Met Cys Leu Ala Leu His Cys Ile Ala Asn
122 127 132 137

gtg ggc agc cgg gag atg ggc gag gcc ttt gcc gct gac atc ccc cgc 603
Val Gly Ser Arg Glu Met Gly Glu Ala Phe Ala Ala Asp Ile Pro Arg
138 143 148 153

atc ctg gtg gcc ggg gac agc atg gac agt gtc aag cag agt gcg gcc 651
Ile Leu Val Ala Gly Asp Ser Met Asp Ser Val Lys Gln Ser Ala Ala
154 159 164 169

ctg tgc ctc ctt cga ctg tac aag gcc tcg cct gac ctg gtg ccc atg 699
Leu Cys Leu Leu Arg Leu Tyr Lys Ala Ser Pro Asp Leu Val Pro Met
170 175 180 185

ggc gag tgg acg gcg cgt gtg gta cac ctg ctc aat gac cag cac atg 747
Gly Glu Trp Thr Ala Arg Val Val His Leu Leu Asn Asp Gln His Met
186 191 196 201

ggg gtg gtc acg gcc gcc gtc agc ctc atc acc tgt ctc tgc aag aag 795

Gly Val Val Thr Ala Ala Val Ser Leu Ile Thr Cys Leu Cys Lys Lys	
202 207 212 217	
aac cca gat gac ttc aag acg tgc gtc tct ctg gct gtg tcg cgc ctg	843
Asn Pro Asp Asp Phe Lys Thr Cys Val Ser Leu Ala Val Ser Arg Leu	
218 223 228 233	
agc cgg atc gtc tcc tct gcc tcc acc gac ctc cag gac tac acc tac	891
Ser Arg Ile Val Ser Ser Ala Ser Thr Asp Leu Gln Asp Tyr Thr Tyr	
234 239 244 249	
tac ttc gtc cca gca ccc tgg ctc tcg gtg aag ctc ctg cgg ctg ctg	939
Tyr Phe Val Pro Ala Pro Trp Leu Ser Val Lys Leu Leu Arg Leu Leu	
250 255 260 265	
cag tgc tac ccg cct cca gag gat gcg gct gtg aag ggg cgg ctg gtg	987
Gln Cys Tyr Pro Pro Pro Glu Asp Ala Ala Val Lys Gly Arg Leu Val	
266 271 276 281	
gaa tgt ctg gag act gtg ctc aac aag gcc cag gag ccc ccc aaa tcc	1035
Glu Cys Leu Glu Thr Val Leu Asn Lys Ala Gln Glu Pro Pro Lys Ser	
282 287 292 297	
aag aag gtg cag cat tcc aac gcc aag aac gcc atc ctc ttc gag acc	1083
Lys Lys Val Gln His Ser Asn Ala Lys Asn Ala Ile Leu Phe Glu Thr	
298 303 308 313	
atc agc ctc atc atc cac tat gac agt gag ccc aac ctc ctg gtt cgg	1131
Ile Ser Leu Ile Ile His Tyr Asp Ser Glu Pro Asn Leu Leu Val Arg	
314 319 324 329	
gcc tgc aac cag ctg ggc cag ttc ctg cag cac cgg gag acc aac ctg	1179
Ala Cys Asn Gln Leu Gly Gln Phe Leu Gln His Arg Glu Thr Asn Leu	
330 335 340 345	
cgc tac ctg gcc ctg gag agc atg tgc acg ctg gcc agc tcc gag ttc	1227
Arg Tyr Leu Ala Leu Glu Ser Met Cys Thr Leu Ala Ser Ser Glu Phe	
346 351 356 361	
tcc cat gaa gcc gtc aag acg cac att gac acc gtc atc aat gcc ctc	1275
Ser His Glu Ala Val Lys Thr His Ile Asp Thr Val Ile Asn Ala Leu	
362 367 372 377	
aag acg gag cgg gac gtc agc gtg cgg cag cgg gcg gct gac ctc ctc	1323
Lys Thr Glu Arg Asp Val Ser Val Arg Gln Arg Ala Ala Asp Leu Leu	
378 383 388 393	
tac gcc atg tgt gac cgg agc aat gcc aag cag atc gtg tcg gag atg	1371
Tyr Ala Met Cys Asp Arg Ser Asn Ala Lys Gln Ile Val Ser Glu Met	
394 399 404 409	
ctg cgg tac ctg gag acg gca gac tac gcc atc cgc gag gag atc gtc	1419
Leu Arg Tyr Leu Glu Thr Ala Asp Tyr Ala Ile Arg Glu Glu Ile Val	
410 415 420 425	
ctg aag gtg gcc atc ctg gcc gag aag tac gcc gtg gac tac agc tgg	1467
Leu Lys Val Ala Ile Leu Ala Glu Lys Tyr Ala Val Asp Tyr Ser Trp	

426	431	436	441	
tac gtg gac acc atc ctc aac ctc atc cgc att gcg ggc gac tac gtg				1515
Tyr Val Asp Thr Ile Leu Asn Leu Ile Arg Ile Ala Gly Asp Tyr Val				
442	447	452	457	
agt gag gag gtg tgg tac cgt gtg cta cag atc gtc acc aac cgt gat				1563
Ser Glu Glu Val Trp Tyr Arg Val Leu Gln Ile Val Thr Asn Arg Asp				
458	463	468	473	
gac gtc cag ggc tat gcc gcc aag acc gtc ttt gag gcg ctc cag gcc				1611
Asp Val Gln Gly Tyr Ala Ala Lys Thr Val Phe Glu Ala Leu Gln Ala				
474	479	484	489	
cct gcc tgt cac gag aac atg gtg aag gtt ggc ggc tac atc ctt ggg				1659
Pro Ala Cys His Glu Asn Met Val Lys Val Gly Gly Tyr Ile Leu Gly				
490	495	500	505	
gag ttt ggg aac ctg att gct ggg gac ccc cgc tcc agc ccc cca gtg				1707
Glu Phe Gly Asn Leu Ile Ala Gly Asp Pro Arg Ser Ser Pro Pro Val				
506	511	516	521	
cag ttc tcc ctg ctc cac tcc aag ttc cat ctg tgc agc gtg gcc acg				1755
Gln Phe Ser Leu Leu His Ser Lys Phe His Leu Cys Ser Val Ala Thr				
522	527	532	537	
cgg gcg ctg ctg ctg tcc acc tac atc aag ttc atc aac ctc tcc ccc				1803
Arg Ala Leu Leu Leu Ser Thr Tyr Ile Lys Phe Ile Asn Leu Ser Pro				
538	543	548	553	
gag acc aag gcc acc atc cag ggc gtc ctg cgg gcc ggc tcc cag ctg				1851
Glu Thr Lys Ala Thr Ile Gln Gly Val Leu Arg Ala Gly Ser Gln Leu				
554	559	564	569	
cgc aat gct gac gtg gag ctg cag cag cga gcc gtg gag tac ctc acc				1899
Arg Asn Ala Asp Val Glu Leu Gln Gln Arg Ala Val Glu Tyr Leu Thr				
570	575	580	585	
ctc agc tca gtg gcc agc acc gac gtc ctg gcc acg gtg ctg gag gag				1947
Leu Ser Ser Val Ala Ser Thr Asp Val Leu Ala Thr Val Leu Glu Glu				
586	591	596	601	
atg ccg ccc ttc ccc gag cgc gag tcg tcc atc ctg gcc aag ctg aaa				1995
Met Pro Pro Phe Pro Glu Arg Glu Ser Ser Ile Leu Ala Lys Leu Lys				
602	607	612	617	
cgc aag aag ggg cca ggg gcc ggc agc gcc ctg gac gat ggc cgg agg				2043
Arg Lys Lys Gly Pro Gly Ala Gly Ser Ala Leu Asp Asp Gly Arg Arg				
618	623	628	633	
gac ccc agc agc aac gac atc aac ggg ggc atg gag ccc acc ccc agc				2091
Asp Pro Ser Ser Asn Asp Ile Asn Gly Gly Met Glu Pro Thr Pro Ser				
634	639	644	649	
act gtg tcg acg ccc tcg ccc tcc gcc gac ctc ctg ggg ctg cgg gca				2139
Thr Val Ser Thr Pro Ser Pro Ser Ala Asp Leu Leu Gly Leu Arg Ala				
650	655	660	665	

gcc cct ccc ccg gca gca ccc ccg gct tct gca gga gca ggg aac ctt	2187
Ala Pro Pro Pro Ala Ala Pro Pro Ala Ser Ala Gly Ala Gly Asn Leu	
666 671 676 681	
ctg gtg gac gtc ttc gat ggc ccg gcc gcc cag ccc agc ctg ggg ccc	2235
Leu Val Asp Val Phe Asp Gly Pro Ala Ala Gln Pro Ser Leu Gly Pro	
682 687 692 697	
acc ccc gag gag gcc ttc ctc agc cca ggt cct gag gac atc ggc cct	2283
Thr Pro Glu Glu Ala Phe Leu Ser Pro Gly Pro Glu Asp Ile Gly Pro	
698 703 708 713	
ccc att ccg gaa gcc gat gag ttg ctg aat aag ttt gtg tgt aag aac	2331
Pro Ile Pro Glu Ala Asp Glu Leu Leu Asn Lys Phe Val Cys Lys Asn	
714 719 724 729	
aac ggg gtc ctg ttc gag aac cag ctg ctg cag atc gga gtc aag tca	2379
Asn Gly Val Leu Phe Glu Asn Gln Leu Leu Gln Ile Gly Val Lys Ser	
730 735 740 745	
gag ttc cga cag aac ctg ggc cgc atg tat ctc ttc tat ggc aac aag	2427
Glu Phe Arg Gln Asn Leu Gly Arg Met Tyr Leu Phe Tyr Gly Asn Lys	
746 751 756 761	
acc tcg gtg cag ttc cag aat ttc tca ccc act gtg gtt cac ccg gga	2475
Thr Ser Val Gln Phe Gln Asn Phe Ser Pro Thr Val Val His Pro Gly	
762 767 772 777	
gac ctc cag act cag ctg gct gtg cag acc aag cgc gtg gcg gcg cag	2523
Asp Leu Gln Thr Gln Leu Ala Val Gln Thr Lys Arg Val Ala Ala Gln	
778 783 788 793	
gtg gac ggc ggc gcg cag gtg cag cag gtg ctc aat atc gag tgc ctg	2571
Val Asp Gly Gly Ala Gln Val Gln Gln Val Leu Asn Ile Glu Cys Leu	
794 799 804 809	
cgg gac ttc ctg acg ccc ccg ctg ctg tcc gtg cgc ttc cgg tac ggt	2619
Arg Asp Phe Leu Thr Pro Pro Leu Leu Ser Val Arg Phe Arg Tyr Gly	
810 815 820 825	
ggc gcc ccc cag gcc ctc acc ctg aag ctc cca gtg acc atc aac aag	2667
Gly Ala Pro Gln Ala Leu Thr Leu Lys Leu Pro Val Thr Ile Asn Lys	
826 831 836 841	
ttc ttc cag ccc acc gag atg gcg gcc cag gat ttc ttc cag cgc tgg	2715
Phe Phe Gln Pro Thr Glu Met Ala Ala Gln Asp Phe Phe Gln Arg Trp	
842 847 852 857	
aag cag ctg agc ctc cct caa cag gag gcg cag aaa atc ttc aaa gcc	2763
Lys Gln Leu Ser Leu Pro Gln Gln Glu Ala Gln Lys Ile Phe Lys Ala	
858 863 868 873	
aac cac ccc atg gac gca gaa gtt act aag gcc aag ctt ctg ggg ttt	2811
Asn His Pro Met Asp Ala Glu Val Thr Lys Ala Lys Leu Leu Gly Phe	
874 879 884 889	

ggc tct gct ctc ctg gac aat gtg gac ccc aac cct gag aac ttc gtg	2859
Gly Ser Ala Leu Leu Asp Asn Val Asp Pro Asn Pro Glu Asn Phe Val	
890 895 900 905	
ggg gcg ggg atc atc cag act aaa gcc ctg cag gtg ggc tgt ctg ctt	2907
Gly Ala Gly Ile Ile Gln Thr Lys Ala Leu Gln Val Gly Cys Leu Leu	
906 911 916 921	
cgg ctg gag ccc aat gcc cag gcc cag atg tac cgg ctg acc ctg cgc	2955
Arg Leu Glu Pro Asn Ala Gln Ala Gln Met Tyr Arg Leu Thr Leu Arg	
922 927 932 937	
acc agc aag gag ccc gtc tcc cgt cac ctg tgt gag ctg ctg gca cag	3003
Thr Ser Lys Glu Pro Val Ser Arg His Leu Cys Glu Leu Leu Ala Gln	
938 943 948 953	
cag ttc tga gccctgg actctgcccc gggggatgtg gccggcactg ggcagcccct	3059
Gln Phe *	
954	
tggactgagg cagttttggt ggatggggga cctccactgg tgacagagaa gacaccaggg	3119
tttgggggat gcctgggact ttcctccggc cttttgtatt tttatTTTTg ttcattctgct	3179
gctgtttaca ttctgggggg ttagggggag tccccctccc tccctttccc cccaagcac	3239
agaggggaga ggggccaggg aagtggatgt ctccctccct cccacccac cctgtttag	3299
cccctctac cccctcccca tccaggggct gtgtattatt gtgagcgaat aaacagagag	3359
acgctaataaa aaaaaaa	3376

<210> 117
 <211> 2616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (261)..(2159)

<400> 117	
caccggcccgaattcccgggtcgacgatttcgtgtggctccttgcggttcctacatcctc	60
tcattctgagaatcagagagcataatcttcttacgggcccgtgatttattaacgtggctta	120
atctgaaggttctcagtcattctttgtgatctactgatgtggggggcattggcaaggtt	180
tgcttaaaggagcttggt	240
ggcagcacac tgctcggaga atg aag gcg ctt ctg ttg ctg gtc ttg cct	290
Met Lys Ala Leu Leu Leu Leu Val Leu Pro	

1

5

tgg ctc agt cct gct aac tac att gac aat gtg ggc aac ctg cac ttc	338
Trp Leu Ser Pro Ala Asn Tyr Ile Asp Asn Val Gly Asn Leu His Phe	
11 16 21 26	
ctg tat tca gaa ctc tgt aaa ggt gcc tcc cac tac ggc ctg acc aaa	386
Leu Tyr Ser Glu Leu Cys Lys Gly Ala Ser His Tyr Gly Leu Thr Lys	
27 32 37 42	
gat agg aag agg cgc tca caa gat ggc tgt cca gac ggc tgt gcg agc	434
Asp Arg Lys Arg Arg Ser Gln Asp Gly Cys Pro Asp Gly Cys Ala Ser	
43 48 53 58	
ctc aca gcc acg gct ccc tcc cca gag gtt tct gca gct gcc acc atc	482
Leu Thr Ala Thr Ala Pro Ser Pro Glu Val Ser Ala Ala Ala Thr Ile	
59 64 69 74	
tcc tta atg aca gac gag cct ggc cta gac aac cct gcc tac gtg tcc	530
Ser Leu Met Thr Asp Glu Pro Gly Leu Asp Asn Pro Ala Tyr Val Ser	
75 80 85 90	
tcg gca gag gac ggg cag cca gca atc agc cca gtg gac tct ggc cgg	578
Ser Ala Glu Asp Gly Gln Pro Ala Ile Ser Pro Val Asp Ser Gly Arg	
91 96 101 106	
agc aac cga act agg gca cgg ccc ttt gag aga tcc act att aga agc	626
Ser Asn Arg Thr Arg Ala Arg Pro Phe Glu Arg Ser Thr Ile Arg Ser	
107 112 117 122	
aga tca ttt aaa aaa ata aat cga gct ttg agt gtt ctt cga agg aca	674
Arg Ser Phe Lys Lys Ile Asn Arg Ala Leu Ser Val Leu Arg Arg Thr	
123 128 133 138	
aag agc ggg agt gca gtt gcc aac cat gcc gac cag ggc agg gaa aat	722
Lys Ser Gly Ser Ala Val Ala Asn His Ala Asp Gln Gly Arg Glu Asn	
139 144 149 154	
tct gaa aac acc act gcc cct gag gtc ttt cca agg ttg tac cac ctg	770
Ser Glu Asn Thr Thr Ala Pro Glu Val Phe Pro Arg Leu Tyr His Leu	
155 160 165 170	
att cca gat ggt gaa att acc agc atc aag atc aat cga gta gat ccc	818
Ile Pro Asp Gly Glu Ile Thr Ser Ile Lys Ile Asn Arg Val Asp Pro	
171 176 181 186	
agt gaa agc ctc tct att atg ctg gtg gga ggt agc gaa acc cca ctg	866
Ser Glu Ser Leu Ser Ile Met Leu Val Gly Gly Ser Glu Thr Pro Leu	
187 192 197 202	
gtc cat atc att atc caa cac att tat cgt gat ggg gtg atc gcc aga	914
Val His Ile Ile Ile Gln His Ile Tyr Arg Asp Gly Val Ile Ala Arg	
203 208 213 218	
gac ggc cgg cta ctg cca gga gac atc att cta aag gtc aac ggg atg	962
Asp Gly Arg Leu Leu Pro Gly Asp Ile Ile Leu Lys Val Asn Gly Met	
219 224 229 234	
gac atc agc aat gtc cct cac aac tac gct gtg cgt ctc ctg cgg cag	1010

Asp Ile Ser Asn Val Pro His Asn Tyr Ala Val Arg Leu Leu Arg Gln	
235 240 245 250	
ccc tgc cag gtg ctg tgg ctg act gtg atg cgt gaa cag aag ttc cgc	1058
Pro Cys Gln Val Leu Trp Leu Thr Val Met Arg Glu Gln Lys Phe Arg	
251 256 261 266	
agc agg aac aat gga cag gcc ccg gat gcc tac aga ccc cga gat gac	1106
Ser Arg Asn Asn Gly Gln Ala Pro Asp Ala Tyr Arg Pro Arg Asp Asp	
267 272 277 282	
agc ttt cat gtg att ctc aac aaa agt agc ccc gag gag cag ctt gga	1154
Ser Phe His Val Ile Leu Asn Lys Ser Ser Pro Glu Glu Gln Leu Gly	
283 288 293 298	
ata aaa ctg gtg cgc aag gtg gat gag cct ggg gtt ttc atc ttc aat	1202
Ile Lys Leu Val Arg Lys Val Asp Glu Pro Gly Val Phe Ile Phe Asn	
299 304 309 314	
gtg ctg gat ggc ggt gtg gca tat cga cat ggt cag ctt gag gag aat	1250
Val Leu Asp Gly Gly Val Ala Tyr Arg His Gly Gln Leu Glu Glu Asn	
315 320 325 330	
gac cgt gtg tta gcc atc aat gga cat gat ctt cga tat ggc agc cca	1298
Asp Arg Val Leu Ala Ile Asn Gly His Asp Leu Arg Tyr Gly Ser Pro	
331 336 341 346	
gaa agt gcg gct cat ctg att cag gcc agt gaa aga cgt gtt cac ctc	1346
Glu Ser Ala Ala His Leu Ile Gln Ala Ser Glu Arg Arg Val His Leu	
347 352 357 362	
gtc gtg tcc cgc cag gtt cgg cag cgg agc cct gac atc ttt cag gaa	1394
Val Val Ser Arg Gln Val Arg Gln Arg Ser Pro Asp Ile Phe Gln Glu	
363 368 373 378	
gcc gcc tgg aac agc aat gcc agc tgg tcc cca ggg cca ggg gag agg	1442
Ala Gly Trp Asn Ser Asn Gly Ser Trp Ser Pro Gly Pro Gly Glu Arg	
379 384 389 394	
agc aac act ccc aag ccc ctc cat cct aca att act tgt cat gag aag	1490
Ser Asn Thr Pro Lys Pro Leu His Pro Thr Ile Thr Cys His Glu Lys	
395 400 405 410	
gtg gta aat atc caa aaa gac ccc ggt gaa tct ctc ggc atg acc gtc	1538
Val Val Asn Ile Gln Lys Asp Pro Gly Glu Ser Leu Gly Met Thr Val	
411 416 421 426	
gca ggg gga gca tca cat aga gaa tgg gat ttg cct atc tat gtc atc	1586
Ala Gly Gly Ala Ser His Arg Glu Trp Asp Leu Pro Ile Tyr Val Ile	
427 432 437 442	
agt gtt gag ccc gga gga gtc ata agc aga gat gga aga ata aaa aca	1634
Ser Val Glu Pro Gly Gly Val Ile Ser Arg Asp Gly Arg Ile Lys Thr	
443 448 453 458	
ggg gac att ttg ttg aat gtg gat ggg gtc gaa ctg aca gag gtc agc	1682
Gly Asp Ile Leu Leu Asn Val Asp Gly Val Glu Leu Thr Glu Val Ser	

459	464	469	474	
cgg agt gag gca gtg	gca tta ttg aaa aga	aca tca tcc tcg ata gta		1730
Arg Ser Glu Ala Val	Ala Leu Leu Lys Arg	Thr Ser Ser Ser Ile Val		
475	480	485	490	
ctc aaa gct ttg gaa gtc	aaa gag tat gag ccc	cag gaa gac tgc agc		1778
Leu Lys Ala Leu Glu Val	Lys Glu Tyr Glu Pro	Gln Glu Asp Cys Ser		
491	496	501	506	
agc cca gca gcc ctg gac	tcc aac cac aac atg gcc	cca ccc agt gac		1826
Ser Pro Ala Ala Leu Asp	Ser Asn His Asn Met	Ala Pro Pro Ser Asp		
507	512	517	522	
tgg tcc cca tcc tgg gtc	atg tgg ctg gaa tta cca	cgg tgc ttg tat		1874
Trp Ser Pro Ser Trp Val	Met Trp Leu Glu Leu	Pro Arg Cys Leu Tyr		
523	528	533	538	
aac tgt aaa gat att gta	tta cga aga aac aca gct	gga agt ctg ggc		1922
Asn Cys Lys Asp Ile Val	Leu Arg Arg Asn Thr	Ala Gly Ser Leu Gly		
539	544	549	554	
ttc tgc att gta gga ggt	tat gaa gaa tac aat gga	aac aaa cct ttt		1970
Phe Cys Ile Val Gly Gly	Tyr Glu Glu Tyr Asn	Gly Asn Lys Pro Phe		
555	560	565	570	
ttc atc aaa tcc att gtt	gaa gga aca cca gca tac	aat gat gga aga		2018
Phe Ile Lys Ser Ile Val	Glu Gly Thr Pro Ala	Tyr Asn Asp Gly Arg		
571	576	581	586	
att aga tgt ggt gat att	ctt ctt gct gtc aat ggt	aga agt aca tca		2066
Ile Arg Cys Gly Asp Ile	Leu Leu Ala Val Asn	Gly Arg Ser Thr Ser		
587	592	597	602	
gga atg ata cat gct tgc	ttg gca aga ctg ctg aaa	gaa ctt aaa gga		2114
Gly Met Ile His Ala Cys	Leu Ala Arg Leu Leu	Lys Glu Leu Lys Gly		
603	608	613	618	
aga att act cta act att	gtt tct tgg cct ggc act	ttt tta tag aat		2162
Arg Ile Thr Leu Thr Ile	Val Ser Trp Pro Gly	Thr Phe Leu *		
619	624	629		
caatgatggg tcagaggaaa	acagaaaaat cacaaatagg	ctaagaagtt gaaacactat		2222
atztatcttg tcagttttta	tatttaaaga aagaatacat	tgtaaaaatg tcaggaaaag		2282
tatgatcatc taatgaaagc	cagttacacc tcagaaaata	tgattccaaa aaaattaaaa		2342
ctactagttt tttttcagtg	tggaggattt ctcattactc	tacaacattg tttatatattt		2402
ttctattcaa taaaaagccc	taaaacaact aaaatgattt	gtatacccca ctgaattcaa		2462
gctgatttaa atttaaaatt	tggtatatgc tgaagtctgc	caagggtaca ttatggccat		2522
ttttaattta /cagctaaaaat	attttttaaa atgcattgct	gagaaacggt gctttcatca		2582
aacaagaata aatatttttc	agaaaaaaaaaaaa	aaaa		2616

<210> 118
 <211> 1431
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (481)..(969)

<400> 118

```

tttgatagct gtacgcctgc aggtaccggt ccggaattcc cgggtcgacg atttcgtgga      60
ggctgcggcg acgggtcctc ctccgccgtc cggtcgcgcc ctcgcggaag ctcggcagtg      120
cgctgcgcc  cgcacccgca ctccaaatta gaaaggggac gtctagtggg ttgcccgga      180
ggggtggcgg gagcggtcct ggaaataatc tgtcctctgt cgccgggaac tggcgaggta      240
gttccttcgc ggtggagaga cctggaatgg ccaaatatca aggtgaagtt caaagtttga      300
aactggatga tgattcagtt atagaaggag taagcgacca agtacttgtg gcagttgtgg      360
tcagtttcgc tttgattgct accctggtat atgcactttt cagaaatgta catcaaaaca      420
ttcaccacaga aaaccaggag ctagtaaggg tacttcgaga acagcttcaa acagaacagg      480

atg cac ctg ctg cca ctc gac agc agt tct aca ctg aca tgt act gtc      528
Met His Leu Leu Pro Leu Asp Ser Ser Ser Thr Leu Thr Cys Thr Val
  1             5             10             15

cca tct gcc tgc acc aag cct cct tcc cgg tgg aga cca act gtg gac      576
Pro Ser Ala Cys Thr Lys Pro Pro Ser Arg Trp Arg Pro Thr Val Asp
 17             22             27             32

atc ttt ttt gtg gta acc tta ctc cta aca gta ttt ggt gaa gat gat      624
Ile Phe Phe Val Val Thr Leu Leu Leu Thr Val Phe Gly Glu Asp Asp
 33             38             43             48

cag tct cag gat gtt ctg aga ttg cat cag gat att aat gat tat aac      672
Gln Ser Gln Asp Val Leu Arg Leu His Gln Asp Ile Asn Asp Tyr Asn
 49             54             59             64

cgg aga ttc tca ggg caa ccc aga tct att atg gag aga att atg gat      720
Arg Arg Phe Ser Gly Gln Pro Arg Ser Ile Met Glu Arg Ile Met Asp
 65             70             75             80

cta ccc act tta ctg agg cat gca ttc agg gaa atg ttt tca gtc ggg      768
Leu Pro Thr Leu Leu Arg His Ala Phe Arg Glu Met Phe Ser Val Gly
 81             86             91             96

ggc ctt ttc tgg atg ttt cgc atc agg ata ata ctt tgt tta atg gga      816
Gly Leu Phe Trp Met Phe Arg Ile Arg Ile Ile Leu Cys Leu Met Gly
 97             102            107            112

```

gct ttt ttc tat ctt ata tca cct cta gat ttt gta cct gaa gcc ttg	864
Ala Phe Phe Tyr Leu Ile Ser Pro Leu Asp Phe Val Pro Glu Ala Leu	
113 118 123 128	
ttt gga att cta ggc ttt cta gat gat ttc ttt gtc atc ttt tta ttg	912
Phe Gly Ile Leu Gly Phe Leu Asp Asp Phe Phe Val Ile Phe Leu Leu	
129 134 139 144	
ctt atc tac atc tct att atg tat cga gaa gtg ata acc caa agg cta	960
Leu Ile Tyr Ile Ser Ile Met Tyr Arg Glu Val Ile Thr Gln Arg Leu	
145 150 155 160	
act aga tga aaaagaa aacaaaactg agtttactag gatattctgag ctaatgtaga	1016
Thr Arg *	
161	
acatcaaaca gaaggaccca tggcagtata aagcaatgaa gcaatggagt attatctcac	1076
aaatataaaa ccactataag acaaacattt gattatcatt tgacaaatac ctaggtataa	1136
ctggaatttt catgtttgaa gttctaatat taagttttaga attataatga tctacagttg	1196
tatcttgatt ctatgttgtc tggaaaaaat atggaattat ataaaaaggg atgcttttat	1256
atatttttct tttccccaga attacttaga ttaattagat gtatagtaaa atattgttaa	1316
atgtcagttt atccatctta tccttctcag caggtaacct tatgataata tatagctgtg	1376
aaactcatct aaatattttt gttccaataa aatattatat actaaaaaaaa aaaaa	1431

<210> 119
 <211> 2236
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (80) .. (1369)

<400> 119	
ccgtccggaa ttcccgggac gagccacgcg tccgcagaca tggccgggag aaggagatca	60
gcaggacgct gcgcacaac atg ggc aac cac ctg ccg ctc ctg cct gca gag	112
Met Gly Asn His Leu Pro Leu Leu Pro Ala Glu	
1 5	
agt gag gaa gaa gat gaa atg gaa gtt gaa gac cag gat agt aaa gaa	160
Ser Glu Glu Glu Asp Glu Met Glu Val Glu Asp Gln Asp Ser Lys Glu	
12 17 22 27	
gcc aaa aaa cca aac atc ata aat ttt gac acc agt ctg ccg acá tca	208
Ala Lys Lys Pro Asn Ile Ile Asn Phe Asp Thr Ser Leu Pro Thr Ser	
28 33 38 43	

cat aca tac cta ggt gct gat atg gaa gaa ttt cat ggc agg act ttg	256
His Thr Tyr Leu Gly Ala Asp Met Glu Glu Phe His Gly Arg Thr Leu	
44 49 54 59	
cac gat gac gac agc tgt cag gtg att cca gtt ctt cca caa gtg atg	304
His Asp Asp Asp Ser Cys Gln Val Ile Pro Val Leu Pro Gln Val Met	
60 65 70 75	
atg atc ctg att ccc gga cag aca tta cct ctt cag ctt ttt cac cct	352
Met Ile Leu Ile Pro Gly Gln Thr Leu Pro Leu Gln Leu Phe His Pro	
76 81 86 91	
caa gaa gtc agt atg gtg cgg aat tta att cag aaa gat aga acc ttt	400
Gln Glu Val Ser Met Val Arg Asn Leu Ile Gln Lys Asp Arg Thr Phe	
92 97 102 107	
gct gtt ctt gca tac agc aat gta cag gaa agg gaa gca cag ttt gga	448
Ala Val Leu Ala Tyr Ser Asn Val Gln Glu Arg Glu Ala Gln Phe Gly	
108 113 118 123	
aca aca gca gag ata tat gcc tat cga gaa gaa cag gat ttt gga att	496
Thr Thr Ala Glu Ile Tyr Ala Tyr Arg Glu Glu Gln Asp Phe Gly Ile	
124 129 134 139	
gag ata gtg aaa gtg aaa gca att gga aga caa agg ttc aaa gtc ctt	544
Glu Ile Val Lys Val Lys Ala Ile Gly Arg Gln Arg Phe Lys Val Leu	
140 145 150 155	
gag cta aga aca cag tca gat gga atc cag caa gct aaa gtg caa att	592
Glu Leu Arg Thr Gln Ser Asp Gly Ile Gln Gln Ala Lys Val Gln Ile	
156 161 166 171	
ctt ccc gaa tgt gtg ttg cct tca acc atg tct gca gtt caa tta gaa	640
Leu Pro Glu Cys Val Leu Pro Ser Thr Met Ser Ala Val Gln Leu Glu	
172 177 182 187	
tcc ctc aat aag tgc cag ata ttt cct tca aaa cct gtc tca aga gaa	688
Ser Leu Asn Lys Cys Gln Ile Phe Pro Ser Lys Pro Val Ser Arg Glu	
188 193 198 203	
gac caa tgt tca tat aaa tgg tgg cag aaa tac cag aag aga aag ttt	736
Asp Gln Cys Ser Tyr Lys Trp Trp Gln Lys Tyr Gln Lys Arg Lys Phe	
204 209 214 219	
cat tgt gca aat cta act tca tgg cct cgc tgg ctg tat tcc tta tat	784
His Cys Ala Asn Leu Thr Ser Trp Pro Arg Trp Leu Tyr Ser Leu Tyr	
220 225 230 235	
gat gct gag acc tta atg gac aga atc aag aaa cag cta cgt gaa tgg	832
Asp Ala Glu Thr Leu Met Asp Arg Ile Lys Lys Gln Leu Arg Glu Trp	
236 241 246 251	
gat gaa aat cta aaa gat gat tct ctt cct tca aat cca ata gat ttt	880
Asp Glu Asn Leu Lys Asp Asp Ser Leu Pro Ser Asn Pro Ile Asp Phe	
252 257 262 267	

tct tac aga gta gct gct tgt ctt cct att gat gat gta ttg aga att	928
Ser Tyr Arg Val Ala Ala Cys Leu Pro Ile Asp Asp Val Leu Arg Ile	
268 273 278 283	
cag ctc ctt aaa att ggc agt gct atc cag cga ctt cgc tgt gaa tta	976
Gln Leu Leu Lys Ile Gly Ser Ala Ile Gln Arg Leu Arg Cys Glu Leu	
284 289 294 299	
gac att atg aat aaa tgt act tcc ctt tgc tgt aaa caa tgt caa gaa	1024
Asp Ile Met Asn Lys Cys Thr Ser Leu Cys Cys Lys Gln Cys Gln Glu	
300 305 310 315	
aca gaa ata aca acc aaa aat gaa ata ttc agt tta tcc tta tgt ggg	1072
Thr Glu Ile Thr Thr Lys Asn Glu Ile Phe Ser Leu Ser Leu Cys Gly	
316 321 326 331	
ccg atg gca gct tat gtg aat cct cat gga tat gtg cat gag aca ctt	1120
Pro Met Ala Ala Tyr Val Asn Pro His Gly Tyr Val His Glu Thr Leu	
332 337 342 347	
act gtg tat aag gct tgc aac ttg aat ctg ata ggc cgg cct tct aca	1168
Thr Val Tyr Lys Ala Cys Asn Leu Asn Leu Ile Gly Arg Pro Ser Thr	
348 353 358 363	
gaa cac agc tgg ttt cct ggg tat gcc tgg act gtt gcc cag tgt aag	1216
Glu His Ser Trp Phe Pro Gly Tyr Ala Trp Thr Val Ala Gln Cys Lys	
364 369 374 379	
atc tgt gca agc cat att gga tgg aag ttt acg gcc acc aaa aaa gac	1264
Ile Cys Ala Ser His Ile Gly Trp Lys Phe Thr Ala Thr Lys Lys Asp	
380 385 390 395	
atg tca cct caa aaa ttt tgg ggc tta acg cga tct gct ctg ttg ccc	1312
Met Ser Pro Gln Lys Phe Trp Gly Leu Thr Arg Ser Ala Leu Leu Pro	
396 401 406 411	
acg atc cca gac act gaa gat gaa ata agt cca gac aaa gta ata ctt	1360
Thr Ile Pro Asp Thr Glu Asp Glu Ile Ser Pro Asp Lys Val Ile Leu	
412 417 422 427	
tgc ttg taa acagatg tgatagagat aaagttagtt atctaacaaa ttggttatat	1416
Cys Leu *	
428	
tctaagatct gctttggaaa ttattgcctc tgatacatat ctaagtaaac ataacattaa	1476
tacctaagta aacataacat tacttggagg gttgcagttt ctaagtgaac ctgtatttga	1536
aacttttaag tatacttttag gaaacaagca tgaacggcag tctagaatac cagaaacatc	1596
tacttgggta gcttgggtgcc attatcctgt ggaatctgat atgtctggta gcatgtcatt	1656
gatggggacat gaagacatct ttggaaatga tgagattatt tctgtgttta aaaaaaaaaa	1716
aaatcttaaa ttctacaat gtgaaactga aactaataat ttgatcctga tgtatgggac	1776
agcgtatctg taccagtgcct ctaaataaca aaagctaggg tgacaagtac atgttccttt	1836

tggaagaag caaggcaatg tatattaatt attctaaaag ggctttgttc ctttccattt	1896
tctttaactt ctctgagata ctgatttgta aattttgaaa attagttaaa atatgcagtt	1956
ttttgagccc acgaatagtt gtcatttcct ttatgtgcct gttagtaaaa agtagtattg	2016
tgtatttgct cagtatctga actataagcc catttatact gttccataca aaagctattt	2076
ttcaaaaatt aatttgaacc aaaactacta ctatagggaa aagatgccaa aacatgtccc	2136
ctcaccagc ctaaacttga tactgtatta ttttgttcaa tgtaaattga agaaaatctg	2196
taagtaagta aaccttaagt gtgaaactaa aaaaaaaaaa	2236

<210> 120
 <211> 2507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (256)..(2091)

<400> 120	
catgcagtag gcgtgccgga actgccgcgg agatcccggc tcgacccacg cgtccgcgga	60
cgcggtgggtc gccacgcgt cgggcggctg gagcagaagt gttagcggcc agagctccca	120
gacccctacc cacagccagg cgggacgcgc acagtccttc cagcgggaaa gaagtacctt	180
cgccggtcac cggctcctgc agggtgcaaa tatatacaga gtttcataat cagcccaaga	240
ccacatagag caaac atg aat gat att tcc caa aag gct gag att aaa gaa	291
Met Asn Asp Ile Ser Gln Lys Ala Glu Ile Lys Glu	
1 5 10	
atg ctt gct tct gat gat gag gaa gat gta tct tct aaa gta gaa aag	339
Met Leu Ala Ser Asp Asp Glu Glu Asp Val Ser Ser Lys Val Glu Lys	
13 18 23 28	
gct tat gtt cca aaa tta aca gga act gtg aag ggt aga ttt gct gaa	387
Ala Tyr Val Pro Lys Leu Thr Gly Thr Val Lys Gly Arg Phe Ala Glu	
29 34 39 44	
atg gag aaa caa aga caa gag gaa caa agg aag aga acg gag gag gaa	435
Met Glu Lys Gln Arg Gln Glu Glu Gln Arg Lys Arg Thr Glu Glu Glu	
45 50 55 60	
cga aaa cgc aga att gag cag gat atg tta gaa aag agg aaa ata cag	483
Arg Lys Arg Arg Ile Glu Gln Asp Met Leu Glu Lys Arg Lys Ile Gln	
61 66 71 76	
cgt gaa tta gca aaa agg gct gaa cag att gag gac ata aac aat acg	531

Arg Glu Leu Ala Lys Arg Ala Glu Gln Ile Glu Asp Ile Asn Asn Thr	
77 82 87 92	
gga act gaa tca gca tca gag gaa gga gat gat tca cta ctt ata act	579
Gly Thr Glu Ser Ala Ser Glu Glu Gly Asp Asp Ser Leu Leu Ile Thr	
93 98 103 108	
gtg gta cct gtc aaa tca tat aaa aca tct gga aaa atg aaa aag aat	627
Val Val Pro Val Lys Ser Tyr Lys Thr Ser Gly Lys Met Lys Lys Asn	
109 114 119 124	
ttt gag gat cta gaa aaa gaa cgt gaa gag aaa gaa agg atc aag tac	675
Phe Glu Asp Leu Glu Lys Glu Arg Glu Glu Lys Glu Arg Ile Lys Tyr	
125 130 135 140	
gag gaa gat aaa aga ata aga tat gaa gaa caa cga cca tct ctc aag	723
Glu Glu Asp Lys Arg Ile Arg Tyr Glu Glu Gln Arg Pro Ser Leu Lys	
141 146 151 156	
gaa gca aag tgt ctt tca tta gtt atg gat gat gaa ata gaa agt gaa	771
Glu Ala Lys Cys Leu Ser Leu Val Met Asp Asp Glu Ile Glu Ser Glu	
157 162 167 172	
gca aaa aaa gaa tca ctt tct ccc gga aaa ttg aaa cta act ttt gaa	819
Ala Lys Lys Glu Ser Leu Ser Pro Gly Lys Leu Lys Leu Thr Phe Glu	
173 178 183 188	
gaa ctg gag cga caa aga caa gaa aac cga aag aag caa gct gaa gag	867
Glu Leu Glu Arg Gln Arg Gln Glu Asn Arg Lys Lys Gln Ala Glu Glu	
189 194 199 204	
gaa gca aga aaa cgt tta gaa gaa gag aag cgt gct ttt gaa gaa gca	915
Glu Ala Arg Lys Arg Leu Glu Glu Glu Lys Arg Ala Phe Glu Glu Ala	
205 210 215 220	
agg cgg caa atg gta aat gaa gat gag gaa aac caa gac aca gca aaa	963
Arg Arg Gln Met Val Asn Glu Asp Glu Glu Asn Gln Asp Thr Ala Lys	
221 226 231 236	
att ttt aaa ggg tac cgc cct ggt aaa ctc aaa ctc agt ttt gaa gaa	1011
Ile Phe Lys Gly Tyr Arg Pro Gly Lys Leu Lys Leu Ser Phe Glu Glu	
237 242 247 252	
atg gaa agg caa aga aga gaa gat gaa aaa agg aaa gca gaa gaa gaa	1059
Met Glu Arg Gln Arg Arg Glu Asp Glu Lys Arg Lys Ala Glu Glu Glu	
253 258 263 268	
gcc aga agg aga ata gag gaa gaa aag aag gcg ttt gct gaa gca agg	1107
Ala Arg Arg Arg Ile Glu Glu Glu Lys Lys Ala Phe Ala Glu Ala Arg	
269 274 279 284	
aga aat atg gta gta gat gat gac tcc cca gag atg tat aag aca atc	1155
Arg Asn Met Val Val Asp Asp Asp Ser Pro Glu Met Tyr Lys Thr Ile	
285 290 295 300	
tct caa gaa ttt ctt aca ccg gga aaa ctg gaa att aat ttt gaa gaa	1203
Ser Gln Glu Phe Leu Thr Pro Gly Lys Leu Glu Ile Asn Phe Glu Glu	

301	306	311	316	
tta tta aaa caa aaa atg gaa gaa gaa aaa cga cga aca gag gag gaa				1251
Leu Leu Lys Gln Lys Met Glu Glu Glu Lys Arg Arg Thr Glu Glu Glu				
317	322	327	332	
cgg aag cat aag cta gaa atg gag aaa caa gaa ttt gaa caa ctg aga				1299
Arg Lys His Lys Leu Glu Met Glu Lys Gln Glu Phe Glu Gln Leu Arg				
333	338	343	348	
cag gaa atg gga gag gaa gag gaa gaa aat gaa acc ttt gga ttg agc				1347
Gln Glu Met Gly Glu Glu Glu Glu Glu Asn Glu Thr Phe Gly Leu Ser				
349	354	359	364	
aga gaa tat gaa gaa ctg atc aaa tta aaa agg agt ggc tct att caa				1395
Arg Glu Tyr Glu Glu Leu Ile Lys Leu Lys Arg Ser Gly Ser Ile Gln				
365	370	375	380	
gct aaa aac cta aaa agc aag ttt gaa aaa att gga cag ttg tct gaa				1443
Ala Lys Asn Leu Lys Ser Lys Phe Glu Lys Ile Gly Gln Leu Ser Glu				
381	386	391	396	
aaa gaa ata cag aaa aaa ata gaa gaa gag cga gca aga agg aga gca				1491
Lys Glu Ile Gln Lys Lys Ile Glu Glu Glu Arg Ala Arg Arg Arg Ala				
397	402	407	412	
att gac ctt gaa att aaa gag cga gaa gct gaa aat ttt cat gag gaa				1539
Ile Asp Leu Glu Ile Lys Glu Arg Glu Ala Glu Asn Phe His Glu Glu				
413	418	423	428	
gat gat gtt gat gtt agg cct gca aga aaa agc gag gct cca ttt act				1587
Asp Asp Val Asp Val Arg Pro Ala Arg Lys Ser Glu Ala Pro Phe Thr				
429	434	439	444	
cac aaa gtg aat atg aaa gct aga ttt gaa caa atg gct aag gca aga				1635
His Lys Val Asn Met Lys Ala Arg Phe Glu Gln Met Ala Lys Ala Arg				
445	450	455	460	
gaa gaa gaa gaa caa aga aga att gaa gaa caa aag tta cta cgc atg				1683
Glu Glu Glu Glu Gln Arg Arg Ile Glu Glu Gln Lys Leu Leu Arg Met				
461	466	471	476	
cag ttt gaa caa agg gaa att gat gca gca cta caa aag aaa aga gaa				1731
Gln Phe Glu Gln Arg Glu Ile Asp Ala Ala Leu Gln Lys Lys Arg Glu				
477	482	487	492	
gag gag gag gag gaa gaa ggt agc atc atg aat ggc tcc act gct gaa				1779
Glu Glu Glu Glu Glu Glu Gly Ser Ile Met Asn Gly Ser Thr Ala Glu				
493	498	503	508	
gat gaa gag caa acc aga tca gga gct cca tgg ttc aag aag cct ctt				1827
Asp Glu Glu Gln Thr Arg Ser Gly Ala Pro Trp Phe Lys Lys Pro Leu				
509	514	519	524	
aaa aac aca tca gtt gta gac agt gag cca gtc aga ttt acg gtt aaa				1875
Lys Asn Thr Ser Val Val Asp Ser Glu Pro Val Arg Phe Thr Val Lys				
525	530	535	540	

gta aca gga gaa ccc aaa cca gaa att aca tgg tgg ttt gaa gga gaa	1923
Val Thr Gly Glu Pro Lys Pro Glu Ile Thr Trp Trp Phe Glu Gly Glu	
541 546 551 556	
ata ctg cag gat gga gaa gac tat caa tat att gaa agg gga gaa act	1971
Ile Leu Gln Asp Gly Glu Asp Tyr Gln Tyr Ile Glu Arg Gly Glu Thr	
557 562 567 572	
tac tgc ctt tac tta cca gaa act ttc cca gaa gat gga gga gag tat	2019
Tyr Cys Leu Tyr Leu Pro Glu Thr Phe Pro Glu Asp Gly Gly Glu Tyr	
573 578 583 588	
atg tgt aaa gca gtc aac aat aaa gga tct gca gct agt acc tgt att	2067
Met Cys Lys Ala Val Asn Asn Lys Gly Ser Ala Ala Ser Thr Cys Ile	
589 594 599 604	
ctt acc att gaa agt aag aat taa tcaactctttt tatcttttat tctattaatt	2121
Leu Thr Ile Glu Ser Lys Asn *	
605 610	
tttttttccct taaaatcact tttcttcttc tcttttttag ctgatgacta ctagctcccc	2181
tccccctctcc ctggaacttt ctctttcact ccaactttct tactacatcc atcttttctg	2241
tggcggggcc aaaaaaggaa accaggagtg ccactatgct gacttcttat tccttttcat	2301
aacagtcttc aaagcacagc tcactctaaag aatgcctact tcttttccaa ataagcatca	2361
gatttatcgc ctattatgca gtaacagtca ataaaatgta cttatggggg ggaattactc	2421
aattattcta tcagaacctt ttataaagac tgtatttccc atagacgttt acagcaacta	2481
tgtttaaaaa acaaaaaaaaa aaaaaa	2507

<210> 121
 <211> 4771
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (3023)..(4771)

<400> 121	
atggcaaagc aacttaacct tccagaaaat acagatgatt ggacaaaaga ggatgtaaat	60
cagtgggttag aaagtcataa gattgaccaa aaacacaggg aaattttgac tgaacaagac	120
gtgaatggag cagtcttgaa gtgggttaaaa aaagaacatc ttgttgatat gggcatcaca	180
catggaccag ctattcaaat agaagaacta ttcaaagaat tggggaaaac agccattgaa	240
gattcgattc agacatctaa gatgggaaaag cccagtaaaa atgctcctaa agaccaaact	300

gtgtctcaaa aggaacgtag agaaacttca aagcaaaaac aaaagggtaa agagaaccca	360
gatatggcta atccgtctgc aatgagtaca actgctaaag gttctaagtc actaaaagtt	420
gagctcatag aagataaaat agattataca aaggaaaggc aaccatccat agacctgaca	480
tgtgtatcat atccatttga tgaattcagt aatccatatac gttacaagtt ggattttagt	540
ctacagcctg aaacaggacc aggcaatctc attgatccga tacatgaatt caaagccttc	600
acaaatacag caacagccac agaagaggat gtcaagatga aatttagcaa tgaggttttc	660
cgatttgctt cagcttgtat gaattcacgt accaatggca ctattcattt tggagtcaaa	720
gacaaaacccc atgggaaaat tgttggcatc aaagtcacca atgataccaa ggaagccctc	780
attaaccatt tcaatctgat gataaacaag tattttgaag accatcaagt ccaacaagca	840
aagaagtgca ttcgagagcc aagatttgtg gaagttttac tgccaaatag tactctatct	900
gacagatttg ttattgaagt ggacattatt ccacagttct ctgaatgcc aatatgattat	960
ttccagatta aaatgcaaaa ttacaacaac aaaatatggg aacaaagtaa aaaattctca	1020
ctatttgtgc gagatgggac cagctctaag gacattacga aaaataaagt tgatttcaga	1080
gcattttaaag cagattttta aacactggca gagtccagaa aagcagcaga agaaaaattc	1140
agagcaaaaa caaataaaaa agaaagagag ggaccaaaagt tggttaaatt attgacagga	1200
aatcaagatt tgtagataa ttcatactat gaacagtaca ttcttgtaac aaataaatgc	1260
caccagatc aaacaaaaca cttagatttc ctgaaggaaa ttaaattggtt tgctgtattg	1320
gagtttgatc ctgagtctaa catcaatgga gtggtcaaag cttacaaaga aagccgagta	1380
gcaaaccttc actttccaag tgtatatgta gaacagaaaa ccacacaaaa tgagacgatt	1440
tctactctaa atctttacca tcaaccagc tggattttct gcaatggcag gttagacctt	1500
gacagtga aaatataaacc ctttgatcca agttcctggc aaagagaaag agcttctgat	1560
gtcaggaaac tgatttcatt tcttacacat gaagacataa tgccaagagg gaagtttttg	1620
gtggtatttc tattactgtc ctctgtggat gacccaagag atccccctcat tgagactttc	1680
tgtgctttct accaggatct caaaggaatg gaaaatatac tgtgtatttg tgtgcacca	1740
cacatatttc agggatggaa agatctactt gaagcaagat taataaaaca ccaagatgaa	1800
atttcaagcc aatgtatttc tgctttaagc cttgaagaga tcaatggcac tattcttaaa	1860
ctaaaatctg tgactcaatc ttcaaaaagg cttttgccat ctattggttt atcgactgtc	1920
cttctgaaaa aggaagaaga tatcatgact gctctggaaa ttatctgtga aaatgaatgt	1980

gaggggtacac tgttagagaa ggacaaaaat aaattccttg aattcaaggc atcaaaagag 2040
gaagacttct atcgaggtgg caaagtgtca tgggtggaact tctacttctc ttctgaaagt 2100
tattcttcac cttttgtcaa aagggataaa tatgaaagac ttgaagcaat gattcaaaac 2160
tgtgcagatt cttctaaacc aacaagtacc aaaattattc atctgtatca tcatccaggc 2220
tgtgggggaa ctaccttggc tatgcacatt ctctgggaac taaggaagaa attcagatgt 2280
gctgtgctga aaaacaagac agtggatttt tctgaaattg gagaacaggc aaccagttta 2340
atcacctatg gggcaatgaa ccgtcaggaa tacgtacctg tactactcct tgttgatgat 2400
tttgaagaac aagataatgt ctatcttctg cagtactota ttcaaacagc tatagctaaa 2460
aagtacattc gatatgaaaa acctctggtg attatcctaa attgtatgag atcacaaaat 2520
cctgaaaaaa gtgcaaggat ccagacagt attgccgtaa tacagcaact ctctcccaaa 2580
gaacagagag cttttgagct taaattgaaa gaaatcaaag aacagcataa aaactttgag 2640
gatttttatt cttttatgat catgaaaacc aattttaata aagaatacat agaaaatgtg 2700
gtccggaata tcttgaaagg gcagaatatt ttcaccaagg aagcaaagct cttttctttt 2760
ctggctcttc ttaattcata tgtgcctgat accaccattt cactatcaca gtgtgaaaaa 2820
ttottaggaa ttggaaacaa gaaggctttc tgggggacag aaaaatttga agacaagatg 2880
ggcacctact ctacaattcc tgataaaaaac agaggtcatc gaatgtggga actactgtgg 2940
agtacgcac attcactctt tgattgcaga gttctcactg gaagaattga agaaaagcta 3000
tcacctgaat aaaagtcaaa tt atg ttg gat atg cta act gag aat ttg ttc 3052
Met Leu Asp Met Leu Thr Glu Asn Leu Phe
1 5
ttc gat act ggt atg gga aaa agt aaa ttt ttg caa gat atg cac aca 3100
Phe Asp Thr Gly Met Gly Lys Ser Lys Phe Leu Gln Asp Met His Thr
11 16 21 26
ctc cta ctc aca aga cac cgc gat gaa cat gaa ggt gaa aca gga aat 3148
Leu Leu Leu Thr Arg His Arg Asp Glu His Glu Gly Glu Thr Gly Asn
27 32 37 42
tgg ttt tcc cca ttt att gaa gca tta cat aaa gat gaa gga aat gaa 3196
Trp Phe Ser Pro Phe Ile Glu Ala Leu His Lys Asp Glu Gly Asn Glu
43 48 53 58
gca gtt gaa gct gta ttg ctt gaa agt atc cat cgg ttc aac cca aat 3244
Ala Val Glu Ala Val Leu Leu Glu Ser Ile His Arg Phe Asn Pro Asn
59 64 69 74
gca ttc att tgc caa gcg ttg gca aga cat ttc tac att aaa aag aag 3292
Ala Phe Ile Cys Gln Ala Leu Ala Arg His Phe Tyr Ile Lys Lys Lys
75 80 85 90

gac ttt ggc aat gct cta aac tgg gca aaa caa gca aaa atc ata gaa	3340
Asp Phe Gly Asn Ala Leu Asn Trp Ala Lys Gln Ala Lys Ile Ile Glu	
91 96 101 106	
cct gac aat tct tat atc tca gat aca ctg ggt caa gtc tac aaa agt	3388
Pro Asp Asn Ser Tyr Ile Ser Asp Thr Leu Gly Gln Val Tyr Lys Ser	
107 112 117 122	
aaa ata aga tgg tgg ata gag gaa aac gga gga aac ggg aac att tca	3436
Lys Ile Arg Trp Trp Ile Glu Glu Asn Gly Gly Asn Gly Asn Ile Ser	
123 128 133 138	
gtt gat gat cta att gct ctt ttg gat tta gca gaa cat gcc tca agt	3484
Val Asp Asp Leu Ile Ala Leu Leu Asp Leu Ala Glu His Ala Ser Ser	
139 144 149 154	
gca ttc aaa gaa tct caa cag caa agt gaa gat aga gag tat gaa gtg	3532
Ala Phe Lys Glu Ser Gln Gln Gln Ser Glu Asp Arg Glu Tyr Glu Val	
155 160 165 170	
aag gaa aga ttg tat ccg aag tca aaa agg cgg tat gat act tac aat	3580
Lys Glu Arg Leu Tyr Pro Lys Ser Lys Arg Arg Tyr Asp Thr Tyr Asn	
171 176 181 186	
ata gct ggt tat caa gga gag ata gaa gtt ggg ctt tac aca atc caa	3628
Ile Ala Gly Tyr Gln Gly Glu Ile Glu Val Gly Leu Tyr Thr Ile Gln	
187 192 197 202	
att ctc cag ctc att cct ttt ttt gat aat aaa aat gag cta tct aaa	3676
Ile Leu Gln Leu Ile Pro Phe Phe Asp Asn Lys Asn Glu Leu Ser Lys	
203 208 213 218	
aga tat atg gtc aat ttt gta tca gga agt agt gat att cca ggg gat	3724
Arg Tyr Met Val Asn Phe Val Ser Gly Ser Ser Asp Ile Pro Gly Asp	
219 224 229 234	
cca aac aat gaa tat aaa tta gcc ctc aaa aac tat att cct tat tta	3772
Pro Asn Asn Glu Tyr Lys Leu Ala Leu Lys Asn Tyr Ile Pro Tyr Leu	
235 240 245 250	
act aaa ttg aaa ttt tct ttg aaa aag tcc ttt gat ttt ttt gat gaa	3820
Thr Lys Leu Lys Phe Ser Leu Lys Lys Ser Phe Asp Phe Phe Asp Glu	
251 256 261 266	
tac ttt gtc ctg cta aaa ccc agg aac aat att aag caa aat gaa gag	3868
Tyr Phe Val Leu Leu Lys Pro Arg Asn Asn Ile Lys Gln Asn Glu Glu	
267 272 277 282	
gcc aaa act cgg aga aag gtg gct gga tat ttt aag aaa tat gta gat	3916
Ala Lys Thr Arg Arg Lys Val Ala Gly Tyr Phe Lys Lys Tyr Val Asp	
283 288 293 298	
ata ttt tgt ctc tta gaa gaa tca caa aac aac aca ggt ctt gga tca	3964
Ile Phe Cys Leu Leu Glu Glu Ser Gln Asn Asn Thr Gly Leu Gly Ser	
299 304 309 314	

aag ttc agt gag cca ctt caa gta gag aga tgc agg aga aac cta gta Lys Phe Ser Glu Pro Leu Gln Val Glu Arg Cys Arg Arg Asn Leu Val 315 320 325 330	4012
gct tta aaa gca gac aag ttt tct ggg ctc ttg gaa tat ctt atc aaa Ala Leu Lys Ala Asp Lys Phe Ser Gly Leu Leu Glu Tyr Leu Ile Lys 331 336 341 346	4060
agt caa gag gat gct ata agc act atg aaa tgt ata gtg aac gaa tat Ser Gln Glu Asp Ala Ile Ser Thr Met Lys Cys Ile Val Asn Glu Tyr 347 352 357 362	4108
act ttt ctc tta gaa caa tgc act gtc aaa atc cag tca aaa gaa aag Thr Phe Leu Leu Glu Gln Cys Thr Val Lys Ile Gln Ser Lys Glu Lys 363 368 373 378	4156
cta aat ttc atc ttg gcc aac att att ctc tcc tgt atc caa cct acc Leu Asn Phe Ile Leu Ala Asn Ile Ile Leu Ser Cys Ile Gln Pro Thr 379 384 389 394	4204
tcc aga tta gta aag cca gtt gaa aaa cta aaa gat cag ctt cga gaa Ser Arg Leu Val Lys Pro Val Glu Lys Leu Lys Asp Gln Leu Arg Glu 395 400 405 410	4252
gtc ttg caa cca ata gga ctg act tat cag ttt tca gaa ccg tat ttt Val Leu Gln Pro Ile Gly Leu Thr Tyr Gln Phe Ser Glu Pro Tyr Phe 411 416 421 426	4300
cta gct tcc ctc tta ttc tgg cca gaa aat caa caa cta gat caa cat Leu Ala Ser Leu Leu Phe Trp Pro Glu Asn Gln Gln Leu Asp Gln His 427 432 437 442	4348
tct gaa caa atg aaa gag tat gct caa gca cta aaa aat tct ttc aag Ser Glu Gln Met Lys Glu Tyr Ala Gln Ala Leu Lys Asn Ser Phe Lys 443 448 453 458	4396
ggg caa tat aaa cat atg cat cgt aca aag caa cca att gca tat ttc Gly Gln Tyr Lys His Met His Arg Thr Lys Gln Pro Ile Ala Tyr Phe 459 464 469 474	4444
ttt ctt gga aaa ggt aaa aga ctg gaa aga ctt gtt cac aaa gga aaa Phe Leu Gly Lys Gly Lys Arg Leu Glu Arg Leu Val His Lys Gly Lys 475 480 485 490	4492
att gac cag tgc ttt aag aag aca cca gat att aat tcc ttg tgg cag Ile Asp Gln Cys Phe Lys Lys Thr Pro Asp Ile Asn Ser Leu Trp Gln 491 496 501 506	4540
agt gga gat gtg tgg aag gag gaa aaa gtc caa gaa ctt ttg ctt cgt Ser Gly Asp Val Trp Lys Glu Glu Lys Val Gln Glu Leu Leu Leu Arg 507 512 517 522	4588
tta caa ggt cga gct gaa aac aat tgt tta tat ata gaa tat gga atc Leu Gln Gly Arg Ala Glu Asn Asn Cys Leu Tyr Ile Glu Tyr Gly Ile 523 528 533 538	4636
aat gaa aaa atc aca ata ccc atc act ccc gct ttt tta ggt caa ctt	4684

	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

```
<220>  
<221> CDS  
<222> (141)..(869)
```

422

cat gga agg act gcc aac ctc tac tcc ctt cac agc tgg ctg ggc atc	506
His Gly Arg Thr Ala Asn Leu Tyr Ser Leu His Ser Trp Leu Gly Ile	
107 112 117 122	
acc act gtc ttc ctc ttc gcc tgc cag tgg ttc ctg ggc ttt gct gtc	554
Thr Thr Val Phe Leu Phe Ala Cys Gln Trp Phe Leu Gly Phe Ala Val	
123 128 133 138	
ttc ctc ctg ccc tgg gcg tcc atg tgg ctg cgc agc ctc cta aaa cct	602
Phe Leu Leu Pro Trp Ala Ser Met Trp Leu Arg Ser Leu Leu Lys Pro	
139 144 149 154	
atc cac gtc ttt ttt gga gcc gcc atc ctc tct ctg tcc atc gca tcc	650
Ile His Val Phe Phe Gly Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser	
155 160 165 170	
gtc att tcg ggc att aat gag aag ctt ttc ttc agt ttg aaa aac acc	698
Val Ile Ser Gly Ile Asn Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr	
171 176 181 186	
acc agg cca tac cac agc ctg ccc agt gag gcg gtc ttt gcc aac agc	746
Thr Arg Pro Tyr His Ser Leu Pro Ser Glu Ala Val Phe Ala Asn Ser	
187 192 197 202	
acc ggg atg ctg gtg gtg gcc ttt ggg ctg ctg gtg ctc tac atc ctt	794
Thr Gly Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu	
203 208 213 218	
ctg gct tca tct tgg aag cgc cca gag ccg ggg atc ctg acc gac aga	842
Leu Ala Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg	
219 224 229 234	
cag ccc ctg ctg cat gat ggg gag tga agcag caggaagggg ctcccaagag	894
Gln Pro Leu Leu His Asp Gly Glu *	
235 240	
ctcctggtgg tgcagcctgt gctcccctca gaagctctgc tcttcccagg gctcccggct	954
ggtttcagca ggcgacttct ttccaatgct gggcccagac ttcttgcttg ggtgctggcc	1014
tgccctctcc ggccgcttgc tgctgtctg ctttccctgg tggctttgcg tgggtgctgg	1074
gcctgccttc tctggctgct tgctgcctgt ctgcttccct tgggtgcttt ggcttctgca	1134
ctccttggcg tcagcctctc aggtcccaag cttcagactg ctgtgcttag taagcaagtg	1194
agaagcctgg ggtttggagc ccacctactc tctggcagca tcagcctcct actcctggca	1254
acatcaggcc aacgtccacc ccagcctcac attgccagat gttggcagaa gggctaatat	1314
tgaccgtctt gactggctgg agccttcaaa gccactggga tgtcctccag gcacctgggt	1374
cccatgacca gctcccgcgc tccatagggg taggcatttc actggtttat gaagctcgag	1434
tttcattaaa tatgttaaga atcaaaaaaa aaaaaa	1470

<210> 123
 <211> 1650
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (88)..(1005)

<400> 123

ccgccgagct cgctgtggcc cggatgttcg gtgcagctgc cagatccgct gatctagcgc 60

ttctcgaaaa aaaccttcag gcggccc atg gca tgc ctt gga ctt tat tgt 111
 Met Ala Cys Leu Gly Leu Tyr Cys
 1 5

ggg aag acc cta tta ttt aaa aat ggc tca act gaa ata tat gga gaa 159
 Gly Lys Thr Leu Leu Phe Lys Asn Gly Ser Thr Glu Ile Tyr Gly Glu
 9 14 19 24

tgt ggg gta tgc cca aga gga cag aga acg aat gca cag aaa tat tgt 207
 Cys Gly Val Cys Pro Arg Gly Gln Arg Thr Asn Ala Gln Lys Tyr Cys
 25 30 35 40

cag cct tgc aca gaa tct cct gaa ctt tat gat tgg ctc tat ctt gga 255
 Gln Pro Cys Thr Glu Ser Pro Glu Leu Tyr Asp Trp Leu Tyr Leu Gly
 41 46 51 56

ttt atg gca atg ctt cct ctg gtt tta cat tgg ttc ttc att gaa tgg 303
 Phe Met Ala Met Leu Pro Leu Val Leu His Trp Phe Phe Ile Glu Trp
 57 62 67 72

tac tcg ggg aaa aag agt tcc agc gca ctt ttc caa cac atc act gca 351
 Tyr Ser Gly Lys Lys Ser Ser Ser Ala Leu Phe Gln His Ile Thr Ala
 73 78 83 88

tta ttt gaa tgc agc atg gca gct att atc acc tta ctt gtg agt gat 399
 Leu Phe Glu Cys Ser Met Ala Ala Ile Ile Thr Leu Leu Val Ser Asp
 89 94 99 104

cca gtt ggt gtt ctt tat att cgt tca tgt cga gta ttg atg ctt tct 447
 Pro Val Gly Val Leu Tyr Ile Arg Ser Cys Arg Val Leu Met Leu Ser
 105 110 115 120

gac tgg tac acg atg ctt tac aac cca agt cca gat tac gtt acc aca 495
 Asp Trp Tyr Thr Met Leu Tyr Asn Pro Ser Pro Asp Tyr Val Thr Thr
 121 126 131 136

gta cac tgt act cat gaa gcc gtc tac cca cta tat acc att gta ttt 543
 Val His Cys Thr His Glu Ala Val Tyr Pro Leu Tyr Thr Ile Val Phe
 137 142 147 152

atc tat tac gca ttc tgc ttg gta tta atg atg ctg ctc cga cct ctt 591
 Ile Tyr Tyr Ala Phe Cys Leu Val Leu Met Met Leu Leu Arg Pro Leu
 153 158 163 168

ctg gtg aag aag att gca tgt ggg tta ggg aaa tct gat cga ttt aaa	639
Leu Val Lys Lys Ile Ala Cys Gly Leu Gly Lys Ser Asp Arg Phe Lys	
169 174 179 184	
agt att tat gct gca ctt tac ttc ttc cca att tta acc gtg ctt cag	687
Ser Ile Tyr Ala Ala Leu Tyr Phe Phe Pro Ile Leu Thr Val Leu Gln	
185 190 195 200	
gca gtt ggt gga ggc ctt tta tat tac gcc ttc cca tac att ata tta	735
Ala Val Gly Gly Gly Leu Leu Tyr Tyr Ala Phe Pro Tyr Ile Ile Leu	
201 206 211 216	
gtg tta tct ttg gtt act ctg gct gtg tac atg tct gct tct gaa ata	783
Val Leu Ser Leu Val Thr Leu Ala Val Tyr Met Ser Ala Ser Glu Ile	
217 222 227 232	
gag aac tgc tat gat ctt ctg gtc aga aag aaa aga ctt att gtt ctc	831
Glu Asn Cys Tyr Asp Leu Leu Val Arg Lys Lys Arg Leu Ile Val Leu	
233 238 243 248	
ttc agc cac tgg tta ctt cat gcc tat gga ata atc tcc att tcc aga	879
Phe Ser His Trp Leu Leu His Ala Tyr Gly Ile Ile Ser Ile Ser Arg	
249 254 259 264	
gtg gat aaa ctt gag caa gat ttg ccc ctt ttg gct ttg gta cct aca	927
Val Asp Lys Leu Glu Gln Asp Leu Pro Leu Leu Ala Leu Val Pro Thr	
265 270 275 280	
cca gcc ctt ttt tac ttg ttc act gca aaa ttt acc gaa cct tca agg	975
Pro Ala Leu Phe Tyr Leu Phe Thr Ala Lys Phe Thr Glu Pro Ser Arg	
281 286 291 296	
ata ctc tca gaa gga gcc aat gga cac tga g tgtagacatg tgaaatgcc	1026
Ile Leu Ser Glu Gly Ala Asn Gly His *	
297 302	
aaaacctgag aagtgtcct aataaaaaag taaatcaatc ttaacagtgt atgagaacta	1086
ttctatcata tatgggaaca agattgtcag tatatcttaa tgtttgggtt tgtctttggt	1146
ttgtttatgg ttagacttac agacttgga aatgcaaaac tctgtaatac tctgttacac	1206
agggtaatat tatctgtac actggaaggc cgctaggaag cccttgcttc tctcaacagt	1266
tcagctgttc tttagggcaa aatcatgttt ctgtgtacct agcaatgtgt toccatttta	1326
ttaagaaaag ctttaacacg tgtaatctgc agtccttaac agtggcgtaa ttgtacgtac	1386
ctgttgtgtt tcagtttggt tttcacctat aatgaattgt aaaaacaaac atacttgtgg	1446
ggtctgatag caaacataga aatgatgtat attgtttttt gttatctatt tattttcatc	1506
aatacagtat tttgatgtat tgcaaaaata gataataatt tatataacag gttttctggt	1566
tatagattgg ttcaagattt gtttgatta ttgttcctgt aaagaaaaca ataataaaaa	1626

gcttacctac ataaaaaaaaa aaaa

1650

<210> 124
<211> 1534
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (138)..(1334)

<400> 124

ggaattcttt ctgtcttgcc ttgcagttat aagttttaaa ggttttatTT ttgtcttctg 60

ctttaggcaa tccttttatca caggatatTC tcaacttata ccaggaccca gatggaacCC 120

gaaagctact gaacttc atg ctt gac aat ctc gca gtt cat cca gag cag 170
Met Leu Asp Asn Leu Ala Val His Pro Glu Gln

1 5

ctt cct ccg agg cca tgg att aca tta aaa gaa cga gac caa att ctg 218
Leu Pro Pro Arg Pro Trp Ile Thr Leu Lys Glu Arg Asp Gln Ile Leu
12 17 22 27

ccg tca gca tca ttc acg gtt atg tgt tac aat gtg tta tgt gat aaa 266
Pro Ser Ala Ser Phe Thr Val Met Cys Tyr Asn Val Leu Cys Asp Lys
28 33 38 43

tac gct acc ccg cag cta tat ggc tat tgc cca tcc tgg gca tta aac 314
Tyr Ala Thr Arg Gln Leu Tyr Gly Tyr Cys Pro Ser Trp Ala Leu Asn
44 49 54 59

tgg gaa tac agg aaa aag gga att atg gaa gaa att gtt aac tgt gac 362
Trp Glu Tyr Arg Lys Lys Gly Ile Met Glu Glu Ile Val Asn Cys Asp
60 65 70 75

gca gat atc att agt ctt cag gaa gtg gaa aca gag caa tac ttc act 410
Ala Asp Ile Ile Ser Leu Gln Glu Val Glu Thr Glu Gln Tyr Phe Thr
76 81 86 91

ctc ttt ctg cca gca ttg aag gag cgt gga tat gat gga ttt ttt tct 458
Leu Phe Leu Pro Ala Leu Lys Glu Arg Gly Tyr Asp Gly Phe Phe Ser
92 97 102 107

cca aag tca cgt gcc aaa atc atg tct gag cag gag aga aag cat gta 506
Pro Lys Ser Arg Ala Lys Ile Met Ser Glu Gln Glu Arg Lys His Val
108 113 118 123

gat ggt tgt gca ata ttc ttc aaa aca gaa aaa ttt aca ttg gtg cag 554
Asp Gly Cys Ala Ile Phe Phe Lys Thr Glu Lys Phe Thr Leu Val Gln
124 129 134 139

aag cat aca gtg gaa ttt aac caa gtg gcg atg gct aat tca gat gga 602
Lys His Thr Val Glu Phe Asn Gln Val Ala Met Ala Asn Ser Asp Gly

140	145	150	155	
tcc gaa gct atg ctg aac aga gtg atg aca aaa gat aac att ggt gtc				650
Ser Glu Ala Met Leu Asn Arg Val Met Thr Lys Asp Asn Ile Gly Val				
156	161	166	171	
gct gtg gta tta gag gtc cac aaa gaa cta ttt gga gca ggt atg aag				698
Ala Val Val Leu Glu Val His Lys Glu Leu Phe Gly Ala Gly Met Lys				
172	177	182	187	
cct att cat gct gca gac aaa cag ctg ctt ata gtg gca aat gcc cac				746
Pro Ile His Ala Ala Asp Lys Gln Leu Leu Ile Val Ala Asn Ala His				
188	193	198	203	
atg cat tgg gac cca gag tat tct gat gtg aag ctc atc cag acc atg				794
Met His Trp Asp Pro Glu Tyr Ser Asp Val Lys Leu Ile Gln Thr Met				
204	209	214	219	
atg ttt gtc tca gag gtt aaa aac att ctg gag aaa gcc tct agt agg				842
Met Phe Val Ser Glu Val Lys Asn Ile Leu Glu Lys Ala Ser Ser Arg				
220	225	230	235	
cct gga agc cca act gca gat cct aat tcc atc ccg ctg gtg cta tgt				890
Pro Gly Ser Pro Thr Ala Asp Pro Asn Ser Ile Pro Leu Val Leu Cys				
236	241	246	251	
gca gat ctt aac tca ttg cca gat tca ggt gtt gtg gaa tac tta agc				938
Ala Asp Leu Asn Ser Leu Pro Asp Ser Gly Val Val Glu Tyr Leu Ser				
252	257	262	267	
aat gga gga gta gct gac aac cat aaa gac ttc aag gaa cta agg tac				986
Asn Gly Gly Val Ala Asp Asn His Lys Asp Phe Lys Glu Leu Arg Tyr				
268	273	278	283	
aat gag tgt ctt atg aac ttc agc tgc aat gga aag aat gga agc tca				1034
Asn Glu Cys Leu Met Asn Phe Ser Cys Asn Gly Lys Asn Gly Ser Ser				
284	289	294	299	
gaa ggg aga atc aca cat ggc ttc caa ctt aag agc gcc tat gaa aat				1082
Glu Gly Arg Ile Thr His Gly Phe Gln Leu Lys Ser Ala Tyr Glu Asn				
300	305	310	315	
aac ttg atg cct tac acc aat tac acc ttt gat ttc aaa ggc gtg att				1130
Asn Leu Met Pro Tyr Thr Asn Tyr Thr Phe Asp Phe Lys Gly Val Ile				
316	321	326	331	
gac tac att ttc tat tcc aag act cat atg aac gtg ctt ggt gtc ctg				1178
Asp Tyr Ile Phe Tyr Ser Lys Thr His Met Asn Val Leu Gly Val Leu				
332	337	342	347	
ggg cct tta gat cct caa tgg ctg gtt gag aac aac atc act ggg tgt				1226
Gly Pro Leu Asp Pro Gln Trp Leu Val Glu Asn Asn Ile Thr Gly Cys				
348	353	358	363	
cca cac cct cac atc cct tca gac cac ttc tca ctg tta aca caa ctt				1274
Pro His Pro His Ile Pro Ser Asp His Phe Ser Leu Leu Thr Gln Leu				
364	369	374	379	

Thr	Glu	Ile	Asp	Cys	Gly	Thr	Pro	Pro	Glu	Val	Pro	Asp	Gly	Tyr	Ile
23					28					33					38

ata	gga	aat	tat	acg	tct	agt	ctg	ggc	agc	cag	gtt	cgt	tat	gct	tgc	796
Ile	Gly	Asn	Tyr	Thr	Ser	Ser	Leu	Gly	Ser	Gln	Val	Arg	Tyr	Ala	Cys	
39					44					49					54	

aga	gaa	gga	ttc	ttc	agt	gtt	cca	gaa	gat	aca	gtt	tca	agc	tgc	aca	844
Arg	Glu	Gly	Phe	Phe	Ser	Val	Pro	Glu	Asp	Thr	Val	Ser	Ser	Cys	Thr	
55					60					65					70	

ggc	ctg	ggc	aca	tgg	gag	tcc	cca	aaa	tta	cat	tgc	caa	gag	atc	aac	892
Gly	Leu	Gly	Thr	Trp	Glu	Ser	Pro	Lys	Leu	His	Cys	Gln	Glu	Ile	Asn	
71					76					81					86	

tgt	ggc	aac	cct	cca	gaa	atg	cgg	cac	gcc	atc	ttg	gta	gga	aat	cac	940
Cys	Gly	Asn	Pro	Pro	Glu	Met	Arg	His	Ala	Ile	Leu	Val	Gly	Asn	His	
87					92					97					102	

agc	tcc	agg	ctg	ggc	ggt	gtg	gct	cgc	tat	gtc	tgt	caa	gag	ggc	ttt	988
Ser	Ser	Arg	Leu	Gly	Gly	Val	Ala	Arg	Tyr	Val	Cys	Gln	Glu	Gly	Phe	
103					108					113					118	

gag	agc	cct	gga	gga	aag	atc	act	tct	gtt	tgc	aca	gag	aaa	ggc	acc	1036
Glu	Ser	Pro	Gly	Gly	Lys	Ile	Thr	Ser	Val	Cys	Thr	Glu	Lys	Gly	Thr	
119					124					129					134	

tgg	aga	gaa	agt	act	tta	aca	tgc	aca	gaa	att	ctg	aca	aag	att	aat	1084
Trp	Arg	Glu	Ser	Thr	Leu	Thr	Cys	Thr	Glu	Ile	Leu	Thr	Lys	Ile	Asn	
135					140					145					150	

gat	gta	tca	ctg	ttt	aat	gat	acc	tgt	gtg	aga	tgg	caa	ata	aac	tca	1132
Asp	Val	Ser	Leu	Phe	Asn	Asp	Thr	Cys	Val	Arg	Trp	Gln	Ile	Asn	Ser	
151					156					161					166	

aga	aga	ata	aac	ccc	aag	atc	tca	tat	gtg	ata	tcc	ata	aaa	gga	caa	1180
Arg	Arg	Ile	Asn	Pro	Lys	Ile	Ser	Tyr	Val	Ile	Ser	Ile	Lys	Gly	Gln	
167					172					177					182	

cgg	ttg	gac	cct	atg	gaa	tca	gtt	cgt	gag	gag	aca	gtc	aac	ttg	acc	1228
Arg	Leu	Asp	Pro	Met	Glu	Ser	Val	Arg	Glu	Glu	Thr	Val	Asn	Leu	Thr	
183					188					193					198	

aca	gac	agc	agg	acc	cca	gaa	gtg	tgc	cta	gcc	ctg	tac	cca	ggc	acc	1276
Thr	Asp	Ser	Arg	Thr	Pro	Glu	Val	Cys	Leu	Ala	Leu	Tyr	Pro	Gly	Thr	
199					204					209					214	

aac	tac	acc	gtg	aac	atc	tcc	aca	gca	cct	ccc	agg	cgc	tcg	atg	cca	1324
Asn	Tyr	Thr	Val	Asn	Ile	Ser	Thr	Ala	Pro	Pro	Arg	Arg	Ser	Met	Pro	
215					220					225					230	

gcc	gtc	atc	ggt	ttc	cag	aca	gct	gaa	gtt	gat	ctc	tta	gaa	gat	gat	1372
Ala	Val	Ile	Gly	Phe	Gln	Thr	Ala	Glu	Val	Asp	Leu	Leu	Glu	Asp	Asp	
231					236					241					246	

gga	agt	ttc	aat	att	tca	ata	ttt	aat	gaa	act	tgt	ttg	aaa	ttg	aac	1420
Gly	Ser	Phe	Asn	Ile	Ser	Ile	Phe	Asn	Glu	Thr	Cys	Leu	Lys	Leu	Asn	

247	252	257	262	
agg cgt tct agg aaa gtt gga tca gaa cac atg tac caa ttt acc gtt				1468
Arg Arg Ser Arg Lys Val Gly Ser Glu His Met Tyr Gln Phe Thr Val				
263	268	273	278	
ctg ggt cag agg tgg tat ctg gct aac ttt tct cat gca aca tcg ttt				1516
Leu Gly Gln Arg Trp Tyr Leu Ala Asn Phe Ser His Ala Thr Ser Phe				
279	284	289	294	
aac ttc aca acg agg gaa caa gtg cct gta gtg tgt ttg gat ctg tac				1564
Asn Phe Thr Thr Arg Glu Gln Val Pro Val Val Cys Leu Asp Leu Tyr				
295	300	305	310	
cct acg act gat tat acg gtg aat gtg acc ctg ctg aga tct cct aag				1612
Pro Thr Thr Asp Tyr Thr Val Asn Val Thr Leu Leu Arg Ser Pro Lys				
311	316	321	326	
cgg cac tca gtg caa ata aca ata gca act ccc cca gca gta aaa cag				1660
Arg His Ser Val Gln Ile Thr Ile Ala Thr Pro Pro Ala Val Lys Gln				
327	332	337	342	
acc atc agt aac att tca gga ttt aat gaa acc tgc ttg aga tgg aga				1708
Thr Ile Ser Asn Ile Ser Gly Phe Asn Glu Thr Cys Leu Arg Trp Arg				
343	348	353	358	
agc atc aag aca gct gat atg gag gag atg tat tta ttc cac att tgg				1756
Ser Ile Lys Thr Ala Asp Met Glu Glu Met Tyr Leu Phe His Ile Trp				
359	364	369	374	
ggc cag aga tgg tat cag aag gaa ttt gcc cag gaa atg acc ttt aat				1804
Gly Gln Arg Trp Tyr Gln Lys Glu Phe Ala Gln Glu Met Thr Phe Asn				
375	380	385	390	
atc agt agc agc agc cga gat ccc gag gtg tgc ttg gac cta cgt ccg				1852
Ile Ser Ser Ser Ser Arg Asp Pro Glu Val Cys Leu Asp Leu Arg Pro				
391	396	401	406	
ggt acc aac tac aat gtc agt ctc cgg gct ctg tct tcg gaa ctt cct				1900
Gly Thr Asn Tyr Asn Val Ser Leu Arg Ala Leu Ser Ser Glu Leu Pro				
407	412	417	422	
gtg gtc atc tcc ctg aca acc cag ata aca gag cct ccc ctc ccg gaa				1948
Val Val Ile Ser Leu Thr Thr Gln Ile Thr Glu Pro Pro Leu Pro Glu				
423	428	433	438	
gta gaa ttt ttt acg gtg cac aga gga cct cta cca cgc ctc aga ctg				1996
Val Glu Phe Phe Thr Val His Arg Gly Pro Leu Pro Arg Leu Arg Leu				
439	444	449	454	
agg aaa gcc aag gag aaa aat gga cca atc agt tca tat cag gtg tta				2044
Arg Lys Ala Lys Glu Lys Asn Gly Pro Ile Ser Ser Tyr Gln Val Leu				
455	460	465	470	
gtg ctt ccc ctg gcc ctc caa agc aca ttt tct tgt gat tct gaa ggc				2092
Val Leu Pro Leu Ala Leu Gln Ser Thr Phe Ser Cys Asp Ser Glu Gly				
471	476	481	486	

gct tcc tcc ttc ttt agc aac gcc tct gat gct gat gga tac gtg gct	2140
Ala Ser Ser Phe Phe Ser Asn Ala Ser Asp Ala Asp Gly Tyr Val Ala	
487 492 497 502	
gca gaa cta ctg gcc aaa gat gtt cca gat gat gcc atg gag ata cct	2188
Ala Glu Leu Leu Ala Lys Asp Val Pro Asp Asp Ala Met Glu Ile Pro	
503 508 513 518	
ata gga gac agg ctg tac tat ggg gaa tat tat aat gca ccc ttg aaa	2236
Ile Gly Asp Arg Leu Tyr Tyr Gly Glu Tyr Tyr Asn Ala Pro Leu Lys	
519 524 529 534	
aga ggg agt gat tac tgc att ata tta cga atc ac ⁴ a agt gaa tgg aat	2284
Arg Gly Ser Asp Tyr Cys Ile Ile Leu Arg Ile Thr Ser Glu Trp Asn	
535 540 545 550	
aag gtg aga aga cac tcc tgt gca gtt tgg gct cag gtg aaa gat tcg	2332
Lys Val Arg Arg His Ser Cys Ala Val Trp Ala Gln Val Lys Asp Ser	
551 556 561 566	
tca ctc atg ctg ctg cag atg gcg ggt gtt gga ctg ggt tcc ctg gct	2380
Ser Leu Met Leu Leu Gln Met Ala Gly Val Gly Leu Gly Ser Leu Ala	
567 572 577 582	
gtt gtg atc att ctc aca ttc ctc tcc ttc tca gcg gtg tga tggcaga	2429
Val Val Ile Ile Leu Thr Phe Leu Ser Phe Ser Ala Val *	
583 588 593	
tggacactga gtggggagga tgcactgctg ctgggcaggt gttctggcag cttctcaggt	2489
gcccgcacag aggctccgtg tgacttccgt ccaggagca tgtgggcctg caactttctc	2549
cattcccagc tgggccccat tcttgattt aagatgggtg ctatccctga ggagtcacca	2609
taaggagaaa actcaggaat tctgagtctt ccctgctaca ggaccagttc tgtgcaatga	2669
acttgagact cctgatgtac actgtgatat tgaccgaagg ctacatacag atctgtgaat	2729
cttggtctggg acttcctctg agtgatgcct gagggtcagc tctctagac attgactgca	2789
agagaatctc tgcaacctcc tatataaaag catttctgtt aattcaaaaa aaaaaaaaaa	2849
a	2850

<210> 126
 <211> 3423
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (53)..(2800)

<400> 126

gcacgagggtt tcaaaggaca caaagagaga tgtggactca aagtcaccgg gg	atg	55
	Met	
	1	
cct tta ttt gaa gca gag gaa gga gtt cta tca cga acc cag ata ttt		103
Pro Leu Phe Glu Ala Glu Glu Gly Val Leu Ser Arg Thr Gln Ile Phe		
2 7 12 17		
cct acc act att aaa gtc att gat cca gaa ttt ctg gag gag cca cct		151
Pro Thr Thr Ile Lys Val Ile Asp Pro Glu Phe Leu Glu Glu Pro Pro		
18 23 28 33		
gca ctt gca ttt tta tat aag gat ctg tat gaa gaa gca gtt gga gag		199
Ala Leu Ala Phe Leu Tyr Lys Asp Leu Tyr Glu Glu Ala Val Gly Glu		
34 39 44 49		
aaa aag aag gaa gag gag aca gct tct gaa ggt gac agt gtg aat tct		247
Lys Lys Lys Glu Glu Glu Thr Ala Ser Glu Gly Asp Ser Val Asn Ser		
50 55 60 65		
gag gca tca ttt ccc agc aga aat tct gac act gat gat gga aca gga		295
Glu Ala Ser Phe Pro Ser Arg Asn Ser Asp Thr Asp Asp Gly Thr Gly		
66 71 76 81		
ata tat ttt gag aag tac ata ctc aaa gat gac att ctc cat gac aca		343
Ile Tyr Phe Glu Lys Tyr Ile Leu Lys Asp Asp Ile Leu His Asp Thr		
82 87 92 97		
tct cta act caa aag gac cag ggc caa ggt ctg gaa gaa aaa cga gtt		391
Ser Leu Thr Gln Lys Asp Gln Gly Gln Gly Leu Glu Glu Lys Arg Val		
98 103 108 113		
ggt aag gat gat tca tac caa ccg ata gct gca gaa ggg gaa att tgg		439
Gly Lys Asp Asp Ser Tyr Gln Pro Ile Ala Ala Glu Gly Glu Ile Trp		
114 119 124 129		
gga aag ttt gga act att tgc agg gag aag agt ctg gaa gaa cag aaa		487
Gly Lys Phe Gly Thr Ile Cys Arg Glu Lys Ser Leu Glu Glu Gln Lys		
130 135 140 145		
ggt gtt tat ggg gaa gga gaa tca gta gac cat gtg gag acc gtt ggt		535
Gly Val Tyr Gly Glu Gly Glu Ser Val Asp His Val Glu Thr Val Gly		
146 151 156 161		
aac gta gcg atg cag aag aaa gct ccc atc aca gag gac gtc aga gtg		583
Asn Val Ala Met Gln Lys Lys Ala Pro Ile Thr Glu Asp Val Arg Val		
162 167 172 177		
gct acc cag aaa ata agt tat gcg gtt cca ttt gaa gac acc cat cat		631
Ala Thr Gln Lys Ile Ser Tyr Ala Val Pro Phe Glu Asp Thr His His		
178 183 188 193		
gtt ctg gag cgt gca gat gaa gca ggc agt cac ggt aat gaa gtc gga		679
Val Leu Glu Arg Ala Asp Glu Ala Gly Ser His Gly Asn Glu Val Gly		
194 199 204 209		

aat gca agt cca gag gtc aat ctg aat gtc cca gta caa gtg tcc ttc	727
Asn Ala Ser Pro Glu Val Asn Leu Asn Val Pro Val Gln Val Ser Phe	
210 215 220 225	
ccg gag gaa gaa ttt gca tct ggt gca act cat gtt caa gaa aca tca	775
Pro Glu Glu Glu Phe Ala Ser Gly Ala Thr His Val Gln Glu Thr Ser	
226 231 236 241	
cta gaa gaa cct aaa atc ctg gtc cca cct gag cca agt gaa gag agg	823
Leu Glu Glu Pro Lys Ile Leu Val Pro Pro Glu Pro Ser Glu Glu Arg	
242 247 252 257	
ctc cgt aat agc cct gtt cag gat gag tat gaa ttt aca gaa tcc ctg	871
Leu Arg Asn Ser Pro Val Gln Asp Glu Tyr Glu Phe Thr Glu Ser Leu	
258 263 268 273	
cat aat gaa gtg gtt cct caa gac ata tta tca gaa gaa ctg tct tca	919
His Asn Glu Val Val Pro Gln Asp Ile Leu Ser Glu Glu Leu Ser Ser	
274 279 284 289	
gaa tcc aca cct gaa gat gtc tta tct caa gga aag gaa tcc ttt gag	967
Glu Ser Thr Pro Glu Asp Val Leu Ser Gln Gly Lys Glu Ser Phe Glu	
290 295 300 305	
cac atc agt gaa aat gaa ttt gcg agt gag gca gaa caa agt aca cct	1015
His Ile Ser Glu Asn Glu Phe Ala Ser Glu Ala Glu Gln Ser Thr Pro	
306 311 316 321	
gct gaa caa aaa gag ttg ggc agc gag agg aaa gaa gaa gac caa tta	1063
Ala Glu Gln Lys Glu Leu Gly Ser Glu Arg Lys Glu Glu Asp Gln Leu	
322 327 332 337	
tca tct gag gta gta act gaa aag gca caa aaa gag ctg aaa aag tcc	1111
Ser Ser Glu Val Val Thr Glu Lys Ala Gln Lys Glu Leu Lys Lys Ser	
338 343 348 353	
cag att gac aca tac tgt tac acc tgc aaa tgt cca att tct gcc act	1159
Gln Ile Asp Thr Tyr Cys Tyr Thr Cys Lys Cys Pro Ile Ser Ala Thr	
354 359 364 369	
gac aag gtg ttt ggc acc cac aaa gac cat gaa gtt tca acg ctt gac	1207
Asp Lys Val Phe Gly Thr His Lys Asp His Glu Val Ser Thr Leu Asp	
370 375 380 385	
aca gct ata agt gct gta aag gtt caa tta gca gaa ttt cta gaa aat	1255
Thr Ala Ile Ser Ala Val Lys Val Gln Leu Ala Glu Phe Leu Glu Asn	
386 391 396 401	
tta caa gaa aag tcc ttg agg att gaa gcc ttt gtt agt gag ata gaa	1303
Leu Gln Glu Lys Ser Leu Arg Ile Glu Ala Phe Val Ser Glu Ile Glu	
402 407 412 417	
tcc ttt ttt aat acc att gag gaa aac tgt agt aaa aat gag aaa agg	1351
Ser Phe Phe Asn Thr Ile Glu Glu Asn Cys Ser Lys Asn Glu Lys Arg	
418 423 428 433	
cta gaa gaa cag aat gag gaa atg atg aag aag gtt tta gca cag tat	1399

Leu Glu Glu Gln Asn Glu Glu Met Met Lys Lys Val Leu Ala Gln Tyr	
434 439 444 449	
gat gag aaa gcc cag agc ttt gag gaa gtg aag aag aag atg gag	1447
Asp Glu Lys Ala Gln Ser Phe Glu Glu Val Lys Lys Lys Lys Met Glu	
450 455 460 465	
ttc ctg cat gag cag atg gtc cac ttt ctg cag agc atg gac act gcc	1495
Phe Leu His Glu Gln Met Val His Phe Leu Gln Ser Met Asp Thr Ala	
466 471 476 481	
aaa gac acc ctg gag acc atc gtg aga gaa gca gag gag ctt gat gag	1543
Lys Asp Thr Leu Glu Thr Ile Val Arg Glu Ala Glu Glu Leu Asp Glu	
482 487 492 497	
gcc gtc ttc ctg act tcg ttt gag gaa atc aat gaa agg ttg ctt tct	1591
Ala Val Phe Leu Thr Ser Phe Glu Glu Ile Asn Glu Arg Leu Leu Ser	
498 503 508 513	
gca atg gag agc act gct tct tta gag aaa atg cct gct gcg ttt tcc	1639
Ala Met Glu Ser Thr Ala Ser Leu Glu Lys Met Pro Ala Ala Phe Ser	
514 519 524 529	
ctt ttc gaa cat tat gat gac agc tcg gca aga agt gac cag atg tta	1687
Leu Phe Glu His Tyr Asp Asp Ser Ser Ala Arg Ser Asp Gln Met Leu	
530 535 540 545	
aaa caa gtg gct gtt cca cag cct cct aga tta gaa cct cag gaa cca	1735
Lys Gln Val Ala Val Pro Gln Pro Pro Arg Leu Glu Pro Gln Glu Pro	
546 551 556 561	
aat tct gcc acc agc aca aca att gca gtt tac tgg agc atg aac aag	1783
Asn Ser Ala Thr Ser Thr Thr Ile Ala Val Tyr Trp Ser Met Asn Lys	
562 567 572 577	
gaa gat gtc att gat tca ttt cag gtt tac tgc atg gag gag cca caa	1831
Glu Asp Val Ile Asp Ser Phe Gln Val Tyr Cys Met Glu Glu Pro Gln	
578 583 588 593	
gat gat caa gaa gta aat gag ttg gta gaa gaa tac aga ctg aca gtg	1879
Asp Asp Gln Glu Val Asn Glu Leu Val Glu Glu Tyr Arg Leu Thr Val	
594 599 604 609	
aaa gaa agc tac tgc att ttt gaa gat ctg gaa cct gac cga tgc tat	1927
Lys Glu Ser Tyr Cys Ile Phe Glu Asp Leu Glu Pro Asp Arg Cys Tyr	
610 615 620 625	
caa gtg tgg gtg atg gct gtg aac ttc act gga tgt agc ctg ccc agt	1975
Gln Val Trp Val Met Ala Val Asn Phe Thr Gly Cys Ser Leu Pro Ser	
626 631 636 641	
gaa agg gcc atc ttt agg aca gca ccc tcc acc cct gtg atc cgc gct	2023
Glu Arg Ala Ile Phe Arg Thr Ala Pro Ser Thr Pro Val Ile Arg Ala	
642 647 652 657	
gag gac tgt act gtg tgt tgg aac aca gcc act atc cga tgg cgg ccc	2071
Glu Asp Cys Thr Val Cys Trp Asn Thr Ala Thr Ile Arg Trp Arg Pro	

658	663	668	673	
acc acc cca gag gcc	acg gag acc tac act	ctg gag tac tgc aga cag		2119
Thr Thr Pro Glu Ala	Thr Glu Thr Tyr Thr	Leu Glu Tyr Cys Arg Gln		
674	679	684	689	
cac tct cct gag gga	gag ggc ctc aga tct	ttc tct gga atc aaa gga		2167
His Ser Pro Glu Gly	Glu Gly Leu Arg Ser	Phe Ser Gly Ile Lys Gly		
690	695	700	705	
ctc cag ctg aaa gtt	aac ctc caa ccc aat	gat aac tac ttt ttc tat		2215
Leu Gln Leu Lys Val	Asn Leu Gln Pro Asn	Asp Asn Tyr Phe Phe Tyr		
706	711	716	721	
gtg agg gcc atc aat	gca ttt ggg aca agt	gaa cag agt gaa gct gct		2263
Val Arg Ala Ile Asn	Ala Phe Gly Thr Ser	Glu Gln Ser Glu Ala Ala		
722	727	732	737	
ctc atc tcc acc aga	gga acc aga ttt ctc	ttg ttg aga gaa aca gct		2311
Leu Ile Ser Thr Arg	Gly Thr Arg Phe Leu	Leu Leu Arg Glu Thr Ala		
738	743	748	753	
cat cct gct cta cac	att tcc tca agt ggg	aca gtg atc agc ttt ggt		2359
His Pro Ala Leu His	Ile Ser Ser Ser Gly	Thr Val Ile Ser Phe Gly		
754	759	764	769	
gag agg aga cgg ctg	acg gaa atc ccg tca	gtg ctg ggt gag gag ctg		2407
Glu Arg Arg Arg Leu	Thr Glu Ile Pro Ser	Val Leu Gly Glu Glu Leu		
770	775	780	785	
cct tcc tgt ggc cag	cat tac tgg gaa acc	aca gtc aca gac tgc cca		2455
Pro Ser Cys Gly Gln	His Tyr Trp Glu Thr	Thr Val Thr Asp Cys Pro		
786	791	796	801	
gca tat cga ctc ggc	atc tgc tcc agc tcg	gct gtg cag gca ggt gcc		2503
Ala Tyr Arg Leu Gly	Ile Cys Ser Ser Ser	Ala Val Gln Ala Gly Ala		
802	807	812	817	
cta gga caa ggg gag	acc tca tgg tac atg	cac tgc tct gag cca cag		2551
Leu Gly Gln Gly Glu	Thr Ser Trp Tyr Met	His Cys Ser Glu Pro Gln		
818	823	828	833	
aga tac aca ttt ttc	tac agt ggt att gtg	agt gat gtt cat gtg act		2599
Arg Tyr Thr Phe Phe	Tyr Ser Gly Ile Val	Ser Asp Val His Val Thr		
834	839	844	849	
gag cgt cca gcc aga	gtg ggc atc ctg ctg	gac tac aac aac cag aga		2647
Glu Arg Pro Ala Arg	Val Gly Ile Leu Leu	Asp Tyr Asn Asn Gln Arg		
850	855	860	865	
ctt atc ttc atc aac	gca gag agc gag cag	ttg ctc ttc atc atc agg		2695
Leu Ile Phe Ile Asn	Ala Glu Ser Glu Gln	Leu Leu Phe Ile Ile Arg		
866	871	876	881	
cac agg ttt aat gag	ggt gtc cac cct gcc	ttt gcc ctg gag aaa cct		2743
His Arg Phe Asn Glu	Gly Val His Pro Ala	Phe Ala Leu Glu Lys Pro		
882	887	892	897	

gga aaa tgt act ttg cac ctg ggg ata gag ccc ccg gat tct gta agg 2791
 Gly Lys Cys Thr Leu His Leu Gly Ile Glu Pro Pro Asp Ser Val Arg
 898 903 908 913

cac aag tga tccttgg ctttcagaat ttgcaagaac agcgatttga attttggggg 2847
 His Lys *
 914

ggctctgctgt tcattccttt aggtgctata cattattcaa aaagtctccc gcgcatttgc 2907

actaatgatg gctgcatgca tagcaatcag catgtgagca aaatcgacaa gaaaaccttg 2967

actttacaga gcagtgtgtg agtaaacaga atgaaaacaa caacctccac tctttagttt 3027

atataagttt gagttctttc cttaaattaaa agatctacac ttgagttggg aaccgaaaga 3087

gaaaaatgga cttccatctg ttttactggg aaaggaaatc ctctgatgga caggtcagag 3147

tgaaggaagg ttgtgctggt aagacatctc tgacgaagag ccatggatgc tttccacaaa 3207

atgtcacctc gctgcactaa aggatgatga atcctaataca ttaaaggaat tgtttcagct 3267

gatttaaatt tataatgaac tcttttgtaa taatgtatac tgtagaacat gagtctctcc 3327

tccctaaaat tttaaatgta gaaaagtgtc atatattaga aatttccatt ttgttaaata 3387

aatgggttaga gtctataaag ccaaaaaaaaa aaaaaa 3423

<210> 127
 <211> 1668
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1668)

<400> 127

atg gcg gcc gcc ggg gct gcg gct aca cac cta gag gtg gcc cgg ggc 48
 Met Ala Ala Ala Gly Ala Ala Ala Thr His Leu Glu Val Ala Arg Gly
 1 5 10

aag cgc gcc gcc ctc ttc ttc gct gcg gtg gcc atc gtg ctg ggg cta 96
 Lys Arg Ala Ala Leu Phe Phe Ala Ala Val Ala Ile Val Leu Gly Leu
 17 22 27 32

ccg ctc tgg tgg aag acc acg gag acc tac cgg gcc tcg ttg cct tac 144
 Pro Leu Trp Trp Lys Thr Thr Glu Thr Tyr Arg Ala Ser Leu Pro Tyr
 33 38 43 48

tcc cag atc agt ggc ctg aat gcc ctt cag ctc cgc ctc atg gtg cct 192
 Ser Gln Ile Ser Gly Leu Asn Ala Leu Gln Leu Arg Leu Met Val Pro
 49 54 59 64

gtc act gtc gtg ttt acg cgg gag tca gtg ccc ctg gac gac cag gag	240
Val Thr Val Val Phe Thr Arg Glu Ser Val Pro Leu Asp Asp Gln Glu	
65 70 75 80	
aag ctg ccc ttc acc gtt gtg cat gaa aga gag att cct ctg aaa tac	288
Lys Leu Pro Phe Thr Val Val His Glu Arg Glu Ile Pro Leu Lys Tyr	
81 86 91 96	
aaa atg aaa atc aaa tgc cgt ttc cag aag gcc tat cgg agg gct ttg	336
Lys Met Lys Ile Lys Cys Arg Phe Gln Lys Ala Tyr Arg Arg Ala Leu	
97 102 107 112	
gac cat gag gag gag gcc ctg tca tcg ggc agt gtg caa gag gca gaa	384
Asp His Glu Glu Glu Ala Leu Ser Ser Gly Ser Val Gln Glu Ala Glu	
113 118 123 128	
gcc atg tta gat gag cct cag gaa caa gcg gag ggc tcc ctg act gtg	432
Ala Met Leu Asp Glu Pro Gln Glu Gln Ala Glu Gly Ser Leu Thr Val	
129 134 139 144	
tac gtg ata tct gaa cac tcc tca ctt ctt ccc cag gac atg atg agc	480
Tyr Val Ile Ser Glu His Ser Ser Leu Leu Pro Gln Asp Met Met Ser	
145 150 155 160	
tac att ggg ccc aag agg aca gca gtg gtg cgg ggg ata atg cac cgg	528
Tyr Ile Gly Pro Lys Arg Thr Ala Val Val Arg Gly Ile Met His Arg	
161 166 171 176	
gag gcc ttt aac atc att ggc cgc cgc ata gtc cag gtg gcc cag gcc	576
Glu Ala Phe Asn Ile Ile Gly Arg Arg Ile Val Gln Val Ala Gln Ala	
177 182 187 192	
atg tct ttg act gag gat gtg ctt gct gct gct ctg gct gac cac ctt	624
Met Ser Leu Thr Glu Asp Val Leu Ala Ala Ala Leu Ala Asp His Leu	
193 198 203 208	
cca gag gac aag tgg agc gct gag aag agg cgg cct ctc aag tcc agc	672
Pro Glu Asp Lys Trp Ser Ala Glu Lys Arg Arg Pro Leu Lys Ser Ser	
209 214 219 224	
ttg ggc tat gag atc acc ttc agt tta ctc aac cca gac ccc aag tcc	720
Leu Gly Tyr Glu Ile Thr Phe Ser Leu Leu Asn Pro Asp Pro Lys Ser	
225 230 235 240	
cat gat gtc tac tgg gac att gag ggg gct gtc cgg cgc tat gtg caa	768
His Asp Val Tyr Trp Asp Ile Glu Gly Ala Val Arg Arg Tyr Val Gln	
241 246 251 256	
cct ttc ctg aat gcc ctc ggt gcc gct ggc aac ttc tct gtg gac tct	816
Pro Phe Leu Asn Ala Leu Gly Ala Ala Gly Asn Phe Ser Val Asp Ser	
257 262 267 272	
cag att ctt tac tat gca atg ttg ggg gtg aat ccc cgc ttt gac tca	864
Gln Ile Leu Tyr Tyr Ala Met Leu Gly Val Asn Pro Arg Phe Asp Ser	
273 278 283 288	

gct tcc tcc agc tac tat ttg gac atg cac agc ctc ccc cat gtc atc	912
Ala Ser Ser Ser Tyr Tyr Leu Asp Met His Ser Leu Pro His Val Ile	
289 294 299 304	
aac cca gtg gag tcc cgg ctg gga tcc agt gct gcc tcc ttg tac cct	960
Asn Pro Val Glu Ser Arg Leu Gly Ser Ser Ala Ala Ser Leu Tyr Pro	
305 310 315 320	
gtg ctc aac ttt cta ctc tac gtg cct gag ctt gca cac tca ccg ctg	1008
Val Leu Asn Phe Leu Leu Tyr Val Pro Glu Leu Ala His Ser Pro Leu	
321 326 331 336	
tac att cag gac aag gat ggc gct cca gtg gcc acg aat gcc ttc cat	1056
Tyr Ile Gln Asp Lys Asp Gly Ala Pro Val Ala Thr Asn Ala Phe His	
337 342 347 352	
agt ccc cgc tgg ggt ggc att atg gta tat aat gtt gac tcc aaa acc	1104
Ser Pro Arg Trp Gly Gly Ile Met Val Tyr Asn Val Asp Ser Lys Thr	
353 358 363 368	
tat aat gcc tca gtg ctg cca gtg aga gtc gag gtg gac atg gtg cga	1152
Tyr Asn Ala Ser Val Leu Pro Val Arg Val Glu Val Asp Met Val Arg	
369 374 379 384	
gtg atg gag gtg ttc ctg gca cag ttg cgg ttg ctc ttt ggg att gct	1200
Val Met Glu Val Phe Leu Ala Gln Leu Arg Leu Leu Phe Gly Ile Ala	
385 390 395 400	
cag ccc cag ctg cct cca aaa tgc ctg ctt tca ggg cct acg agt gaa	1248
Gln Pro Gln Leu Pro Pro Lys Cys Leu Leu Ser Gly Pro Thr Ser Glu	
401 406 411 416	
ggg cta atg acc tgg gag cta gac cgg ctg ctc tgg gct cgg tca gtg	1296
Gly Leu Met Thr Trp Glu Leu Asp Arg Leu Leu Trp Ala Arg Ser Val	
417 422 427 432	
gag aac ctg gcc aca gcc acc acc acc ctt acc tcc ctg gcg cag ctt	1344
Glu Asn Leu Ala Thr Ala Thr Thr Thr Leu Thr Ser Leu Ala Gln Leu	
433 438 443 448	
ctg ggc aag atc agc aac att gtc att aag gac gac gtg gca tct gag	1392
Leu Gly Lys Ile Ser Asn Ile Val Ile Lys Asp Asp Val Ala Ser Glu	
449 454 459 464	
gtg tac aag gct gta gct gcc gtc cag aag tgc gca gaa gag ttg gcg	1440
Val Tyr Lys Ala Val Ala Ala Val Gln Lys Ser Ala Glu Glu Leu Ala	
465 470 475 480	
tct ggg cac ctg gca tct gcc ttt gtc gcc agc cag gaa gct gtg aca	1488
Ser Gly His Leu Ala Ser Ala Phe Val Ala Ser Gln Glu Ala Val Thr	
481 486 491 496	
tcc tct gag ctt gcc ttc ttt gac ccg tca ctc ctc cac ctc ctt tat	1536
Ser Ser Glu Leu Ala Phe Phe Asp Pro Ser Leu Leu His Leu Leu Tyr	
497 502 507 512	
ttc cct gat gac cag aag ttt gcc atc tac atc cca ctc ttc ctg cct	1584

Phe Pro Asp Asp Gln Lys Phe Ala Ile Tyr Ile Pro Leu Phe Leu Pro
513 518 523 528

atg gct gtg ccc atc ctc ctg tcc ctg gtc aag atc ttc ctg gag acc 1632
Met Ala Val Pro Ile Leu Leu Ser Leu Val Lys Ile Phe Leu Glu Thr
529 534 539 544

cgc aag tcc tgg aga aag cct gag aag aca gac tga 1668
Arg Lys Ser Trp Arg Lys Pro Glu Lys Thr Asp *
545 550 555

<210> 128
<211> 3964
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (174)..(2540)

<400> 128

actgttggag gtgacctata gaacaagttt gtacaaaaaa gcaggctggt accggtccgg 60

aattccccggg atggcgcggg ggacgtcagc gctgccagcg tggaaggagc tgcggggcg 120

gggaggagga agtagagccc gggaccgcca ggccaccacc ggccgcctca gcc atg 176
Met
1

gac gcg tcc ctg gag aag ata gca gac ccc acg tta gct gaa atg gga 224
Asp Ala Ser Leu Glu Lys Ile Ala Asp Pro Thr Leu Ala Glu Met Gly
2 7 12 17

aaa aac ttg aag gag gca gtg aag atg ctg gag gac agt cag aga aga 272
Lys Asn Leu Lys Glu Ala Val Lys Met Leu Glu Asp Ser Gln Arg Arg
18 23 28 33

aca gaa gag gaa aat gga aag aag ctc ata tcc gga gat att cca ggc 320
Thr Glu Glu Glu Asn Gly Lys Lys Leu Ile Ser Gly Asp Ile Pro Gly
34 39 44 49

cca ctc cag ggc agt ggg caa gat atg gtg agc atc ctc cag tta gtt 368
Pro Leu Gln Gly Ser Gly Gln Asp Met Val Ser Ile Leu Gln Leu Val
50 55 60 65

cag aat ctc atg cat gga gat gaa gat gag gag ccc cag agc ccc aga 416
Gln Asn Leu Met His Gly Asp Glu Asp Glu Glu Pro Gln Ser Pro Arg
66 71 76 81

atc caa aat att gga gaa caa ggt cat atg gct ttg ttg gga cat agt 464
Ile Gln Asn Ile Gly Glu Gln Gly His Met Ala Leu Leu Gly His Ser
82 87 92 97

ctg gga gct tat att tca act ctg gac aaa gag aag ctg aga aaa ctt	512
Leu Gly Ala Tyr Ile Ser Thr Leu Asp Lys Glu Lys Leu Arg Lys Leu	
98 103 108 113	
aca act agg ata ctt tca gat acc acc tta tgg cta tgc aga att ttc	560
Thr Thr Arg Ile Leu Ser Asp Thr Thr Leu Trp Leu Cys Arg Ile Phe	
114 119 124 129	
aga tat gaa aat ggg tgt gct tat ttc cac gaa gag gaa aga gaa gga	608
Arg Tyr Glu Asn Gly Cys Ala Tyr Phe His Glu Glu Glu Arg Glu Gly	
130 135 140 145	
ctt gca aag ata tgt agg ctt gcc att cat tct cga tat gaa gac ttc	656
Leu Ala Lys Ile Cys Arg Leu Ala Ile His Ser Arg Tyr Glu Asp Phe	
146 151 156 161	
gta gtg gat ggc ttc aat gtg tta tat aac aag aag cct gtc ata tat	704
Val Val Asp Gly Phe Asn Val Leu Tyr Asn Lys Lys Pro Val Ile Tyr	
162 167 172 177	
ctt agt gct gct gct aga cct ggc ctg ggc caa tac ctt tgt aat cag	752
Leu Ser Ala Ala Ala Arg Pro Gly Leu Gly Gln Tyr Leu Cys Asn Gln	
178 183 188 193	
ctc ggc ttg ccc ttc ccc tgc ttg tgc cgt gta ccc tgt aac act gtg	800
Leu Gly Leu Pro Phe Pro Cys Leu Cys Arg Val Pro Cys Asn Thr Val	
194 199 204 209	
ttt gga tcc cag cat cag atg gat gtt gcc ttc ctg gag aaa ctg att	848
Phe Gly Ser Gln His Gln Met Asp Val Ala Phe Leu Glu Lys Leu Ile	
210 215 220 225	
aaa gat gat ata gag cga gga aga ctg ccc ctg ttg ctt gtc gca aat	896
Lys Asp Asp Ile Glu Arg Gly Arg Leu Pro Leu Leu Leu Val Ala Asn	
226 231 236 241	
gca gga acg gca gca gta gga cac aca gac aag att ggg aga ttg aaa	944
Ala Gly Thr Ala Ala Val Gly His Thr Asp Lys Ile Gly Arg Leu Lys	
242 247 252 257	
gaa ctc tgt gag cag tat ggc ata tgg ctt cat gtg gag ggt gtg aat	992
Glu Leu Cys Glu Gln Tyr Gly Ile Trp Leu His Val Glu Gly Val Asn	
258 263 268 273	
ctg gca aca ttg gct ctg ggt tat gtc tcc tca tca gtg ctg gct gca	1040
Leu Ala Thr Leu Ala Leu Gly Tyr Val Ser Ser Ser Val Leu Ala Ala	
274 279 284 289	
gcc aaa tgt gat agc atg acg atg act cct ggc ccg tgg ctg ggt ttg	1088
Ala Lys Cys Asp Ser Met Thr Met Thr Pro Gly Pro Trp Leu Gly Leu	
290 295 300 305	
cca gct gtt cct gcg gtg aca ctg tat aaa cac gat gac cct gcc ttg	1136
Pro Ala Val Pro Ala Val Thr Leu Tyr Lys His Asp Asp Pro Ala Leu	
306 311 316 321	
act tta gtt gct ggt ctt aca tca aat aag ccc aca gac aaa ctc cgt	1184

Thr Leu Val Ala Gly Leu Thr Ser Asn Lys Pro Thr Asp Lys Leu Arg
322 327 332 337

gcc ctg cct ctg tgg tta tct tta caa tac ttg gga ctt gat ggg ttt 1232
Ala Leu Pro Leu Trp Leu Ser Leu Gln Tyr Leu Gly Leu Asp Gly Phe
338 343 348 353

gtg gag agg atc aag cat gcc tgt caa ctg agt caa cgg ttg cag gaa 1280
Val Glu Arg Ile Lys His Ala Cys Gln Leu Ser Gln Arg Leu Gln Glu
354 359 364 369

agt ttg aag aaa gtg aat tac atc aaa atc ttg gtg gaa gat gag ctc 1328
Ser Leu Lys Lys Val Asn Tyr Ile Lys Ile Leu Val Glu Asp Glu Leu
370 375 380 385

agc tcc cca gtg gtg gtg ttc aga ttt ttc cag gaa tta cca ggc tca 1376
Ser Ser Pro Val Val Val Phe Arg Phe Phe Gln Glu Leu Pro Gly Ser
386 391 396 401

gat ccg gtg ttt aaa gcc gtc cca gtg ccc aac atg aca cct tca gga 1424
Asp Pro Val Phe Lys Ala Val Pro Val Pro Asn Met Thr Pro Ser Gly
402 407 412 417

gtc ggc cgg gag agg cac tcg tgt gac gcg ctg aat cgc tgg ctg gga 1472
Val Gly Arg Glu Arg His Ser Cys Asp Ala Leu Asn Arg Trp Leu Gly
418 423 428 433

gaa cag ctg aag cag ctg gtg cct gca agc ggc ctc aca gtc atg gat 1520
Glu Gln Leu Lys Gln Leu Val Pro Ala Ser Gly Leu Thr Val Met Asp
434 439 444 449

ctg gaa gct gag ggc acg tgt ttg cgg ttc agc cct ttg atg acc gca 1568
Leu Glu Ala Glu Gly Thr Cys Leu Arg Phe Ser Pro Leu Met Thr Ala
450 455 460 465

gca gtt tta gga act cgg gga gag gat gtg gat cag ctc gta gcc tgc 1616
Ala Val Leu Gly Thr Arg Gly Glu Asp Val Asp Gln Leu Val Ala Cys
466 471 476 481

ata gaa agc aaa ctg cca gtg ctg tgc tgt acg ctc cag ttg cgt gaa 1664
Ile Glu Ser Lys Leu Pro Val Leu Cys Cys Thr Leu Gln Leu Arg Glu
482 487 492 497

gag ttc aag cag gaa gtg gaa gca aca gca ggt ctc cta tat gtt gat 1712
Glu Phe Lys Gln Glu Val Glu Ala Thr Ala Gly Leu Leu Tyr Val Asp
498 503 508 513

gac cct aac tgg tct gga ata ggg gtt gtc agg tat gaa cat gct aat 1760
Asp Pro Asn Trp Ser Gly Ile Gly Val Val Arg Tyr Glu His Ala Asn
514 519 524 529

gat gat aag agc agt ttg aaa tca gat ccc gaa ggg gaa aac atc cat 1808
Asp Asp Lys Ser Ser Leu Lys Ser Asp Pro Glu Gly Glu Asn Ile His
530 535 540 545

gct gga ctc ctg aag aag tta aat gaa ctg gaa tct gac cta acc ttt 1856
Ala Gly Leu Leu Lys Lys Leu Asn Glu Leu Glu Ser Asp Leu Thr Phe

546	551	556	561	
aaa ata ggc cct gag tat aag agc atg aag agc tgc ctt tat gtc ggc				1904
Lys Ile Gly Pro Glu Tyr Lys Ser Met Lys Ser Cys Leu Tyr Val Gly				
562	567	572	577	
atg gcg agc gac aac gtc gat gct gct gag ctc gtg gag acc att gcg				1952
Met Ala Ser Asp Asn Val Asp Ala Ala Glu Leu Val Glu Thr Ile Ala				
578	583	588	593	
gcc aca gcc cgg gag ata gag gag aac tcg agg ctt ctg gaa aac atg				2000
Ala Thr Ala Arg Glu Ile Glu Glu Asn Ser Arg Leu Leu Glu Asn Met				
594	599	604	609	
aca gaa gtg gtt cgg aaa ggc att cag gaa gct caa gtg gag ctg cag				2048
Thr Glu Val Val Arg Lys Gly Ile Gln Glu Ala Gln Val Glu Leu Gln				
610	615	620	625	
aag gca agt gaa gaa cgg ctt ctg gaa gag ggg gtg ttg cgg cag atc				2096
Lys Ala Ser Glu Glu Arg Leu Leu Glu Glu Gly Val Leu Arg Gln Ile				
626	631	636	641	
cct gta gtg ggc tcc gtg ctg aat tgg ttt tct ccg gtc cag gct tta				2144
Pro Val Val Gly Ser Val Leu Asn Trp Phe Ser Pro Val Gln Ala Leu				
642	647	652	657	
cag aag gga aga act ttt aac ttg aca gca ggc tct ctg gag tcc aca				2192
Gln Lys Gly Arg Thr Phe Asn Leu Thr Ala Gly Ser Leu Glu Ser Thr				
658	663	668	673	
gaa ccc ata tat gtc tac aaa gca caa ggt gca gga gtc acg ctg cct				2240
Glu Pro Ile Tyr Val Tyr Lys Ala Gln Gly Ala Gly Val Thr Leu Pro				
674	679	684	689	
cca acg ccc tcg ggc agt cgc acc aag cag agg ctt cca ggc cag aag				2288
Pro Thr Pro Ser Gly Ser Arg Thr Lys Gln Arg Leu Pro Gly Gln Lys				
690	695	700	705	
cct ttt aaa agg tcc ctg cga ggt tca gat gct ttg agt gag acc agc				2336
Pro Phe Lys Arg Ser Leu Arg Gly Ser Asp Ala Leu Ser Glu Thr Ser				
706	711	716	721	
tca gtc agt cac att gaa gac tta gaa aag gtg gag cgc cta tcc agt				2384
Ser Val Ser His Ile Glu Asp Leu Glu Lys Val Glu Arg Leu Ser Ser				
722	727	732	737	
ggg ccg gag cag atc acc ctc gag gcc agc agc act gag gga cac cca				2432
Gly Pro Glu Gln Ile Thr Leu Glu Ala Ser Ser Thr Glu Gly His Pro				
738	743	748	753	
ggg gct ccc agc cct cag cac acc gac cag acc gag gcc ttc cag aaa				2480
Gly Ala Pro Ser Pro Gln His Thr Asp Gln Thr Glu Ala Phe Gln Lys				
754	759	764	769	
ggg gtc cca cac cca gaa gat gac cac tca cag gta gaa gga ccg gag				2528
Gly Val Pro His Pro Glu Asp Asp His Ser Gln Val Glu Gly Pro Glu				
770	775	780	785	

agc tta aga tga gac tcattgtgtg gtttgagact gtactgagta ttgtttcagg 2583
 Ser Leu Arg *
 786

gaagatgaag ttctattgga aatgtgaact gtgccacata ctaatataaa ttactgttgt 2643
 ttgtgcttca ctgggatttt ggcacaaata tgtgcctgaa aggtaggctt tctaggaggg 2703
 gagtcagctt gtctaacttc atgtacatgt agaaccacgt ttgctgtcct actacgactt 2763
 ttccctaagt taccataaac acattttatt cacaaaaaac acttcgaatt tcaagtgtct 2823
 accagtagca ccocttgcctt ttctaaacat aagcctaagt atatgaggtt gcccgtaggca 2883
 acttttttggg aaaacagctt ttcattagca ctctccaggt tctctgcaac acttcacaga 2943
 ggcgagactg gctgtatcct ttgctgtcgg tcttttagtac gatcaagttg caatatacag 3003
 tgggactgct agacttgaag gagagcagtg attgtgggat tgtaaataag agcatcagaa 3063
 gccctcccca gctactgctc ttctgtggaga cttagtaagg actgtgtcta cttgagctgt 3123
 ggcaaggctg ctgtctggga ctgtcctctg ccacaaggcc atttctccca ttatataccg 3183
 tttgtaaaga gaaactgtaa agtctcctcc tgaccatata tttttaaata ctggcaaagc 3243
 ttttaaaatt ggcacacaag tacagactgt gctcatttct gtttagtata tgaaaacctg 3303
 atagatgcta cccttaagag cttgctcttc cgtgtgctac gtagcacca cctgggttaa 3363
 atctgaaaac aagtaccctt ttgacctgtc tcccactgaa gcttctactg cctgggcagc 3423
 tcgcctgggc ccaactcaga aacaggagcc agcagagcac tctctcacgc tgatccagcc 3483
 gggcacccctg ctttaagtcag tagaagctcg ctggcactgc ccgttctac ttttccgaag 3543
 tactgcgtca ctttgtcgta agtaatggcc cctgtgcctt cttaatccag cagtcaagct 3603
 tttgggagac ctgaaaatgg gaaaattcac actgggtttc tggactgtag tattggaagc 3663
 cttagttata gtatattaag cctataatta tactctgatt tgatgggatt tttgacattt 3723
 acacttgtca aaatgcaggg ggtttttttt ggtgcagatg attaaacagt cttccctatt 3783
 tgggtgcaatg aagtatagca gataaaatgg gggaggggta aattatcacc ttcaagaaga 3843
 tgacatgttt ttatatatat ttggaattgt taaattgggt ttgctgaaac atttcaccct 3903
 tgagatatta tttgaatgtt ggtttcaata aaggttcttg aaattgttaa aaaaaaaaaa 3963
 a 3964

<211> 2905
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (87)..(2216)

<400> 129

gccacagaga cgggtgtcagt ggtagcctag agaggccgct aacagacagg agccgaacgg 60

gggctttcgc tcagcagaga ggcaag atg gct acg gca ggg ggt ggc tct ggg 113
 Met Ala Thr Ala Gly Gly Gly Ser Gly
 1 5

gct gac ccg gga agt cgg ggt ctc ctt cgc ctt ctg tct ttc tgc gtc 161
 Ala Asp Pro Gly Ser Arg Gly Leu Leu Arg Leu Leu Ser Phe Cys Val
 10 15 20 25

cta cta gca ggt ttg tgc agg gga aac tca gtg gag agg aag ata tat 209
 Leu Leu Ala Gly Leu Cys Arg Gly Asn Ser Val Glu Arg Lys Ile Tyr
 26 31 36 41

atc ccc tta aat aaa aca gct ccc tgt gtt cgc ctg ctc aac gcc act 257
 Ile Pro Leu Asn Lys Thr Ala Pro Cys Val Arg Leu Leu Asn Ala Thr
 42 47 52 57

cat cag att ggc tgc cag tct tca att agt gga gac aca ggg gtt atc 305
 His Gln Ile Gly Cys Gln Ser Ser Ile Ser Gly Asp Thr Gly Val Ile
 58 63 68 73

cac gta gta gag aaa gag gag gac cta cag tgg gta ttg act gat ggc 353
 His Val Val Glu Lys Glu Glu Asp Leu Gln Trp Val Leu Thr Asp Gly
 74 79 84 89

ccc aac ccc cct tac atg gtt ctg ctg gag agc aag cat ttt acc agg 401
 Pro Asn Pro Pro Tyr Met Val Leu Leu Glu Ser Lys His Phe Thr Arg
 90 95 100 105

gat tta atg gag aag ctg aaa ggg aga acc agc cga att gct ggt ctt 449
 Asp Leu Met Glu Lys Leu Lys Gly Arg Thr Ser Arg Ile Ala Gly Leu
 106 111 116 121

gca gtg tcc ttg acc aag ccc agt cct gcc tca ggc ttc tct cct agt 497
 Ala Val Ser Leu Thr Lys Pro Ser Pro Ala Ser Gly Phe Ser Pro Ser
 122 127 132 137

gta cag tgc cca aat gat ggg ttt ggt gtt tac tcc aat tcc tat ggg 545
 Val Gln Cys Pro Asn Asp Gly Phe Gly Val Tyr Ser Asn Ser Tyr Gly
 138 143 148 153

cca gag ttt gct cac tgc aga gaa ata cag tgg aat tcg ctg ggc aat 593
 Pro Glu Phe Ala His Cys Arg Glu Ile Gln Trp Asn Ser Leu Gly Asn
 154 159 164 169

ggt ttg gct tat gaa gac ttt agt ttc ccc atc ttt ctt ctt gaa gat 641
 Gly Leu Ala Tyr Glu Asp Phe Ser Phe Pro Ile Phe Leu Leu Glu Asp

170	175	180	185	
gaa aat gaa acc aaa gtc atc aag cag tgc tat caa gat cac aac ctg				689
Glu Asn Glu Thr Lys Val Ile Lys Gln Cys Tyr Gln Asp His Asn Leu				
186	191	196	201	
agt cag aat ggc tca gca cca acc ttc cca cta tgt gcc atg cag ctc				737
Ser Gln Asn Gly Ser Ala Pro Thr Phe Pro Leu Cys Ala Met Gln Leu				
202	207	212	217	
ttt tca cac atg cat gct gtc atc agc act gcc acc tgc atg cgg cgc				785
Phe Ser His Met His Ala Val Ile Ser Thr Ala Thr Cys Met Arg Arg				
218	223	228	233	
agc tcc atc caa agc acc ttc agc atc aac cca gaa atc gtc tgt gac				833
Ser Ser Ile Gln Ser Thr Phe Ser Ile Asn Pro Glu Ile Val Cys Asp				
234	239	244	249	
ccc ctg tct gat tac aat gtg tgg agc atg cta aag cct ata aat aca				881
Pro Leu Ser Asp Tyr Asn Val Trp Ser Met Leu Lys Pro Ile Asn Thr				
250	255	260	265	
act ggg aca tta aag cct gac gac agg gtt gtg gtt gct gcc acc cgg				929
Thr Gly Thr Leu Lys Pro Asp Asp Arg Val Val Val Ala Ala Thr Arg				
266	271	276	281	
ctg gat agt cgt tcc ttt ttc tgg aat gtg gcc cca ggg gct gaa agc				977
Leu Asp Ser Arg Ser Phe Phe Trp Asn Val Ala Pro Gly Ala Glu Ser				
282	287	292	297	
gca gtg gct tcc ttt gtc acc cag ctg gct gct gct gaa gct ttg caa				1025
Ala Val Ala Ser Phe Val Thr Gln Leu Ala Ala Ala Glu Ala Leu Gln				
298	303	308	313	
aag gca cct gat gtg acc acc ctg ccc cgc aat gtc atg ttt gtc ttc				1073
Lys Ala Pro Asp Val Thr Thr Leu Pro Arg Asn Val Met Phe Val Phe				
314	319	324	329	
ttt caa ggg gaa act ttt gac tac att ggc agc tcg agg atg gtc tac				1121
Phe Gln Gly Glu Thr Phe Asp Tyr Ile Gly Ser Ser Arg Met Val Tyr				
330	335	340	345	
gat atg gag aag ggc aag ttt ccc gtg cag tta gag aat gtt gac tca				1169
Asp Met Glu Lys Gly Lys Phe Pro Val Gln Leu Glu Asn Val Asp Ser				
346	351	356	361	
ttt gtg gag ctg gga cag gtg gcc tta aga act tca tta gag ctt tgg				1217
Phe Val Glu Leu Gly Gln Val Ala Leu Arg Thr Ser Leu Glu Leu Trp				
362	367	372	377	
atg cac aca gat cct gtt tct cag aaa aat gag tct gta cgg aac cag				1265
Met His Thr Asp Pro Val Ser Gln Lys Asn Glu Ser Val Arg Asn Gln				
378	383	388	393	
gtg gag gat ctc ctg gcc aca ttg gag aag agt ggt gct ggt gtc cct				1313
Val Glu Asp Leu Leu Ala Thr Leu Glu Lys Ser Gly Ala Gly Val Pro				
394	399	404	409	

gct gtc atc ctc agg agg cca aat cag tcc cag cct ctc cca cca tct	1361
Ala Val Ile Leu Arg Arg Pro Asn Gln Ser Gln Pro Leu Pro Pro Ser	
410 415 420 425	
tcc ctg cag cga ttt ctt cga gct cga aac atc tct ggc gtt gtt ctg	1409
Ser Leu Gln Arg Phe Leu Arg Ala Arg Asn Ile Ser Gly Val Val Leu	
426 431 436 441	
gct gac cac tct ggt gcc ttc cat aac aaa tat tac cag agt att tac	1457
Ala Asp His Ser Gly Ala Phe His Asn Lys Tyr Tyr Gln Ser Ile Tyr	
442 447 452 457	
gac act gct gag aac att aat gtg agc tat ccc gaa ³ tgg ctg agc cct	1505
Asp Thr Ala Glu Asn Ile Asn Val Ser Tyr Pro Glu Trp Leu Ser Pro	
458 463 468 473	
gaa gag gac ctg aac ttt gta aca gac act gcc aag gcc ctg gca gat	1553
Glu Glu Asp Leu Asn Phe Val Thr Asp Thr Ala Lys Ala Leu Ala Asp	
474 479 484 489	
gtg gcc acg gtg ctg gga cgt gct ctg tat gag ctt gca gga gga acc	1601
Val Ala Thr Val Leu Gly Arg Ala Leu Tyr Glu Leu Ala Gly Gly Thr	
490 495 500 505	
aac ttc agc gac aca gtt cag gct gat ccc caa acg gtt acc cgc ctg	1649
Asn Phe Ser Asp Thr Val Gln Ala Asp Pro Gln Thr Val Thr Arg Leu	
506 511 516 521	
ctc tat ggg ttc ctg att aaa gcc aac aac tca tgg ttc cag tct atc	1697
Leu Tyr Gly Phe Leu Ile Lys Ala Asn Asn Ser Trp Phe Gln Ser Ile	
522 527 532 537	
ctc agg cag gac cta agg tcc tac ttg ggt gac ggg cct ctt caa cat	1745
Leu Arg Gln Asp Leu Arg Ser Tyr Leu Gly Asp Gly Pro Leu Gln His	
538 543 548 553	
tac atc gct gtc tcc agc ccc acc aac acc act tat gtt gta cag tat	1793
Tyr Ile Ala Val Ser Ser Pro Thr Asn Thr Thr Tyr Val Val Gln Tyr	
554 559 564 569	
gcc ttg gca aat ttg act ggc aca gtg gtc aac ctc acc cga gag cag	1841
Ala Leu Ala Asn Leu Thr Gly Thr Val Val Asn Leu Thr Arg Glu Gln	
570 575 580 585	
tgc cag gat cca agt aaa gtc cca agt gaa aac aag gat ctg tat gag	1889
Cys Gln Asp Pro Ser Lys Val Pro Ser Glu Asn Lys Asp Leu Tyr Glu	
586 591 596 601	
tac tca tgg gtc cag ggc cct ttg cat tct aat gag acg gac cga ctc	1937
Tyr Ser Trp Val Gln Gly Pro Leu His Ser Asn Glu Thr Asp Arg Leu	
602 607 612 617	
ccc cgg tgt gtg cgt tct act gca cga tta gcc agg gcc ttg tct cct	1985
Pro Arg Cys Val Arg Ser Thr Ala Arg Leu Ala Arg Ala Leu Ser Pro	
618 623 628 633	

gcc ttt gaa ctg agt cag tgg agc tct act gaa tac tct aca tgg act	2033
Ala Phe Glu Leu Ser Gln Trp Ser Ser Thr Glu Tyr Ser Thr Trp Thr	
634 639 644 649	
gag agc cgc tgg aaa gat atc cgt gcc cgg ata ttt ctc atc gcc agc	2081
Glu Ser Arg Trp Lys Asp Ile Arg Ala Arg Ile Phe Leu Ile Ala Ser	
650 655 660 665	
aaa gag ctt gag ttg atc acc ctg aca gtg ggc ttc ggc atc ctc atc	2129
Lys Glu Leu Glu Leu Ile Thr Leu Thr Val Gly Phe Gly Ile Leu Ile	
666 671 676 681	
ttc tcc ctc atc gtc acc tac tgc atc aat gcc aaa gct gat gtc ctt	2177
Phe Ser Leu Ile Val Thr Tyr Cys Ile Asn Ala Lys Ala Asp Val Leu	
682 687 692 697	
ttc att gct ccc cgg gag cca gga gct gtg tca tac tga ggaggacccc	2226
Phe Ile Ala Pro Arg Glu Pro Gly Ala Val Ser Tyr *	
698 703 708	
agctttttctt gccagctcag cagttcactt cctagagcat ctgtcccact gggacacaac	2286
cactaatttg tctactggaac ctccctgggc ctgtctcaga ttgggattaa cataaaaagag	2346
tggaactatc caaaagagac agggagaaat aaataaatg cctcccttcc tccgctcccc	2406
tttcccatca ccccttcccc atttctctct ccttctctac tcatgccaga ttttgggatt	2466
acaaatagaa gcttcttget cctgtttaac tccctagtta cccaccctaa tttgcccttc	2526
aggacccttc tactttttcc ttcttgcct gtacctctct ctgtctctca cccccacccc	2586
tgtaccagc caccttctg actgggaagg acataaaagg tttaatgtca gggtaaact	2646
acattgagcc cctgaggaca ggggcatctc tgggctgagc ctactgtctc cttcccactg	2706
tcctttctcc aggcctcag atggcacatt aggggtggcg tgctgcgggt gggatatcca	2766
cctccagccc acagtgtca gttgtacttt ttattaagct gtaatatcta tttttgtttt	2826
tgtctttttc ctttattctt tttgtaaata tatatataat gagtttcatt aaaatagatt	2886
atcccacaaa aaaaaaaaaa	2905

<210> 130
 <211> 8503
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (91)..(8082)

<400> 130

taaattttaa	ggcggggcgg	cctgtgagcc	ctgaagtgcc	ggccgcggag	ggtcctggcc	60
atatttggtgg	gaccagttca	gcctgatagg	atg gcg gag gaa gga gcc gtg			111
			Met Ala Glu Glu Gly Ala Val			
			1	5		
gcc gtc tgc gtg cga gtg cgg ccg ctg aac agc aga gaa gaa tca ctt						159
Ala Val Cys Val Arg Val Arg Pro Leu Asn Ser Arg Glu Glu Ser Leu						
8		13		18	23	
gga gaa act gcc caa gtt tac tgg aaa act gac aat aat gtc att tat						207
Gly Glu Thr Ala Gln Val Tyr Trp Lys Thr Asp Asn Asn Val Ile Tyr						
24		29		34	39	
caa gtt gat gga agt aaa tcc ttc aat ttt gat cgt gtc ttt cat ggt						255
Gln Val Asp Gly Ser Lys Ser Phe Asn Phe Asp Arg Val Phe His Gly						
40		45		50	55	
aat gaa act acc aaa aat gtg tat gaa gaa ata gca gca cca atc atc						303
Asn Glu Thr Thr Lys Asn Val Tyr Glu Glu Ile Ala Ala Pro Ile Ile						
56		61		66	71	
gat tct gcc ata caa ggc tac aat ggt act ata ttt gcc tat gga cag						351
Asp Ser Ala Ile Gln Gly Tyr Asn Gly Thr Ile Phe Ala Tyr Gly Gln						
72		77		82	87	
act gct tca gga aaa aca tat acc atg atg ggt tca gaa gat cat ttg						399
Thr Ala Ser Gly Lys Thr Tyr Thr Met Met Gly Ser Glu Asp His Leu						
88		93		98	103	
gga gtt ata ccc agg gca att cat gac att ttc caa aaa att aag aag						447
Gly Val Ile Pro Arg Ala Ile His Asp Ile Phe Gln Lys Ile Lys Lys						
104		109		114	119	
ttt cct gat agg gaa ttt ctc tta cgt gta tct tac atg gaa ata tac						495
Phe Pro Asp Arg Glu Phe Leu Leu Arg Val Ser Tyr Met Glu Ile Tyr						
120		125		130	135	
aat gaa acc att aca gat tta ctc tgt ggc act caa aaa atg aaa cct						543
Asn Glu Thr Ile Thr Asp Leu Leu Cys Gly Thr Gln Lys Met Lys Pro						
136		141		146	151	
tta att att cga gaa gat gtc aat agg aat gtg tat gtt gct gat ctc						591
Leu Ile Ile Arg Glu Asp Val Asn Arg Asn Val Tyr Val Ala Asp Leu						
152		157		162	167	
aca gaa gaa gtt gta tat aca tca gaa atg gct ttg aaa tgg att aca						639
Thr Glu Glu Val Val Tyr Thr Ser Glu Met Ala Leu Lys Trp Ile Thr						
168		173		178	183	
aag gga gaa aag agc agg cat tat gga gaa aca aaa atg aat caa aga						687
Lys Gly Glu Lys Ser Arg His Tyr Gly Glu Thr Lys Met Asn Gln Arg						
184		189		194	199	
agc agt cgt tct cat acc atc ttt agg atg att ttg gaa agc aga gag						735
Ser Ser Arg Ser His Thr Ile Phe Arg Met Ile Leu Glu Ser Arg Glu						
200		205		210	215	

aag ggt gaa cct tct aat tgt gaa gga tct gtt aag gta tcc cat ttg	783
Lys Gly Glu Pro Ser Asn Cys Glu Gly Ser Val Lys Val Ser His Leu	
216 221 226 231	
aat ttg gtt gat ctt gca ggc agt gaa aga gct gct caa aca ggc gct	831
Asn Leu Val Asp Leu Ala Gly Ser Glu Arg Ala Ala Gln Thr Gly Ala	
232 237 242 247	
gca ggt gtg cgg ctc aag gaa ggc tgt aat ata aat cga agc tta ttt	879
Ala Gly Val Arg Leu Lys Glu Gly Cys Asn Ile Asn Arg Ser Leu Phe	
248 253 258 263	
att ttg gga caa gtg atc aag aaa ctt agt gat gga caa gtt ggt ggt	927
Ile Leu Gly Gln Val Ile Lys Lys Leu Ser Asp Gly Gln Val Gly Gly	
264 269 274 279	
ttc ata aat tat cga gat agc aag tta aca cga att ctt cag aat tcc	975
Phe Ile Asn Tyr Arg Asp Ser Lys Leu Thr Arg Ile Leu Gln Asn Ser	
280 285 290 295	
ttg gga gga aat cca aag aca cgt att atc tgc aca att act cca gta	1023
Leu Gly Gly Asn Pro Lys Thr Arg Ile Ile Cys Thr Ile Thr Pro Val	
296 301 306 311	
tct ttt gat gaa act ctt act gct ctc cag ttt gcc agt act gct aaa	1071
Ser Phe Asp Glu Thr Leu Thr Ala Leu Gln Phe Ala Ser Thr Ala Lys	
312 317 322 327	
tat atg aag aat act cct tat gtt aat gag gta tca act gat gaa gct	1119
Tyr Met Lys Asn Thr Pro Tyr Val Asn Glu Val Ser Thr Asp Glu Ala	
328 333 338 343	
ctc ctg aaa agg tat aga aaa gaa ata atg gat ctt aaa aaa caa tta	1167
Leu Leu Lys Arg Tyr Arg Lys Glu Ile Met Asp Leu Lys Lys Gln Leu	
344 349 354 359	
gag gag gtt tct tta gag acg cgg gct cag gca atg gaa aaa gac caa	1215
Glu Glu Val Ser Leu Glu Thr Arg Ala Gln Ala Met Glu Lys Asp Gln	
360 365 370 375	
ttg gcc caa ctt ttg gaa gaa aaa gat ttg ctt cag aaa gta cag aat	1263
Leu Ala Gln Leu Leu Glu Glu Lys Asp Leu Leu Gln Lys Val Gln Asn	
376 381 386 391	
gag aaa att gaa aac tta aca cgg atg ctg gtg acc tct tct tcc ctc	1311
Glu Lys Ile Glu Asn Leu Thr Arg Met Leu Val Thr Ser Ser Ser Leu	
392 397 402 407	
acg ttg caa cag gaa tta aag gct aaa aga aaa cga aga gtt act tgg	1359
Thr Leu Gln Gln Glu Leu Lys Ala Lys Arg Lys Arg Arg Val Thr Trp	
408 413 418 423	
tgc ctt ggc aaa att aac aaa atg aag aac tca aac tat gca gat caa	1407
Cys Leu Gly Lys Ile Asn Lys Met Lys Asn Ser Asn Tyr Ala Asp Gln	
424 429 434 439	

ttt aat ata cca aca aat ata aca aca aaa aca cat aag ctt tct ata	1455
Phe Asn Ile Pro Thr Asn Ile Thr Thr Lys Thr His Lys Leu Ser Ile	
440 445 450 455	
aat tta tta cga gaa att gat gaa tct gtc tgt tca gag tct gat gtt	1503
Asn Leu Leu Arg Glu Ile Asp Glu Ser Val Cys Ser Glu Ser Asp Val	
456 461 466 471	
ttc agt aac act ctt gat aca tta agt gag ata gaa tgg aat cca gca	1551
Phe Ser Asn Thr Leu Asp Thr Leu Ser Glu Ile Glu Trp Asn Pro Ala	
472 477 482 487	
aca aag cta cta aat cag gag aat ata gaa agt gag ttg aac tca ctt	1599
Thr Lys Leu Leu Asn Gln Glu Asn Ile Glu Ser Glu Leu Asn Ser Leu	
488 493 498 503	
cgt gct gac tat gat aat ctg gta tta gac tat gaa caa cta cga aca	1647
Arg Ala Asp Tyr Asp Asn Leu Val Leu Asp Tyr Glu Gln Leu Arg Thr	
504 509 514 519	
gaa aaa aaa aaa atg gaa ttg aaa tta aaa gaa aag aat gat ttg gat	1695
Glu Lys Lys Lys Met Glu Leu Lys Leu Lys Glu Lys Asn Asp Leu Asp	
520 525 530 535	
gaa ttt gag gct cta gaa aga aaa act aaa aaa gat caa gag atg caa	1743
Glu Phe Glu Ala Leu Glu Arg Lys Thr Lys Lys Asp Gln Glu Met Gln	
536 541 546 551	
cta att cat gaa att tcg aac tta aag aat tta gtt aag cat cga gaa	1791
Leu Ile His Glu Ile Ser Asn Leu Lys Asn Leu Val Lys His Arg Glu	
552 557 562 567	
gta tat aat caa gat ctt gag aat gaa ctc agt tca aaa gta gag ctg	1839
Val Tyr Asn Gln Asp Leu Glu Asn Glu Leu Ser Ser Lys Val Glu Leu	
568 573 578 583	
ctt aga gaa aag gaa gac cag att aag aag cta cag gaa tac ata gac	1887
Leu Arg Glu Lys Glu Asp Gln Ile Lys Lys Leu Gln Glu Tyr Ile Asp	
584 589 594 599	
tct caa aag cta gaa aat ata aaa atg gac ttg tca tac tca ttg gaa	1935
Ser Gln Lys Leu Glu Asn Ile Lys Met Asp Leu Ser Tyr Ser Leu Glu	
600 605 610 615	
agc att gaa gac cca aaa caa atg aag cag act ctg ttt gat gct gaa	1983
Ser Ile Glu Asp Pro Lys Gln Met Lys Gln Thr Leu Phe Asp Ala Glu	
616 621 626 631	
act gta gcc ctt gat gcc aag aga gaa tca gcc ttt ctt aga agt gaa	2031
Thr Val Ala Leu Asp Ala Lys Arg Glu Ser Ala Phe Leu Arg Ser Glu	
632 637 642 647	
aat ctg gag ttg aag gag aaa atg aaa gaa ctt gca act aca tac aag	2079
Asn Leu Glu Leu Lys Glu Lys Met Lys Glu Leu Ala Thr Thr Tyr Lys	
648 653 658 663	
caa atg gaa aat gat att cag tta tat caa agc caa ttg gag gca aaa	2127

Gln Met Glu Asn Asp	Ile Gln Leu Tyr Gln Ser Gln Leu Glu Ala Lys	
664	669	674 679
aag aaa atg caa gtt gat ctg gag aaa gaa tta caa tct gct ttt aat		2175
Lys Lys Met Gln Val Asp Leu Glu Lys Glu Leu Gln Ser Ala Phe Asn		
680	685 690	695
gag ata aca aaa ctc acc tcc ctt ata gat ggc aaa gtt cca aaa gat		2223
Glu Ile Thr Lys Leu Thr Ser Leu Ile Asp Gly Lys Val Pro Lys Asp		
696	701 706	711
ttg ctc tgt aat ttg gaa ttg gaa gga aag att act gat ctt cag aaa		2271
Leu Leu Cys Asn Leu Glu Leu Glu Gly Lys Ile Thr Asp Leu Gln Lys		
712	717 722	727
gaa cta aat aaa gaa gtt gaa gaa aat gaa gct ttg cgg gaa gaa gtc		2319
Glu Leu Asn Lys Glu Val Glu Glu Asn Glu Ala Leu Arg Glu Glu Val		
728	733 738	743
att ttg ctt tca gaa ttg aaa tct tta cct tct gaa gta gaa agg ctg		2367
Ile Leu Leu Ser Glu Leu Lys Ser Leu Pro Ser Glu Val Glu Arg Leu		
744	749 754	759
agg aaa gag ata caa gac aaa tct gaa gag ctc cat ata ata aca tca		2415
Arg Lys Glu Ile Gln Asp Lys Ser Glu Glu Leu His Ile Ile Thr Ser		
760	765 770	775
gaa aaa gat aaa ttg ttt tct gaa gta gtt cat aag gag agt aga gtt		2463
Glu Lys Asp Lys Leu Phe Ser Glu Val Val His Lys Glu Ser Arg Val		
776	781 786	791
caa ggt tta ctt gaa gaa att ggg aaa aca aaa gat gac cta gca act		2511
Gln Gly Leu Leu Glu Glu Ile Gly Lys Thr Lys Asp Asp Leu Ala Thr		
792	797 802	807
aca cag tcg aat tat aaa agc act gat caa gaa ttc caa aat ttc aaa		2559
Thr Gln Ser Asn Tyr Lys Ser Thr Asp Gln Glu Phe Gln Asn Phe Lys		
808	813 818	823
acc ctt cat atg gac ttt gag caa aag tat aag atg gtc ctt gag gag		2607
Thr Leu His Met Asp Phe Glu Gln Lys Tyr Lys Met Val Leu Glu Glu		
824	829 834	839
aat gag aga atg aat cag gaa ata gtt aat ctc tct aaa gaa gcc caa		2655
Asn Glu Arg Met Asn Gln Glu Ile Val Asn Leu Ser Lys Glu Ala Gln		
840	845 850	855
aaa ttt gat tcg agt ttg ggt gct ttg aag acc gag ctt tct tac aag		2703
Lys Phe Asp Ser Ser Leu Gly Ala Leu Lys Thr Glu Leu Ser Tyr Lys		
856	861 866	871
acc caa gaa ctt cag gag aaa aca cgt gag gtt caa gaa aga cta aat		2751
Thr Gln Glu Leu Gln Glu Lys Thr Arg Glu Val Gln Glu Arg Leu Asn		
872	877 882	887
gag atg gaa cag ctg aag gaa caa tta gaa aat aga gat tct ccg ctg		2799
Glu Met Glu Gln Leu Lys Glu Gln Leu Glu Asn Arg Asp Ser Pro Leu		

888	893	898	903	
caa act gta gaa agg gag aaa aca ctg att act gag aaa ctg cag caa				2847
Gln Thr Val Glu Arg Glu Lys Thr Leu Ile Thr Glu Lys Leu Gln Gln				
904	909	914	919	
act tta gaa gaa gta aaa act tta act caa gaa aaa gat gat cta aaa				2895
Thr Leu Glu Glu Val Lys Thr Leu Thr Gln Glu Lys Asp Asp Leu Lys				
920	925	930	935	
caa ctc caa gaa agc ttg caa att gag agg gac caa ctc aaa agt gat				2943
Gln Leu Gln Glu Ser Leu Gln Ile Glu Arg Asp Gln Leu Lys Ser Asp				
936	941	946	951	
att cac gat act gtt aac atg aat ata gat act caa gaa caa tta cga				2991
Ile His Asp Thr Val Asn Met Asn Ile Asp Thr Gln Glu Gln Leu Arg				
952	957	962	967	
aat gct ctt gag tct ctg aaa caa cat caa gaa aca att aat aca cta				3039
Asn Ala Leu Glu Ser Leu Lys Gln His Gln Glu Thr Ile Asn Thr Leu				
968	973	978	983	
aaa tcg aaa att tct gag gaa gtt tcc agg aat ttg cat atg gag gaa				3087
Lys Ser Lys Ile Ser Glu Glu Val Ser Arg Asn Leu His Met Glu Glu				
984	989	994	999	
aat aca gga gaa act aaa gat gaa ttt cag caa aag atg gtt ggc ata				3135
Asn Thr Gly Glu Thr Lys Asp Glu Phe Gln Gln Lys Met Val Gly Ile				
1000	1005	1010	1015	
gat aaa aaa cag gat ttg gaa gct aaa aat acc caa aca cta act gca				3183
Asp Lys Lys Gln Asp Leu Glu Ala Lys Asn Thr Gln Thr Leu Thr Ala				
1016	1021	1026	1031	
gat gtt aag gat aat gag ata att gag caa caa agg aag ata ttt tct				3231
Asp Val Lys Asp Asn Glu Ile Ile Glu Gln Gln Arg Lys Ile Phe Ser				
1032	1037	1042	1047	
tta ata cag gag aaa aat gaa ctc caa caa atg tta gag agt gtt ata				3279
Leu Ile Gln Glu Lys Asn Glu Leu Gln Gln Met Leu Glu Ser Val Ile				
1048	1053	1058	1063	
gca gaa aag gaa caa ttg aag act gac cta aag gaa aat att gaa atg				3327
Ala Glu Lys Glu Gln Leu Lys Thr Asp Leu Lys Glu Asn Ile Glu Met				
1064	1069	1074	1079	
acc att gaa aac cag gaa gaa tta aga ctt ctt ggg gat gaa ctt aaa				3375
Thr Ile Glu Asn Gln Glu Glu Leu Arg Leu Leu Gly Asp Glu Leu Lys				
1080	1085	1090	1095	
aag caa caa gag ata gtt gca caa gaa aag aac cat gcc ata aag aaa				3423
Lys Gln Gln Glu Ile Val Ala Gln Glu Lys Asn His Ala Ile Lys Lys				
1096	1101	1106	1111	
gaa gga gag ctt tct agg acc tgt gac aga ctg gca gaa gtt gaa gaa				3471
Glu Gly Glu Leu Ser Arg Thr Cys Asp Arg Leu Ala Glu Val Glu Glu				
1112	1117	1122	1127	

aaa cta aag gaa aag agc cag caa ctc caa gaa aaa cag caa caa ctt	3519
Lys Leu Lys Glu Lys Ser Gln Gln Leu Gln Glu Lys Gln Gln Gln Leu	
1128 1133 1138 1143	
ctt aat gta caa gaa gag atg agt gag atg cag aaa aag att aat gaa	3567
Leu Asn Val Gln Glu Glu Met Ser Glu Met Gln Lys Lys Ile Asn Glu	
1144 1149 1154 1159	
ata gag aat tta aag aat gaa tta aag aac aaa gaa ttg aca ttg gaa	3615
Ile Glu Asn Leu Lys Asn Glu Leu Lys Asn Lys Glu Leu Thr Leu Glu	
1160 1165 1170 1175	
cat atg gaa aca gag agg ctt gag ttg gct cag aaa ctt aat gaa aat	3663
His Met Glu Thr Glu Arg Leu Glu Leu Ala Gln Lys Leu Asn Glu Asn	
1176 1181 1186 1191	
tat gag gaa gtg aaa tct ata acc aaa gaa aga aaa gtt cta aag gaa	3711
Tyr Glu Glu Val Lys Ser Ile Thr Lys Glu Arg Lys Val Leu Lys Glu	
1192 1197 1202 1207	
tta cag aag tca ttt gaa aca gag aga gac cac ctt aga gga tat ata	3759
Leu Gln Lys Ser Phe Glu Thr Glu Arg Asp His Leu Arg Gly Tyr Ile	
1208 1213 1218 1223	
aga gaa att gaa gct aca ggc cta caa acc aaa gaa gaa cta aaa att	3807
Arg Glu Ile Glu Ala Thr Gly Leu Gln Thr Lys Glu Glu Leu Lys Ile	
1224 1229 1234 1239	
gct cat att cac cta aaa gaa cac caa gaa act att gat gaa cta aga	3855
Ala His Ile His Leu Lys Glu His Gln Glu Thr Ile Asp Glu Leu Arg	
1240 1245 1250 1255	
aga agc gta tct gag aag aca gct caa ata ata aat act cag gac tta	3903
Arg Ser Val Ser Glu Lys Thr Ala Gln Ile Ile Asn Thr Gln Asp Leu	
1256 1261 1266 1271	
gaa aaa tcc cat acc aaa tta caa gaa gag atc cca gtg ctt cat gag	3951
Glu Lys Ser His Thr Lys Leu Gln Glu Glu Ile Pro Val Leu His Glu	
1272 1277 1282 1287	
gaa caa gag tta ctg cct aat gtg aaa aaa gtc agt gag act cag gaa	3999
Glu Gln Glu Leu Leu Pro Asn Val Lys Lys Val Ser Glu Thr Gln Glu	
1288 1293 1298 1303	
aca atg aat gaa ctg gag tta tta aca gaa cag tcc aca acc aag gac	4047
Thr Met Asn Glu Leu Glu Leu Leu Thr Glu Gln Ser Thr Thr Lys Asp	
1304 1309 1314 1319	
tca aca aca ctg gca aga ata gaa atg gaa agg ctc agg ttg aat gaa	4095
Ser Thr Thr Leu Ala Arg Ile Glu Met Glu Arg Leu Arg Leu Asn Glu	
1320 1325 1330 1335	
aaa ttt caa gaa agt cag gaa gag ata aaa tct cta acc aag gaa aga	4143
Lys Phe Gln/Glu Ser Gln Glu Glu Ile Lys Ser Leu Thr Lys Glu Arg	
1336 1341 1346 1351	

gac aac ctt aaa acg ata aaa gaa gcc ctt gaa gtt aaa cat gac cag	4191
Asp Asn Leu Lys Thr Ile Lys Glu Ala Leu Glu Val Lys His Asp Gln	
1352 1357 1362 1367	
ctg aaa gaa cat att aga gaa act ttg gct aaa atc cag gag tct caa	4239
Leu Lys Glu His Ile Arg Glu Thr Leu Ala Lys Ile Gln Glu Ser Gln	
1368 1373 1378 1383	
agc aaa caa gaa cag tcc tta aat atg aaa gaa aaa gac aat gaa act	4287
Ser Lys Gln Glu Gln Ser Leu Asn Met Lys Glu Lys Asp Asn Glu Thr	
1384 1389 1394 1399	
acc aaa atc gtg agt gag atg gag caa ttc aaa ccg aaa gat tca gca	4335
Thr Lys Ile Val Ser Glu Met Glu Gln Phe Lys Pro Lys Asp Ser Ala	
1400 1405 1410 1415	
cta cta agg ata gaa ata gaa atg ctc gga ttg tcc aaa aga ctt caa	4383
Leu Leu Arg Ile Glu Ile Glu Met Leu Gly Leu Ser Lys Arg Leu Gln	
1416 1421 1426 1431	
gaa agt cat gat gaa atg aaa tct gta gct aag gag aaa gat gac cta	4431
Glu Ser His Asp Glu Met Lys Ser Val Ala Lys Glu Lys Asp Asp Leu	
1432 1437 1442 1447	
cag agg ctg caa gaa gtt ctt caa tct gaa agt gac cag ctc aaa gaa	4479
Gln Arg Leu Gln Glu Val Leu Gln Ser Glu Ser Asp Gln Leu Lys Glu	
1448 1453 1458 1463	
aac ata aaa gaa att gta gct aaa cac ctg gaa act gaa gag gaa ctt	4527
Asn Ile Lys Glu Ile Val Ala Lys His Leu Glu Thr Glu Glu Glu Leu	
1464 1469 1474 1479	
aaa gtt gct cat tgt tgc ctg aaa gaa caa gag gaa act att aat gag	4575
Lys Val Ala His Cys Cys Leu Lys Glu Gln Glu Glu Thr Ile Asn Glu	
1480 1485 1490 1495	
tta aga gtg aat ctt tca gag aag gaa act gaa ata tca acc att caa	4623
Leu Arg Val Asn Leu Ser Glu Lys Glu Thr Glu Ile Ser Thr Ile Gln	
1496 1501 1506 1511	
aag cag tta gaa gca atc aat gat aaa tta cag aac aag atc caa gag	4671
Lys Gln Leu Glu Ala Ile Asn Asp Lys Leu Gln Asn Lys Ile Gln Glu	
1512 1517 1522 1527	
att tat gag aaa gag gaa caa ctt aat ata aaa caa att agt gag gtt	4719
Ile Tyr Glu Lys Glu Glu Gln Leu Asn Ile Lys Gln Ile Ser Glu Val	
1528 1533 1538 1543	
cag gaa aaa gtg aat gaa ctg aaa caa ttc aag gag cat cgc aaa gcc	4767
Gln Glu Lys Val Asn Glu Leu Lys Gln Phe Lys Glu His Arg Lys Ala	
1544 1549 1554 1559	
aag gat tca gca cta caa agt ata gaa agt aag atg ctc gag ttg acc	4815
Lys Asp Ser Ala Leu Gln Ser Ile Glu Ser Lys Met Leu Glu Leu Thr	
1560 1565 1570 1575	
aac aga ctt caa gaa agt caa gaa gaa ata caa att atg att aag gaa	4863

Asn Arg Leu Gln Glu Ser Gln Glu Glu Ile Gln Ile Met Ile Lys Glu	
1576 1581 1586 1591	
aaa gag gaa atg aaa aga gta cag gag gcc ctt cag ata gag aga gac	4911
Lys Glu Glu Met Lys Arg Val Gln Glu Ala Leu Gln Ile Glu Arg Asp	
1592 1597 1602 1607	
caa ctg aaa gaa aac act aaa gaa att gta gct aaa atg aaa gaa tct	4959
Gln Leu Lys Glu Asn Thr Lys Glu Ile Val Ala Lys Met Lys Glu Ser	
1608 1613 1618 1623	
caa gaa aaa gaa tat cag ttt ctt aag atg aca gct gtc aat gag act	5007
Gln Glu Lys Glu Tyr Gln Phe Leu Lys Met Thr Ala Val Asn Glu Thr	
1624 1629 1634 1639	
cag gag aaa atg tgt gaa ata gaa cac ttg aag gag caa ttt gag acc	5055
Gln Glu Lys Met Cys Glu Ile Glu His Leu Lys Glu Gln Phe Glu Thr	
1640 1645 1650 1655	
cag aag tta aac ctg gaa aac ata gaa acg gag aat ata agg ttg act	5103
Gln Lys Leu Asn Leu Glu Asn Ile Glu Thr Glu Asn Ile Arg Leu Thr	
1656 1661 1666 1671	
cag ata cta cat gaa aac ctt gaa gaa atg aga tct gta aca aaa gaa	5151
Gln Ile Leu His Glu Asn Leu Glu Glu Met Arg Ser Val Thr Lys Glu	
1672 1677 1682 1687	
aga gat gac ctt agg agt gtg gag gag act ctc aaa gta gag aga gac	5199
Arg Asp Asp Leu Arg Ser Val Glu Glu Thr Leu Lys Val Glu Arg Asp	
1688 1693 1698 1703	
cag ctc aag gaa aac ctt aga gaa act ata act aga gac cta gaa aaa	5247
Gln Leu Lys Glu Asn Leu Arg Glu Thr Ile Thr Arg Asp Leu Glu Lys	
1704 1709 1714 1719	
caa gag gag cta aaa att gtt cac atg cat ctg aag gag cac caa gaa	5295
Gln Glu Glu Leu Lys Ile Val His Met His Leu Lys Glu His Gln Glu	
1720 1725 1730 1735	
act att gat aaa cta aga ggg att gtt tca gag aaa aca aat gaa ata	5343
Thr Ile Asp Lys Leu Arg Gly Ile Val Ser Glu Lys Thr Asn Glu Ile	
1736 1741 1746 1751	
tca aat atg caa aag gac tta gaa cac tca aat gat gcc tta aaa gca	5391
Ser Asn Met Gln Lys Asp Leu Glu His Ser Asn Asp Ala Leu Lys Ala	
1752 1757 1762 1767	
cag gat ctg aaa ata caa gag gaa cta aga att gct cac atg cat ctg	5439
Gln Asp Leu Lys Ile Gln Glu Glu Leu Arg Ile Ala His Met His Leu	
1768 1773 1778 1783	
aaa gag cag cag gaa act att gac aaa ctc aga gga att gtt tct gag	5487
Lys Glu Gln Gln Glu Thr Ile Asp Lys Leu Arg Gly Ile Val Ser Glu	
1784 1789 1794 1799	
aag aca gat aaa cta tca aat atg caa aaa gat tta gaa aat tca aat	5535
Lys Thr Asp Lys Leu Ser Asn Met Gln Lys Asp Leu Glu Asn Ser Asn	

1800	1805	1810	1815	
gct aaa tta caa gaa aag att caa gaa ctt aag gca aat gaa cat caa				5583
Ala Lys Leu Gln Glu Lys Ile Gln Glu Leu Lys Ala Asn Glu His Gln				
1816	1821	1826	1831	
ctt att acg tta aaa aaa gat gtc aat gag aca cag aaa aaa gtg tct				5631
Leu Ile Thr Leu Lys Lys Asp Val Asn Glu Thr Gln Lys Lys Val Ser				
1832	1837	1842	1847	
gaa atg gag caa cta aag aaa caa ata aaa gac caa agc tta act ctg				5679
Glu Met Glu Gln Leu Lys Lys Gln Ile Lys Asp Gln Ser Leu Thr Leu				
1848	1853	1858	1863	
agt aaa tta gaa ata gag aat tta aat ttg gct caa gaa ctt cat gaa				5727
Ser Lys Leu Glu Ile Glu Asn Leu Asn Leu Ala Gln Glu Leu His Glu				
1864	1869	1874	1879	
aac ctt gaa gaa atg aaa tct gta atg aaa gaa aga gat aat cta aga				5775
Asn Leu Glu Glu Met Lys Ser Val Met Lys Glu Arg Asp Asn Leu Arg				
1880	1885	1890	1895	
aga gta gag gag aca ctg aaa ctg gag aga gac caa ctg aag gaa agc				5823
Arg Val Glu Glu Thr Leu Lys Leu Glu Arg Asp Gln Leu Lys Glu Ser				
1896	1901	1906	1911	
ctg caa gaa acc aaa gct aga gat ctg gaa ata caa cag gaa cta aaa				5871
Leu Gln Glu Thr Lys Ala Arg Asp Leu Glu Ile Gln Gln Glu Leu Lys				
1912	1917	1922	1927	
act gct cgt atg cta tca aaa gaa cac aaa gaa act gtt gat aaa ctt				5919
Thr Ala Arg Met Leu Ser Lys Glu His Lys Glu Thr Val Asp Lys Leu				
1928	1933	1938	1943	
aga gaa aaa att tca gaa aag aca att caa att tca gac att caa aag				5967
Arg Glu Lys Ile Ser Glu Lys Thr Ile Gln Ile Ser Asp Ile Gln Lys				
1944	1949	1954	1959	
gat tta gat aaa tca aaa gat gaa tta cag aaa aag atc caa gaa ctt				6015
Asp Leu Asp Lys Ser Lys Asp Glu Leu Gln Lys Lys Ile Gln Glu Leu				
1960	1965	1970	1975	
cag aaa aaa gaa ctt caa ctg ctt aga gtg aaa gaa gat gtc aat atg				6063
Gln Lys Lys Glu Leu Gln Leu Leu Arg Val Lys Glu Asp Val Asn Met				
1976	1981	1986	1991	
agt cat aaa aaa att aat gaa atg gaa cag ttg aag aag caa ttt gag				6111
Ser His Lys Lys Ile Asn Glu Met Glu Gln Leu Lys Lys Gln Phe Glu				
1992	1997	2002	2007	
cca aac tat cta tgc aag tgt gag atg gat aac ttc cag ttg act aag				6159
Pro Asn Tyr Leu Cys Lys Cys Glu Met Asp Asn Phe Gln Leu Thr Lys				
2008	2013	2018	2023	
aaa ctt cat gaa agc ctt gaa gaa ata aga att gta gct aaa gaa aga				6207
Lys Leu His Glu Ser Leu Glu Glu Ile Arg Ile Val Ala Lys Glu Arg				
2024	2029	2034	2039	

gat gag cta agg agg ata aaa gaa tct ctc aaa atg gaa agg gac caa	6255
Asp Glu Leu Arg Arg Ile Lys Glu Ser Leu Lys Met Glu Arg Asp Gln	
2040 2045 2050 2055	
ttc ata gca acc tta agg gaa atg ata gct aga gac cga cag aac cac	6303
Phe Ile Ala Thr Leu Arg Glu Met Ile Ala Arg Asp Arg Gln Asn His	
2056 2061 2066 2071	
caa gta aaa cct gaa aaa agg tta cta agt gat gga caa cag cac ctt	6351
Gln Val Lys Pro Glu Lys Arg Leu Leu Ser Asp Gly Gln Gln His Leu	
2072 2077 2082 2087	
atg gaa agc ctg aga gaa aag tgc tct aga ata aaa gag ctt ttg aag	6399
Met Glu Ser Leu Arg Glu Lys Cys Ser Arg Ile Lys Glu Leu Leu Lys	
2088 2093 2098 2103	
aga tac tca gag atg gat gat cat tat gag tgc ttg aat aga ttg tct	6447
Arg Tyr Ser Glu Met Asp Asp His Tyr Glu Cys Leu Asn Arg Leu Ser	
2104 2109 2114 2119	
ctt gac ttg gag aag gaa att gaa ttc cac aga atc atg aag aaa ctg	6495
Leu Asp Leu Glu Lys Glu Ile Glu Phe His Arg Ile Met Lys Lys Leu	
2120 2125 2130 2135	
aag tat gtg tta agc tat gtt aca aaa ata aaa gaa gaa caa cat gaa	6543
Lys Tyr Val Leu Ser Tyr Val Thr Lys Ile Lys Glu Glu Gln His Glu	
2136 2141 2146 2151	
tcc atc aat aaa ttt gaa atg gat ttt att gat gaa gtg gaa aag caa	6591
Ser Ile Asn Lys Phe Glu Met Asp Phe Ile Asp Glu Val Glu Lys Gln	
2152 2157 2162 2167	
aag gaa ttg cta att aaa ata cag cac ctt caa caa gat tgt gat gta	6639
Lys Glu Leu Leu Ile Lys Ile Gln His Leu Gln Gln Asp Cys Asp Val	
2168 2173 2178 2183	
cca tcc aga gaa tta agg gat ctc aaa ttg aac cag aat atg gat cta	6687
Pro Ser Arg Glu Leu Arg Asp Leu Lys Leu Asn Gln Asn Met Asp Leu	
2184 2189 2194 2199	
cat att gag gaa att ctc aaa gat ttc tca gaa agt gag ttc cct agc	6735
His Ile Glu Glu Ile Leu Lys Asp Phe Ser Glu Ser Glu Phe Pro Ser	
2200 2205 2210 2215	
ata aag act gaa ttt caa caa gta cta agt aat agg aaa gaa atg aca	6783
Ile Lys Thr Glu Phe Gln Gln Val Leu Ser Asn Arg Lys Glu Met Thr	
2216 2221 2226 2231	
cag ttt ttg gaa gag tgg tta aat act cgt ttt gat ata gaa aag ctt	6831
Gln Phe Leu Glu Glu Trp Leu Asn Thr Arg Phe Asp Ile Glu Lys Leu	
2232 2237 2242 2247	
aaa aat ggc atc cag aaa gaa aat gat agg att tgt caa gtg aat aac	6879
Lys Asn Gly Ile Gln Lys Glu Asn Asp Arg Ile Cys Gln Val Asn Asn	
2248 2253 2258 2263	

ttc ttt aat aac aga ata att gcc ata atg aat gaa tca aca gag ttt	6927
Phe Phe Asn Asn Arg Ile Ile Ala Ile Met Asn Glu Ser Thr Glu Phe	
2264 2269 2274 2279	
gag gaa aga agt gct acc ata tcc aaa gag tgg gaa cag gac ctg aaa	6975
Glu Glu Arg Ser Ala Thr Ile Ser Lys Glu Trp Glu Gln Asp Leu Lys	
2280 2285 2290 2295	
tca ctg aaa gag aaa aat gaa aaa cta ttt aaa aac tac caa aca ttg	7023
Ser Leu Lys Glu Lys Asn Glu Lys Leu Phe Lys Asn Tyr Gln Thr Leu	
2296 2301 2306 2311	
aag act tcc ttg gca tct ggt gcc cag gtt aat cct acc aca caa gac	7071
Lys Thr Ser Leu Ala Ser Gly Ala Gln Val Asn Pro Thr Thr Gln Asp	
2312 2317 2322 2327	
aat aag aat cct cat gtt aca tca aga gct aca cag tta acc aca gag	7119
Asn Lys Asn Pro His Val Thr Ser Arg Ala Thr Gln Leu Thr Thr Glu	
2328 2333 2338 2343	
aaa att cga gag ctg gaa aat tca ctg cat gaa gct aaa gaa agt gct	7167
Lys Ile Arg Glu Leu Glu Asn Ser Leu His Glu Ala Lys Glu Ser Ala	
2344 2349 2354 2359	
atg cat aag gaa agc aag att ata aag atg cag aaa gaa ctt gag gtg	7215
Met His Lys Glu Ser Lys Ile Ile Lys Met Gln Lys Glu Leu Glu Val	
2360 2365 2370 2375	
act aat gac ata ata gca aaa ctt caa gcc aaa gtt cat gaa tca aat	7263
Thr Asn Asp Ile Ile Ala Lys Leu Gln Ala Lys Val His Glu Ser Asn	
2376 2381 2386 2391	
aaa tgc ctt gaa aaa aca aaa gag aca att caa gta ctt cag gac aaa	7311
Lys Cys Leu Glu Lys Thr Lys Glu Thr Ile Gln Val Leu Gln Asp Lys	
2392 2397 2402 2407	
gtt gct tta gga gct aag cca tat aaa gaa gaa att gaa gat ctc aaa	7359
Val Ala Leu Gly Ala Lys Pro Tyr Lys Glu Glu Ile Glu Asp Leu Lys	
2408 2413 2418 2423	
atg aag ctt gtg aaa ata gac cta gag aaa atg aaa aat gcc aaa gaa	7407
Met Lys Leu Val Lys Ile Asp Leu Glu Lys Met Lys Asn Ala Lys Glu	
2424 2429 2434 2439	
ttt gaa aag gaa atc agt gct aca aaa gcc act gta gaa tat caa aag	7455
Phe Glu Lys Glu Ile Ser Ala Thr Lys Ala Thr Val Glu Tyr Gln Lys	
2440 2445 2450 2455	
gaa gtt ata agg cta ttg aga gaa aat ctc aga aga agt caa cag gcc	7503
Glu Val Ile Arg Leu Leu Arg Glu Asn Leu Arg Arg Ser Gln Gln Ala	
2456 2461 2466 2471	
caa gat acc tca gtg ata tca gaa cat act gat cct cag cct tca aat	7551
Gln Asp Thr Ser Val Ile Ser Glu His Thr Asp Pro Gln Pro Ser Asn	
2472 2477 2482 2487	
aaa ccc tta act tgt gga ggt ggc agc ggc att gta caa aac aca aaa	7599

aaaattgtaa atgttttttaa taccttacac attcaataaa tgttttagtag ttctgaaaaa 8496
 aaaaaaa 8503

<210> 131
 <211> 1693
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (88)..(1512)

<400> 131
 atttgaacgc ttgaggtccc ggtccggaat tcccgggtcg acccagcgt ccgcggaacgc 60

gtgggattct tttaatcaga gttagta atg tgg aca gta caa aat cga gag 111
 Met Trp Thr Val Gln Asn Arg Glu
 1 5

agt ctg ggg ctt ctc tct ttc cct gtg atg att acc atg gtc tgt tgt 159
 Ser Leu Gly Leu Leu Ser Phe Pro Val Met Ile Thr Met Val Cys Cys
 9 14 19 24

gca cac agc acc aat gaa ccc agc aac atg tca tac gtg aaa gag aca 207
 Ala His Ser Thr Asn Glu Pro Ser Asn Met Ser Tyr Val Lys Glu Thr
 25 30 35 40

gtg gac aga ttg ctc aaa gga tat gac att cgc ttg cgg ccg gac ttc 255
 Val Asp Arg Leu Leu Lys Gly Tyr Asp Ile Arg Leu Arg Pro Asp Phe
 41 46 51 56

gga ggg ccc ccc gtc gac gtt ggg atg cgg atc gat gtc gcc agc ata 303
 Gly Gly Pro Pro Val Asp Val Gly Met Arg Ile Asp Val Ala Ser Ile
 57 62 67 72

gac atg gtc tcc gaa gtg aat atg gat tat aca ctc acc atg tat ttc 351
 Asp Met Val Ser Glu Val Asn Met Asp Tyr Thr Leu Thr Met Tyr Phe
 73 78 83 88

cag cag tct tgg aaa gac aaa agg ctt tct tat tct gga atc cca ctg 399
 Gln Gln Ser Trp Lys Asp Lys Arg Leu Ser Tyr Ser Gly Ile Pro Leu
 89 94 99 104

aac ctc acc cta gac aat agg gta gct gac caa ctc tgg gta cca gac 447
 Asn Leu Thr Leu Asp Asn Arg Val Ala Asp Gln Leu Trp Val Pro Asp
 105 110 115 120

acc tac ttt ctg aat gac aag aaa tca ttt gtg cat ggg gtc aca gtg 495
 Thr Tyr Phe Leu Asn Asp Lys Lys Ser Phe Val His Gly Val Thr Val
 121 126 131 136

aaa aat cga atg att cga ctg cat cct gat gga aca gtt ctc tat gga 543
 Lys Asn Arg Met Ile Arg Leu His Pro Asp Gly Thr Val Leu Tyr Gly

137	142	147	152	
ctc cga atc aca acc aca gct gca tgt atg atg gat ctt cga aga tat				591
Leu Arg Ile Thr Thr Thr Ala Ala Cys Met Met Asp Leu Arg Arg Tyr				
153	158	163	168	
cca ctg gat gag cag aac tgc acc ctg gag atc gaa agt tat ggc tat				639
Pro Leu Asp Glu Gln Asn Cys Thr Leu Glu Ile Glu Ser Tyr Gly Tyr				
169	174	179	184	
acc act gat gac att gaa ttt tac tgg aat gga gga gaa ggg gca gtc				687
Thr Thr Asp Asp Ile Glu Phe Tyr Trp Asn Gly Gly Glu Gly Ala Val				
185	190	195	200	
act ggt gtt aat aaa atc gaa ctt cct caa ttt tca att gtt gac tac				735
Thr Gly Val Asn Lys Ile Glu Leu Pro Gln Phe Ser Ile Val Asp Tyr				
201	206	211	216	
aag atg gtg tct aag aag gtg gag ttc aca aca gga gcg tat cca cga				783
Lys Met Val Ser Lys Lys Val Glu Phe Thr Thr Gly Ala Tyr Pro Arg				
217	222	227	232	
ctg tca cta agt ttt cgt cta aag aga aac att ggt tac ttc att ttg				831
Leu Ser Leu Ser Phe Arg Leu Lys Arg Asn Ile Gly Tyr Phe Ile Leu				
233	238	243	248	
caa acc tac atg cct tct aca ctg att aca att ctg tcc tgg gtg tct				879
Gln Thr Tyr Met Pro Ser Thr Leu Ile Thr Ile Leu Ser Trp Val Ser				
249	254	259	264	
ttt tgg atc aac tat gat gca tct gca gcc aga gtc gca cta gga atc				927
Phe Trp Ile Asn Tyr Asp Ala Ser Ala Ala Arg Val Ala Leu Gly Ile				
265	270	275	280	
acg acg gtg ctt aca atg aca acc atc agc acc cac ctc agg gag acc				975
Thr Thr Val Leu Thr Met Thr Thr Ile Ser Thr His Leu Arg Glu Thr				
281	286	291	296	
ctg cca aag atc cct tat gtc aaa gcg att gat att tat ctg atg ggt				1023
Leu Pro Lys Ile Pro Tyr Val Lys Ala Ile Asp Ile Tyr Leu Met Gly				
297	302	307	312	
tgc ttt gtg ttt gtg ttc ctg gct ctg ctg gag tat gcc ttt gta aat				1071
Cys Phe Val Phe Val Phe Leu Ala Leu Leu Glu Tyr Ala Phe Val Asn				
313	318	323	328	
tac atc ttc ttt ggg aaa ggc cct cag aaa aag gga gct agc aaa caa				1119
Tyr Ile Phe Phe Gly Lys Gly Pro Gln Lys Lys Gly Ala Ser Lys Gln				
329	334	339	344	
gac cag agt gcc aat gag aag aat aaa ctg gag atg aat aaa gtc cag				1167
Asp Gln Ser Ala Asn Glu Lys Asn Lys Leu Glu Met Asn Lys Val Gln				
345	350	355	360	
gtc gac gcc cac ggt aac att ctc ctc agc acc ctg gaa atc cgg aat				1215
Val Asp Ala His Gly Asn Ile Leu Leu Ser Thr Leu Glu Ile Arg Asn				
361	366	371	376	

gag acg agt ggc tgc gaa gtg ctc acg agc gtg agc gac ccc aag gcc	1263
Glu Thr Ser Gly Ser Glu Val Leu Thr Ser Val Ser Asp Pro Lys Ala	
377 382 387 392	
acc atg tac tcc tat gac agc gcc agc atc cag tac cgc aag ccc ctg	1311
Thr Met Tyr Ser Tyr Asp Ser Ala Ser Ile Gln Tyr Arg Lys Pro Leu	
393 398 403 408	
agc agc cgc gag gcc tac ggg cgc gcc ctg gac cgg cac ggg gta ccc	1359
Ser Ser Arg Glu Ala Tyr Gly Arg Ala Leu Asp Arg His Gly Val Pro	
409 414 419 424	
agc aag ggg cgc atc cgc agg cgt gcc tcc cag ctc ¹ aaa gtc aag atc	1407
Ser Lys Gly Arg Ile Arg Arg Arg Ala Ser Gln Leu Lys Val Lys Ile	
425 430 435 440	
ccc gac ttg act gat gtg aat tcc ata gac aag tgg tcc cga atg ttt	1455
Pro Asp Leu Thr Asp Val Asn Ser Ile Asp Lys Trp Ser Arg Met Phe	
441 446 451 456	
ttc ccc atc acc ttt tct ctt ttt aat gtc gtc tat tgg ctt tac tat	1503
Phe Pro Ile Thr Phe Ser Leu Phe Asn Val Val Tyr Trp Leu Tyr Tyr	
457 462 467 472	
gta cac tga ggtctgt tctaattggtt ccatttagac tactttcctc ttctattggt	1559
Val His *	
473	
ttttaacctt acaggtcccc aacagcgata ctgctgtttc tcgaggtaag agattcagcc	1619
atccaattgg ttttaggtct tgcataatcag ttttattact gcaccatggt tactttcaaaa	1679
agacaaaaaa aaaa	1693

<210> 132
 <211> 920
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (171)..(737)

<400> 132	
tgagttatgt gattggagac catggaacgc ctgcggtacc ggtccggaat tcccgggtcg	60
acccacgcgt ccggactagt tctagatcgc gagccgccgc ccaggaaggg gatgcggaaa	120
cccctggctc ggtggagcgg agaggcaggc gggcaggagc cgaggacggc atg tcc	176
	Met Ser
	1
cag gcc ccg gga gca cag ccg agc cca ccc acc gtg tac cac gaa cgg	224

Gln	Ala	Pro	Gly	Ala	Gln	Pro	Ser	Pro	Pro	Thr	Val	Tyr	His	Glu	Arg		
3					8					13					18		
cag	cgc	ctg	gag	ctg	tgt	gct	gtc	cac	gcc	ctc	aac	aac	gtt	ctg	cag	272	
Gln	Arg	Leu	Glu	Leu	Cys	Ala	Val	His	Ala	Leu	Asn	Asn	Val	Leu	Gln		
19					24					29					34		
cag	cag	ctc	ttt	agc	cag	gag	gct	gcc	gat	gag	atc	tgc	aag	agg	ttg	320	
Gln	Gln	Leu	Phe	Ser	Gln	Glu	Ala	Ala	Asp	Glu	Ile	Cys	Lys	Arg	Leu		
35					40					45					50		
gcc	cca	gac	tcc	cgg	ctg	aac	cct	cat	cgc	agc	ctc	ctg	ggc	acc	ggc	368	
Ala	Pro	Asp	Ser	Arg	Leu	Asn	Pro	His	Arg	Ser	Leu	Leu	Gly	Thr	Gly		
51					56					61					66		
aac	tat	gat	gtc	aat	gtg	atc	atg	gcc	gct	ctg	cag	ggg	ctg	ggc	ctg	416	
Asn	Tyr	Asp	Val	Asn	Val	Ile	Met	Ala	Ala	Leu	Gln	Gly	Leu	Gly	Leu		
67					72					77					82		
gcc	gcc	gtg	tgg	tgg	gac	agg	agg	agg	ccc	ctg	tcc	cag	ctg	gcc	ctg	464	
Ala	Ala	Val	Trp	Trp	Asp	Arg	Arg	Arg	Pro	Leu	Ser	Gln	Leu	Ala	Leu		
83					88					93					98		
ccc	cag	gta	ctg	ggg	ctg	atc	ctg	aac	ctg	ccc	tgc	ccc	gtg	tgc	ctg	512	
Pro	Gln	Val	Leu	Gly	Leu	Ile	Leu	Asn	Leu	Pro	Ser	Pro	Val	Ser	Leu		
99					104					109					114		
ggg	ctg	ctg	tca	ctg	ccg	ctg	cgc	cgg	cgg	cac	tgg	gtg	gcc	ctg	cgc	560	
Gly	Leu	Leu	Ser	Leu	Pro	Leu	Arg	Arg	Arg	His	Trp	Val	Ala	Leu	Arg		
115					120					125					130		
cag	gtg	gac	ggg	gtc	tac	tac	aac	ctg	gac	tcc	aag	ctg	cgg	gcg	ccc	608	
Gln	Val	Asp	Gly	Val	Tyr	Tyr	Asn	Leu	Asp	Ser	Lys	Leu	Arg	Ala	Pro		
131					136					141					146		
gag	gcc	ctg	ggg	gat	gag	gac	gga	gtc	agg	gcc	ttc	ctg	gcg	gct	gcg	656	
Glu	Ala	Leu	Gly	Asp	Glu	Asp	Gly	Val	Arg	Ala	Phe	Leu	Ala	Ala	Ala		
147					152					157					162		
ctg	gcc	cag	ggc	ctg	tgc	gag	gtg	ctg	ctg	gta	gtg	acc	aag	gag	gtg	704	
Leu	Ala	Gln	Gly	Leu	Cys	Glu	Val	Leu	Leu	Val	Val	Thr	Lys	Glu	Val		
163					168					173					178		
gag	gag	aag	ggc	agc	tgg	ctg	cgg	aca	gac	tga	ccatggct	gaccatcggc				755	
Glu	Glu	Lys	Gly	Ser	Trp	Leu	Arg	Thr	Asp	*							
179					184					189							
gcccacagcg	cagtcctctgc	acatccccct	ccggctgcgc	acactgcctg	cctgggaaag											815	
gccagcactt	catggaccct	ggggaggccc	cgccccctcc	ccacaccct	gctccccact											875	
gcccgtgctg	cctcaataaa	tctgctgatt	tgcaaaaaaa	aaaaa												920	

<210> 133

<211> 1005
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (276)..(584)

<400> 133

ttcgggtaccg ctccggaatt cccgggtcga cccacgcgtc cgcagaaatc tccaggccac	60
cggctttccg ctaccggatt ggctgcgtcc ggggtgctgag gcccggccca tttccccggg	120
tcctttgatc acgcgcctga cggcttttcc gggggccggg agccaaccga gggcgttcct	180
gtcggggctg cagcggcggg agggagccca gtggaggcgc cctcccgaag cgccactgcc	240
catgctgacc acccagccct ccggctgctg atgtc atg agt aac acc act gtg	293
Met Ser Asn Thr Thr Val	
1	
ccc aat gcc ccc cag gcc aac agc gac tcc atg gtg ggc tat gtg ttg	341
Pro Asn Ala Pro Gln Ala Asn Ser Asp Ser Met Val Gly Tyr Val Leu	
7 12 17 22	
ggg ccc ttc ttc ctc atc acc ctg gtc ggg gtg gtg gtg gct gtg gta	389
Gly Pro Phe Phe Leu Ile Thr Leu Val Gly Val Val Val Ala Val Val	
23 28 33 38	
atg tat gta cag aaa aaa aag cgg gtg gac cgg ctg cgc cat cac ctg	437
Met Tyr Val Gln Lys Lys Lys Arg Val Asp Arg Leu Arg His His Leu	
39 44 49 54	
ctc ccc atg tac agc tat gac cca gct gag gaa ctg cat gag gct gag	485
Leu Pro Met Tyr Ser Tyr Asp Pro Ala Glu Glu Leu His Glu Ala Glu	
55 60 65 70	
cag gag ctg ctc tct gac atg gga gac ccc aag gtg gta cat ggc tgg	533
Gln Glu Leu Leu Ser Asp Met Gly Asp Pro Lys Val Val His Gly Trp	
71 76 81 86	
cag agt ggc tac cag cac aag cgg atg cca ctg ctg gat gtc aag acg	581
Gln Ser Gly Tyr Gln His Lys Arg Met Pro Leu Leu Asp Val Lys Thr	
87 92 97 102	
tga cctg acccccttgc cccacccttc agagcctggg gtccctggact gcttggggcc	638
*	
103	
ctgccatttg cttcccttgc tgtcacctgg ctcccccctgc tgggtgctgg gtttccattt	698
ttccctccac ccaccctcaa cagcatttgc tttccatgcc ctcaccatca cctcaactgcc	758
cccaggcctt ttgccctttg tgggtgttga gctccccgcc cccccccagg cactcatagg	818
aaaaggcttt ccttttggga tggcggcggc tggtaaacct ctttgctttt tctagccctc	878

ctgggctggg cttgggccc aatccccagg caggctttgg agttgtttcc atggtgatgg 938
ggccagatgt atagtattca gtatatattt tgtaaataaa atgttttgtg gctaggaaaa 998
aaaaaaa 1005

<210> 134
<211> 4323
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (81)..(3920)

<400> 134
tccaggctct gcggtgataag ctgtggatct tcctgggtca gtcttttat gctgttcgtc 60
acacagaaaag ctggaagctg atg agc aca gat gat caa cag aaa atc caa 110
Met Ser Thr Asp Asp Gln Gln Lys Ile Gln
1 5
gca gct gca ttt gac aaa ggt gat gat cga aga ctt ggc aaa aag cct 158
Ala Ala Ala Phe Asp Lys Gly Asp Asp Arg Arg Leu Gly Lys Lys Pro
11 16 21 26
ata ttc agt agc tcg cag caa agg aaa caa gtt tct gac tct ggt gat 206
Ile Phe Ser Ser Ser Gln Gln Arg Lys Gln Val Ser Asp Ser Gly Asp
27 32 37 42
ata aaa atc aaa tct tgg agg gga aat aac aag aaa gag tgt tgg agt 254
Ile Lys Ile Lys Ser Trp Arg Gly Asn Asn Lys Lys Glu Cys Trp Ser
43 48 53 58
tat ctc tct act aat aaa aag atg aaa tct gat gga tta gga gca tct 302
Tyr Leu Ser Thr Asn Lys Lys Met Lys Ser Asp Gly Leu Gly Ala Ser
59 64 69 74
gga cat tcg tca agt acc aat aga aat agt ata aat aaa act ctg aag 350
Gly His Ser Ser Ser Thr Asn Arg Asn Ser Ile Asn Lys Thr Leu Lys
75 80 85 90
caa gat gat gta aag gaa aaa gat ggt aca aaa ata gca tct aag att 398
Gln Asp Asp Val Lys Glu Lys Asp Gly Thr Lys Ile Ala Ser Lys Ile
91 96 101 106
aca aaa gaa cta aaa act ggg gga aaa aat gtt tct gga aag ccc aaa 446
Thr Lys Glu Leu Lys Thr Gly Gly Lys Asn Val Ser Gly Lys Pro Lys
107 112 117 122
act gta aca aaa tcc aaa aca gaa aat ggt gat aag gca cgg ttg gaa 494
Thr Val Thr Lys Ser Lys Thr Glu Asn Gly Asp Lys Ala Arg Leu Glu
123 128 133 138

aac atg tca cct aga caa gtt gta gaa aga tca gca aca gca gca gca	542
Asn Met Ser Pro Arg Gln Val Val Glu Arg Ser Ala Thr Ala Ala Ala	
139 144 149 154	
gca gca act gga cag aag aat tta cta aat gga aaa gga gtg aga aat	590
Ala Ala Thr Gly Gln Lys Asn Leu Leu Asn Gly Lys Gly Val Arg Asn	
155 160 165 170	
cag gaa ggg caa att tca ggt gcc aga ccc aag gta ctc aca gga aac	638
Gln Glu Gly Gln Ile Ser Gly Ala Arg Pro Lys Val Leu Thr Gly Asn	
171 176 181 186	
tta aat gtg caa gcc aaa gca aag cct ttg aag aaa gct aca ggg aag	686
Leu Asn Val Gln Ala Lys Ala Lys Pro Leu Lys Lys Ala Thr Gly Lys	
187 192 197 202	
gat tca cca tgc ctc agc atc gca gga ccc tcc agc aga tcc aca gat	734
Asp Ser Pro Cys Leu Ser Ile Ala Gly Pro Ser Ser Arg Ser Thr Asp	
203 208 213 218	
tca agt atg gaa ttc tca att tcc act gaa tgt ctg gat gaa ccg aaa	782
Ser Ser Met Glu Phe Ser Ile Ser Thr Glu Cys Leu Asp Glu Pro Lys	
219 224 229 234	
gaa aat gga tca aca gaa gaa gaa aag cct tct gga cat aaa cta tcc	830
Glu Asn Gly Ser Thr Glu Glu Glu Lys Pro Ser Gly His Lys Leu Ser	
235 240 245 250	
ttt tgt gat tct cca gga cag atg atg aaa aac agt gta gat agt gtc	878
Phe Cys Asp Ser Pro Gly Gln Met Met Lys Asn Ser Val Asp Ser Val	
251 256 261 266	
aaa aat tcc act gta gcc ata aaa tct cga cct gtt tca aga gtt acc	926
Lys Asn Ser Thr Val Ala Ile Lys Ser Arg Pro Val Ser Arg Val Thr	
267 272 277 282	
aat gga act tcc aat aaa aaa agt att cat gaa caa gac act aat gta	974
Asn Gly Thr Ser Asn Lys Lys Ser Ile His Glu Gln Asp Thr Asn Val	
283 288 293 298	
aat aac agt gta cta aag aaa gtc agt ggc aaa gga tgt agt gag cca	1022
Asn Asn Ser Val Leu Lys Lys Val Ser Gly Lys Gly Cys Ser Glu Pro	
299 304 309 314	
gta cca cag gca att ttg aag aaa aga gga act agc aat gga tgt act	1070
Val Pro Gln Ala Ile Leu Lys Lys Arg Gly Thr Ser Asn Gly Cys Thr	
315 320 325 330	
gca gct cag cag agg aca aag agt acc cca tct aat ctt act aaa act	1118
Ala Ala Gln Gln Arg Thr Lys Ser Thr Pro Ser Asn Leu Thr Lys Thr	
331 336 341 346	
caa gga tcc caa gga gag tca cca aac tca gta aaa tct tca gtc tct	1166
Gln Gly Ser Gln Gly Glu Ser Pro Asn Ser Val Lys Ser Ser Val Ser	
347 352 357 362	
tca agg cag tct gat gaa aat gtg gca aag ttg gac cac aat aca act	1214

Ser Arg Gln Ser Asp Glu Asn Val Ala Lys Leu Asp His Asn Thr Thr	
363 368 373 378	
aca gag aaa caa gca cct aag aga aaa atg gtc aag caa gta cac aca	1262
Thr Glu Lys Gln Ala Pro Lys Arg Lys Met Val Lys Gln Val His Thr	
379 384 389 394	
gct ttg cct aag gtt aat gca aaa ata gtg gca atg cct aaa aat cta	1310
Ala Leu Pro Lys Val Asn Ala Lys Ile Val Ala Met Pro Lys Asn Leu	
395 400 405 410	
aat cag tca aaa aaa ggt gaa act ttg aat aat aaa gat tca aaa cag	1358
Asn Gln Ser Lys Lys Gly Glu Thr Leu Asn Asn Lys Asp Ser Lys Gln	
411 416 421 426	
aaa atg cct cct gga cag gtt ata tca aaa act cag cct tcc tcc caa	1406
Lys Met Pro Pro Gly Gln Val Ile Ser Lys Thr Gln Pro Ser Ser Gln	
427 432 437 442	
aga cct tta aaa cat gaa aca tct act gtc caa aaa agt atg ttt cat	1454
Arg Pro Leu Lys His Glu Thr Ser Thr Val Gln Lys Ser Met Phe His	
443 448 453 458	
gat gtg cgt gat aat aac aac aag gac agt gtt tct gaa cag aag cct	1502
Asp Val Arg Asp Asn Asn Asn Lys Asp Ser Val Ser Glu Gln Lys Pro	
459 464 469 474	
cac aaa cct ctc att aat ctt gca tct gaa ata agt gat gca gaa gca	1550
His Lys Pro Leu Ile Asn Leu Ala Ser Glu Ile Ser Asp Ala Glu Ala	
475 480 485 490	
ctc cag tca tcc tgc agg cct gac cca caa aag cca tta aac gat caa	1598
Leu Gln Ser Ser Cys Arg Pro Asp Pro Gln Lys Pro Leu Asn Asp Gln	
491 496 501 506	
gaa aaa gag aag ttg gcg tta gaa tgc caa aat att tca aag ctg gat	1646
Glu Lys Glu Lys Leu Ala Leu Glu Cys Gln Asn Ile Ser Lys Leu Asp	
507 512 517 522	
aaa tca tta aaa cac gaa ctg gaa tca aaa cag att tgt tta gat aaa	1694
Lys Ser Leu Lys His Glu Leu Glu Ser Lys Gln Ile Cys Leu Asp Lys	
523 528 533 538	
agt gaa aca aaa ttt ccc aat cac aaa gaa aca gat gat tgc gat gca	1742
Ser Glu Thr Lys Phe Pro Asn His Lys Glu Thr Asp Asp Cys Asp Ala	
539 544 549 554	
gct aac ata tgt tgt cat tct gtt ggg agt gat aat gta aat tca aaa	1790
Ala Asn Ile Cys Cys His Ser Val Gly Ser Asp Asn Val Asn Ser Lys	
555 560 565 570	
ttt tat agc acc aca gcc cta aaa tac atg gtt tca aat cca aat gaa	1838
Phe Tyr Ser Thr Thr Ala Leu Lys Tyr Met Val Ser Asn Pro Asn Glu	
571 576 581 586	
aac tcc ttg aac tct aat cca gtt tgt gat tta gac tca aca agt gca	1886
Asn Ser Leu Asn Ser Asn Pro Val Cys Asp Leu Asp Ser Thr Ser Ala	

587	592	597	602	
ggg caa atc cat ttg Gly Gln Ile His Leu 603	ata tca gat agg gag aac caa gta ggg aga aaa Ile Ser Asp Arg Glu Asn Gln Val Gly Arg Lys 608			1934
gat aca aac aaa caa tca agt att aaa tgt gtg gaa gat gtt tca ctg Asp Thr Asn Lys Gln Ser Ser Ile Lys Cys Val Glu Asp Val Ser Leu 619				1982
tgt aat cct gaa agg aca aat ggt acc tta aat tct gct caa gaa gac Cys Asn Pro Glu Arg Thr Asn Gly Thr Leu Asn Ser Ala Gln Glu Asp 635				2030
aaa aaa tcg aaa gtt cct gtg gaa gga ctg aca att cct agt aag ttg Lys Lys Ser Lys Val Pro Val Glu Gly Leu Thr Ile Pro Ser Lys Leu 651				2078
tca gat gaa tct gct atg gat gaa gac aaa cat gct aca gca gac tca Ser Asp Glu Ser Ala Met Asp Glu Asp Lys His Ala Thr Ala Asp Ser 667				2126
gat gta tct tcc aag tgt ttt tcg gga cag cta tca gaa aaa aat tct Asp Val Ser Ser Lys Cys Phe Ser Gly Gln Leu Ser Glu Lys Asn Ser 683				2174
cct aaa aat atg gaa aca tca gaa tct cca gag agc cat gaa act cca Pro Lys Asn Met Glu Thr Ser Glu Ser Pro Glu Ser His Glu Thr Pro 699				2222
gaa act cca ttt gtg ggt cac tgg aat ttg agt act ggt gtt ctg cat Glu Thr Pro Phe Val Gly His Trp Asn Leu Ser Thr Gly Val Leu His 715				2270
cag cga gag agt cct gaa tct gac act ggc agt gct acc acc tcc tcc Gln Arg Glu Ser Pro Glu Ser Asp Thr Gly Ser Ala Thr Thr Ser Ser 731				2318
gat gac ata aag ccc aga tct gaa gac tat gat gct gga ggg tct cag Asp Asp Ile Lys Pro Arg Ser Glu Asp Tyr Asp Ala Gly Gly Ser Gln 747				2366
gat gat gat ggg tca aat gac aga ggt atc tct aaa tgt ggc act atg Asp Asp Asp Gly Ser Asn Asp Arg Gly Ile Ser Lys Cys Gly Thr Met 763				2414
ctg tgc cat gat ttt ctt gga aga agt agc agt gat acc agt act cct Leu Cys His Asp Phe Leu Gly Arg Ser Ser Ser Asp Thr Ser Thr Pro 779				2462
gaa gaa tta aaa att tat gat agt aat tta aga att gaa gta aaa atg Glu Glu Leu Lys Ile Tyr Asp Ser Asn Leu Arg Ile Glu Val Lys Met 795				2510
aaa aag caa agt agt aat gat ctt ttc caa gtt aat tca acg agt gat Lys Lys Gln Ser Ser Asn Asp Leu Phe Gln Val Asn Ser Thr Ser Asp 811				2558

gat gaa atc cct agg aaa agg cca gaa att tgg tct cga tct gca ata	2606
Asp Glu Ile Pro Arg Lys Arg Pro Glu Ile Trp Ser Arg Ser Ala Ile	
827 832 837 842	
ggt cac tct agg gaa aga gaa aat att cca cga ggc agt gtc cag ttt	2654
Val His Ser Arg Glu Arg Glu Asn Ile Pro Arg Gly Ser Val Gln Phe	
843 848 853 858	
gct cag gaa ata gat cag gta tct tct tca gca gat gaa aca gaa gat	2702
Ala Gln Glu Ile Asp Gln Val Ser Ser Ser Ala Asp Glu Thr Glu Asp	
859 864 869 874	
gaa aga tct gaa gct gaa aac gtt gca gaa aat ttc tct ata tct aac	2750
Glu Arg Ser Glu Ala Glu Asn Val Ala Glu Asn Phe Ser Ile Ser Asn	
875 880 885 890	
cca gct cct cag cag ttt cag gga ata att aat tta gct ttt gaa gat	2798
Pro Ala Pro Gln Gln Phe Gln Gly Ile Ile Asn Leu Ala Phe Glu Asp	
891 896 901 906	
gca act gaa aat gaa tgt cgt gaa ttt tct gca aat aaa aag ttt aaa	2846
Ala Thr Glu Asn Glu Cys Arg Glu Phe Ser Ala Asn Lys Lys Phe Lys	
907 912 917 922	
agg tca gtt tta ctt tca gtc gat gaa tgt gaa gag ctg gga tca gat	2894
Arg Ser Val Leu Leu Ser Val Asp Glu Cys Glu Glu Leu Gly Ser Asp	
923 928 933 938	
gaa gga gaa gtc cat act ccc ttt cag gct tct gta gat tct ttt tca	2942
Glu Gly Glu Val His Thr Pro Phe Gln Ala Ser Val Asp Ser Phe Ser	
939 944 949 954	
cct tct gat gtt ttt gat ggc att tct cat gaa cat cat gga agg acc	2990
Pro Ser Asp Val Phe Asp Gly Ile Ser His Glu His His Gly Arg Thr	
955 960 965 970	
tgc tat tcc aga ttc tca cga gaa agt gaa gat aat att tta gaa tgt	3038
Cys Tyr Ser Arg Phe Ser Arg Glu Ser Glu Asp Asn Ile Leu Glu Cys	
971 976 981 986	
aaa caa aat aaa ggc aat agt gta tgt aaa aat gaa agc act gtc ttg	3086
Lys Gln Asn Lys Gly Asn Ser Val Cys Lys Asn Glu Ser Thr Val Leu	
987 992 997 1002	
gat ctt agt agc att gac tct tca aga aaa aat aaa cag agt gtt tca	3134
Asp Leu Ser Ser Ile Asp Ser Ser Arg Lys Asn Lys Gln Ser Val Ser	
1003 1008 1013 1018	
gcc aca gaa aaa aag aac aca ata gac gtc cta tcc agt aga agc aga	3182
Ala Thr Glu Lys Lys Asn Thr Ile Asp Val Leu Ser Ser Arg Ser Arg	
1019 1024 1029 1034	
cag ctt ctt cga gaa gat aaa aaa gta aac aat gga agc aat gtg gaa	3230
Gln Leu Leu Arg Glu Asp Lys Lys Val Asn Asn Gly Ser Asn Val Glu	
1035 1040 1045 1050	

aat gac att cag caa cgc agc aaa ttc ttg gat agt gat gta aaa tct	3278
Asn Asp Ile Gln Gln Arg Ser Lys Phe Leu Asp Ser Asp Val Lys Ser	
1051 1056 1061 1066	
caa gaa aga cca tgt cac ttg gat ctt cat caa aga gaa ccc aat tct	3326
Gln Glu Arg Pro Cys His Leu Asp Leu His Gln Arg Glu Pro Asn Ser	
1067 1072 1077 1082	
gac ata cca aag aac agc tct aca aaa tct cta gac tcc ttt cgg agt	3374
Asp Ile Pro Lys Asn Ser Ser Thr Lys Ser Leu Asp Ser Phe Arg Ser	
1083 1088 1093 1098	
caa gtt ctg cct cag gaa ggt cca gtg aaa gag agc cat tct aca act	3422
Gln Val Leu Pro Gln Glu Gly Pro Val Lys Glu Ser His Ser Thr Thr	
1099 1104 1109 1114	
act gaa aaa gct aat att gct tta tct gca gga gac ata gat gat tgt	3470
Thr Glu Lys Ala Asn Ile Ala Leu Ser Ala Gly Asp Ile Asp Asp Cys	
1115 1120 1125 1130	
gac aca ctg gca caa acc cgc atg tat gac cat cgg cct tca aaa acc	3518
Asp Thr Leu Ala Gln Thr Arg Met Tyr Asp His Arg Pro Ser Lys Thr	
1131 1136 1141 1146	
ctg tct cca ata tat gag atg gat gta ata gaa gca ttt gag cag aaa	3566
Leu Ser Pro Ile Tyr Glu Met Asp Val Ile Glu Ala Phe Glu Gln Lys	
1147 1152 1157 1162	
gtg gaa tca gaa aca cat gtt aca gat atg gat ttt gaa gat gac caa	3614
Val Glu Ser Glu Thr His Val Thr Asp Met Asp Phe Glu Asp Asp Gln	
1163 1168 1173 1178	
cat ttt gca aaa caa gat tgg aca cta cta aag caa ctg ctc tct gaa	3662
His Phe Ala Lys Gln Asp Trp Thr Leu Leu Lys Gln Leu Leu Ser Glu	
1179 1184 1189 1194	
cag gat tca aac tta gat gtt aca aat tcc gtt cct gaa gac tta agt	3710
Gln Asp Ser Asn Leu Asp Val Thr Asn Ser Val Pro Glu Asp Leu Ser	
1195 1200 1205 1210	
tta gca cag tat cta atc aat cag aca cta ctt tta gca cga gat agc	3758
Leu Ala Gln Tyr Leu Ile Asn Gln Thr Leu Leu Leu Ala Arg Asp Ser	
1211 1216 1221 1226	
tca aaa cct cag ggt ata aca cat att gac act ttg aac aga tgg agt	3806
Ser Lys Pro Gln Gly Ile Thr His Ile Asp Thr Leu Asn Arg Trp Ser	
1227 1232 1237 1242	
gaa cta aca tct cca ctt gat tcc tca gcg agc atc acc atg gct agt	3854
Glu Leu Thr Ser Pro Leu Asp Ser Ser Ala Ser Ile Thr Met Ala Ser	
1243 1248 1253 1258	
ttt tcc tct gaa gat tgt tcg cct caa ggc gag tgg aca att ctg gaa	3902
Phe Ser Ser Glu Asp Cys Ser Pro Gln Gly Glu Trp Thr Ile Leu Glu	
1259 1264 1269 1274	
ctg gaa act cag cat taa gtgtta acatttttga aaaatttatg ccactccttt	3956

Leu Glu Thr Gln His *
1275 1280

atTTTTtgat gcctatatta tatccaaatg ataattgcat tagccggata taaactttct 4016
ttaatattga gtctttccaa tttaatgagg taaacatagt ttatttatta atatatcaca 4076
tatagaaaaa tgtttttcta aagtttttga gcatgttttc tctaattatt agagaaatta 4136
gaagacttat aaggaaacco tagcttcagt tttcctttcc tagctgatga tttgttcact 4196
taatcattat tcaagaattt aaaatgtgaa tgcagaagta gatcagtccc tttacttttt 4256
gctctgcata gggtaacata gtaatttaac aataaaaact taccgtgctt gtgtccaaaa 4316
aaaaaaa 4323

<210> 135
<211> 6320
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (237) .. (5549)

<400> 135
taagcttgcg gccgccggcc tcctaggagc gctgcacctg gtgatgaccc tcgtagtggc 60
tgcggcgcgcg cgccgagaag gaagcattcg ttcagtcaga gagcataata gaagtactgc 120
gttttgatga tggaggggcta ctacagaccg agacaacact tggactcagt tcatatcage 180
agaaaagtat atctctctac cgggggaatt gcaggcccat acgatttgag ccacca 236
atg ctg gat ttc cat gaa caa cca gtt gga atg cca aaa atg gaa aaa 284
Met Leu Asp Phe His Glu Gln Pro Val Gly Met Pro Lys Met Glu Lys
1 5 10 15
gtc tac tta cat aat cct agt tct gaa gaa acg att act tta gta tca 332
Val Tyr Leu His Asn Pro Ser Ser Glu Glu Thr Ile Thr Leu Val Ser
17 22 27 32
ata tct gct aca aca tca cat ttt cat gca tca ttt ttt caa aat agg 380
Ile Ser Ala Thr Thr Ser His Phe His Ala Ser Phe Phe Gln Asn Arg
33 38 43 48
aaa att ctt oca gga gga aat aca tca ttt gat gta gtt ttt ctt gca 428
Lys Ile Leu Pro Gly Gly Asn Thr Ser Phe Asp Val Val Phe Leu Ala
49 54 59 64
aga gta gta gga aat gta gaa aat act tta ttt att aat aca tct aat 476
Arg Val Val Gly Asn Val Glu Asn Thr Leu Phe Ile Asn Thr Ser Asn
65 70 75 80

cat ggg gta ttt act tac cag gta ttt ggt gtt gga gtt cca aat cca	524
His Gly Val Phe Thr Tyr Gln Val Phe Gly Val Gly Val Pro Asn Pro	
81 86 91 96	
tat cga ttg agg ccg ttc ctt ggg gcc aga gtc cct gtg aat agc agt	572
Tyr Arg Leu Arg Pro Phe Leu Gly Ala Arg Val Pro Val Asn Ser Ser	
97 102 107 112	
ttc tca cct ata ata aac atc cac aat cct cac agt gag cct tta cag	620
Phe Ser Pro Ile Ile Asn Ile His Asn Pro His Ser Glu Pro Leu Gln	
113 118 123 128	
gtt gta gaa atg tac tct agt gga gga gac ctt cac cta gaa ctc cca	668
Val Val Glu Met Tyr Ser Ser Gly Gly Asp Leu His Leu Glu Leu Pro	
129 134 139 144	
acg ggt caa caa gga ggt acc aga aaa ctg tgg gaa att cct cct tat	716
Thr Gly Gln Gln Gly Gly Thr Arg Lys Leu Trp Glu Ile Pro Pro Tyr	
145 150 155 160	
gaa acc aag gga gtg atg aga gcc agt ttt tca tct aga gaa gca gat	764
Glu Thr Lys Gly Val Met Arg Ala Ser Phe Ser Ser Arg Glu Ala Asp	
161 166 171 176	
aat cac aca gcc ttc ata aga ata aag act aat gct tca gac agc aca	812
Asn His Thr Ala Phe Ile Arg Ile Lys Thr Asn Ala Ser Asp Ser Thr	
177 182 187 192	
gag ttt atc att ctt cct gtt gag gtt gaa gtt aca aca gct cct gga	860
Glu Phe Ile Ile Leu Pro Val Glu Val Glu Val Thr Thr Ala Pro Gly	
193 198 203 208	
att tat tcc tca act gaa atg tta gat ttt ggt aca cta aga aca caa	908
Ile Tyr Ser Ser Thr Glu Met Leu Asp Phe Gly Thr Leu Arg Thr Gln	
209 214 219 224	
gat cta cca aaa gtt tta aac ctt cat tta tta aat tca gga aca aaa	956
Asp Leu Pro Lys Val Leu Asn Leu His Leu Leu Asn Ser Gly Thr Lys	
225 230 235 240	
gat gta cca ata aca agt gtt cga cct aca cca caa aat gat gct ata	1004
Asp Val Pro Ile Thr Ser Val Arg Pro Thr Pro Gln Asn Asp Ala Ile	
241 246 251 256	
acg gta cac ttt aaa cca att aca tta aaa gca tca gaa agt aaa tac	1052
Thr Val His Phe Lys Pro Ile Thr Leu Lys Ala Ser Glu Ser Lys Tyr	
257 262 267 272	
acc aag gtt gca agc att agt ttt gat gca tcg aag gca aaa aag cca	1100
Thr Lys Val Ala Ser Ile Ser Phe Asp Ala Ser Lys Ala Lys Lys Pro	
273 278 283 288	
tct cag ttt tct ggg aaa ata aca gtt aaa gca aag gaa aag agt tat	1148
Ser Gln Phe Ser Gly Lys Ile Thr Val Lys Ala Lys Glu Lys Ser Tyr	
289 294 299 304	
tct aaa ctt gaa ata cca tat caa gca gaa gtt tta gat ggt tat ttg	1196

Ser Lys Leu Glu Ile Pro Tyr Gln Ala Glu Val Leu Asp Gly Tyr Leu	
305 310 315 320	
gga ttt gat cat gct gca aca tta ttt cac atc cga gac agc cct gct	1244
Gly Phe Asp His Ala Ala Thr Leu Phe His Ile Arg Asp Ser Pro Ala	
321 326 331 336	
gat cct gtg gaa agg cca att tac ctt act aac act ttc agt ttt gcg	1292
Asp Pro Val Glu Arg Pro Ile Tyr Leu Thr Asn Thr Phe Ser Phe Ala	
337 342 347 352	
atc ctc att cac gat gtg ttg cta cca gaa gaa gcc aaa aca atg ttt	1340
Ile Leu Ile His Asp Val Leu Leu Pro Glu Glu Ala Lys Thr Met Phe	
353 358 363 368	
aaa gtt cac aac ttc agc aaa cca gtc tta att ctt cct aat gaa tca	1388
Lys Val His Asn Phe Ser Lys Pro Val Leu Ile Leu Pro Asn Glu Ser	
369 374 379 384	
gga tac att ttt acc ctg ctt ttt atg cct tcc aca tca tcc atg cac	1436
Gly Tyr Ile Phe Thr Leu Leu Phe Met Pro Ser Thr Ser Ser Met His	
385 390 395 400	
att gat aac aac att tta ctt att acc aat gct tct aaa ttt cat tta	1484
Ile Asp Asn Asn Ile Leu Leu Ile Thr Asn Ala Ser Lys Phe His Leu	
401 406 411 416	
ccc gtg cgg gta tac aca ggc ttt tta gat tac ttt gta ttg ccc ccc	1532
Pro Val Arg Val Tyr Thr Gly Phe Leu Asp Tyr Phe Val Leu Pro Pro	
417 422 427 432	
aaa ata gag gaa cgt ttc ata gat ttt gga gta ctg agt gct aca gaa	1580
Lys Ile Glu Glu Arg Phe Ile Asp Phe Gly Val Leu Ser Ala Thr Glu	
433 438 443 448	
gca agt aat att tta ttt gca att ata aac agc aat cca att gag ttg	1628
Ala Ser Asn Ile Leu Phe Ala Ile Ile Asn Ser Asn Pro Ile Glu Leu	
449 454 459 464	
gct ata aaa agt tgg cat atc ata gga gac ggt tta tca ata gaa ctt	1676
Ala Ile Lys Ser Trp His Ile Ile Gly Asp Gly Leu Ser Ile Glu Leu	
465 470 475 480	
gta gct gtg gaa aga ggc aat aga act aca ata att tca agc ctg cca	1724
Val Ala Val Glu Arg Gly Asn Arg Thr Thr Ile Ile Ser Ser Leu Pro	
481 486 491 496	
gag ttt gaa aaa tcc tct tta tca gat caa tca tcg gta aca tta gct	1772
Glu Phe Glu Lys Ser Ser Leu Ser Asp Gln Ser Ser Val Thr Leu Ala	
497 502 507 512	
tca ggc tat ttt gca gtc ttc aga gtc aaa ctt act gca aaa aaa tta	1820
Ser Gly Tyr Phe Ala Val Phe Arg Val Lys Leu Thr Ala Lys Lys Leu	
513 518 523 528	
gag ggg att cat gat gga gcc atc cag atc aca aca gac tat gag atc	1868
Glu Gly Ile His Asp Gly Ala Ile Gln Ile Thr Thr Asp Tyr Glu Ile	

529	534	539	544	
ctg aca atc cct gtg aag gct gtg att gca gta ggc tca ctg acc tgc				1916
Leu Thr Ile Pro Val Lys Ala Val Ile Ala Val Gly Ser Leu Thr Cys				
545	550	555	560	
ttc cct aag cac gtg gtt ctt cca cct tcc ttt cca ggg aaa ata gtt				1964
Phe Pro Lys His Val Val Leu Pro Pro Ser Phe Pro Gly Lys Ile Val				
561	566	571	576	
cat caa agt tta aat att atg aat tcc ttc tca cag aag gta aaa ata				2012
His Gln Ser Leu Asn Ile Met Asn Ser Phe Ser Gln Lys Val Lys Ile				
577	582	587	592	
cag caa ata cga tct ttg tca gaa gat gtg cga ttt tac tat aaa cga				2060
Gln Gln Ile Arg Ser Leu Ser Glu Asp Val Arg Phe Tyr Tyr Lys Arg				
593	598	603	608	
tta cgg ggc aat aag gaa gac ttg gag cca gga aaa aaa tca aag att				2108
Leu Arg Gly Asn Lys Glu Asp Leu Glu Pro Gly Lys Lys Ser Lys Ile				
609	614	619	624	
gca aac att tat ttt gat cct gga cta cag tgt ggg gat cat tgc tat				2156
Ala Asn Ile Tyr Phe Asp Pro Gly Leu Gln Cys Gly Asp His Cys Tyr				
625	630	635	640	
gtt ggc ttg cct ttt cta tcc aaa tct gaa ccc aaa gtg cag cct ggt				2204
Val Gly Leu Pro Phe Leu Ser Lys Ser Glu Pro Lys Val Gln Pro Gly				
641	646	651	656	
gta gcc atg cag gaa gat atg tgg gat gct gac tgg gat ttg cat caa				2252
Val Ala Met Gln Glu Asp Met Trp Asp Ala Asp Trp Asp Leu His Gln				
657	662	667	672	
agc ctg ttc aag gga tgg aca gga ata aag gaa aat tca ggt cat aga				2300
Ser Leu Phe Lys Gly Trp Thr Gly Ile Lys Glu Asn Ser Gly His Arg				
673	678	683	688	
ttg agt gct ata ttt gaa gta aat aca gac ctt caa aaa aat ata ata				2348
Leu Ser Ala Ile Phe Glu Val Asn Thr Asp Leu Gln Lys Asn Ile Ile				
689	694	699	704	
tca aaa atc act gct gag ctc tcc tgg cct tcc ata ctt agc tca ccc				2396
Ser Lys Ile Thr Ala Glu Leu Ser Trp Pro Ser Ile Leu Ser Ser Pro				
705	710	715	720	
cgg cac ttg aaa ttt cca ctt act aat aca aac tgc tcc tca gaa gaa				2444
Arg His Leu Lys Phe Pro Leu Thr Asn Thr Asn Cys Ser Ser Glu Glu				
721	726	731	736	
gag att act tta gaa aat cct gca gat gtt cct gtc tat gtt cag ttt				2492
Glu Ile Thr Leu Glu Asn Pro Ala Asp Val Pro Val Tyr Val Gln Phe				
737	742	747	752	
att cct ctg gct tta tat tcc aac cct tca gtg ttt gta gat aag tta				2540
Ile Pro Leu Ala Leu Tyr Ser Asn Pro Ser Val Phe Val Asp Lys Leu				
753	758	763	768	

gta tca agg ttt aac ttg agt aag gtg gca aag ata gat ttg aga aca	2588
Val Ser Arg Phe Asn Leu Ser Lys Val Ala Lys Ile Asp Leu Arg Thr	
769 774 779 784	
cta gaa ttt caa gtc ttc aga aac agt gct cat cca ctg cag agt tca	2636
Leu Glu Phe Gln Val Phe Arg Asn Ser Ala His Pro Leu Gln Ser Ser	
785 790 795 800	
aca gga ttt atg gag ggc ctc tct cga cat tta att tta aac cta att	2684
Thr Gly Phe Met Glu Gly Leu Ser Arg His Leu Ile Leu Asn Leu Ile	
801 806 811 816	
tta aaa cct gga gaa aag aaa tct gtc aaa gta aag ttt act cca gtt	2732
Leu Lys Pro Gly Glu Lys Lys Ser Val Lys Val Lys Phe Thr Pro Val	
817 822 827 832	
cac aac aga act gtt tct tca ctt atc ata gtc aga aat aac ctg act	2780
His Asn Arg Thr Val Ser Ser Leu Ile Ile Val Arg Asn Asn Leu Thr	
833 838 843 848	
gtg atg gat gct gtg atg gtc caa gga caa gga aca act gag aac ttg	2828
Val Met Asp Ala Val Met Val Gln Gly Gln Gly Thr Thr Glu Asn Leu	
849 854 859 864	
agg gtg gca ggc aag ctt cca ggt cca gga agc tcc tta cgc ttt aaa	2876
Arg Val Ala Gly Lys Leu Pro Gly Pro Gly Ser Ser Leu Arg Phe Lys	
865 870 875 880	
atc acg gaa gca ttg tta aaa gat tgt aca gat agt tta aaa cta aga	2924
Ile Thr Glu Ala Leu Leu Lys Asp Cys Thr Asp Ser Leu Lys Leu Arg	
881 886 891 896	
gaa cca aat ttc aca ttg aaa aga aca ttt aag gta gag aat aca gga	2972
Glu Pro Asn Phe Thr Leu Lys Arg Thr Phe Lys Val Glu Asn Thr Gly	
897 902 907 912	
caa ctt caa att cac ata gaa acc att gaa atc agt gga tac tca tgt	3020
Gln Leu Gln Ile His Ile Glu Thr Ile Glu Ile Ser Gly Tyr Ser Cys	
913 918 923 928	
gaa gga tat ggc ttt aaa gtt gtt aat tgt caa gag ttt act cta agt	3068
Glu Gly Tyr Gly Phe Lys Val Val Asn Cys Gln Glu Phe Thr Leu Ser	
929 934 939 944	
gcc aat gct tct aga gat ata atc ata ttg ttt act cct gat ttt aca	3116
Ala Asn Ala Ser Arg Asp Ile Ile Ile Leu Phe Thr Pro Asp Phe Thr	
945 950 955 960	
gct tct aga gtt att cgg gaa ctg aag ttt ata aca acc agt ggc tct	3164
Ala Ser Arg Val Ile Arg Glu Leu Lys Phe Ile Thr Thr Ser Gly Ser	
961 966 971 976	
gag ttt gta ttt ata ttg aat gca tcc ctt cct tac cat atg tta gca	3212
Glu Phe Val Phe Ile Leu Asn Ala Ser Leu Pro Tyr His Met Leu Ala	
977 982 987 992	

acc tgt gca gaa gcc cta ccc aga cct aac tgg gaa ctg gct ctg tat	3260
Thr Cys Ala Glu Ala Leu Pro Arg Pro Asn Trp Glu Leu Ala Leu Tyr	
993 998 1003 1008	
atc atc atc tca gga ata atg agt gca ctg ttt ctt ttg gtc att gga	3308
Ile Ile Ile Ser Gly Ile Met Ser Ala Leu Phe Leu Leu Val Ile Gly	
1009 1014 1019 1024	
aca gcc tat ttg gaa gct caa gga ata tgg gag cca ttt cga agg cgg	3356
Thr Ala Tyr Leu Glu Ala Gln Gly Ile Trp Glu Pro Phe Arg Arg Arg	
1025 1030 1035 1040	
cta tcc ttt gag gcc tcg aac ccg ccc ttc gat gtg gga agg cca ttt	3404
Leu Ser Phe Glu Ala Ser Asn Pro Pro Phe Asp Val Gly Arg Pro Phe	
1041 1046 1051 1056	
gat ctc agg aga atc gtt ggt att tca tct gaa gga aac ttg aac aca	3452
Asp Leu Arg Arg Ile Val Gly Ile Ser Ser Glu Gly Asn Leu Asn Thr	
1057 1062 1067 1072	
ctc agc tgt gac ccc ggt cac agt agg ggg ttc tgt gga gca ggc ggt	3500
Leu Ser Cys Asp Pro Gly His Ser Arg Gly Phe Cys Gly Ala Gly Gly	
1073 1078 1083 1088	
tca tca tcc cga ccc agt gcc ggg agt cat aag cag tgt ggc cca tcg	3548
Ser Ser Ser Arg Pro Ser Ala Gly Ser His Lys Gln Cys Gly Pro Ser	
1089 1094 1099 1104	
gtc cac cca cac agc agt cac agc aat aga aac tca gct gac gtg gaa	3596
Val His Pro His Ser Ser His Ser Asn Arg Asn Ser Ala Asp Val Glu	
1105 1110 1115 1120	
aac gtc aga gcc aaa aac agt tca agt acc tct agt agg act tct gct	3644
Asn Val Arg Ala Lys Asn Ser Ser Ser Thr Ser Ser Arg Thr Ser Ala	
1121 1126 1131 1136	
caa gca gct tct tca cag tct gct aac aaa aca agc ccc ctt gtc tta	3692
Gln Ala Ala Ser Ser Gln Ser Ala Asn Lys Thr Ser Pro Leu Val Leu	
1137 1142 1147 1152	
gat tcg aac aca gtg act caa ggt cat aca gcg ggc aga aag tcc aaa	3740
Asp Ser Asn Thr Val Thr Gln Gly His Thr Ala Gly Arg Lys Ser Lys	
1153 1158 1163 1168	
ggg gca aag cag agc cag cac ggc agc cag cac cat gcc cac agc ccg	3788
Gly Ala Lys Gln Ser Gln His Gly Ser Gln His His Ala His Ser Pro	
1169 1174 1179 1184	
ctg gag cag cac cct cag cct cct ctg cca ccg cca gtg cct cag ccc	3836
Leu Glu Gln His Pro Gln Pro Pro Leu Pro Pro Pro Val Pro Gln Pro	
1185 1190 1195 1200	
cag gag ccg cag cct gaa agg ctg tct ccc gcc ccc ctc gca cac cct	3884
Gln Glu Pro Gln Pro Glu Arg Leu Ser Pro Ala Pro Leu Ala His Pro	
1201 1206 1211 1216	
tcc cac cca gaa cgt gcc agc agc gcg agg cac agt tcc gag gac tcg	3932

1011
 1012
 1013
 1014
 1015
 1016
 1017
 1018
 1019
 1020
 1021
 1022
 1023
 1024
 1025
 1026
 1027
 1028
 1029
 1030
 1031
 1032
 1033
 1034
 1035
 1036
 1037
 1038
 1039
 1040
 1041
 1042
 1043
 1044
 1045
 1046
 1047
 1048
 1049
 1050
 1051
 1052
 1053
 1054
 1055
 1056
 1057
 1058
 1059
 1060
 1061
 1062
 1063
 1064
 1065
 1066
 1067
 1068
 1069
 1070
 1071
 1072
 1073
 1074
 1075
 1076
 1077
 1078
 1079
 1080
 1081
 1082
 1083
 1084
 1085
 1086
 1087
 1088
 1089
 1090
 1091
 1092
 1093
 1094
 1095
 1096
 1097
 1098
 1099
 1100
 1101
 1102
 1103
 1104
 1105
 1106
 1107
 1108
 1109
 1110
 1111
 1112
 1113
 1114
 1115
 1116
 1117
 1118
 1119
 1120
 1121
 1122
 1123
 1124
 1125
 1126
 1127
 1128
 1129
 1130
 1131
 1132
 1133
 1134
 1135
 1136
 1137
 1138
 1139
 1140
 1141
 1142
 1143
 1144
 1145
 1146
 1147
 1148
 1149
 1150
 1151
 1152
 1153
 1154
 1155
 1156
 1157
 1158
 1159
 1160
 1161
 1162
 1163
 1164
 1165
 1166
 1167
 1168
 1169
 1170
 1171
 1172
 1173
 1174
 1175
 1176
 1177
 1178
 1179
 1180
 1181
 1182
 1183
 1184
 1185
 1186
 1187
 1188
 1189
 1190
 1191
 1192
 1193
 1194
 1195
 1196
 1197
 1198
 1199
 1200
 1201
 1202
 1203
 1204
 1205
 1206
 1207
 1208
 1209
 1210
 1211
 1212
 1213
 1214
 1215
 1216
 1217
 1218
 1219
 1220
 1221
 1222
 1223
 1224
 1225
 1226
 1227
 1228
 1229
 1230
 1231
 1232
 1233
 1234
 1235
 1236
 1237
 1238
 1239
 1240
 1241
 1242
 1243
 1244
 1245
 1246
 1247
 1248
 1249
 1250
 1251
 1252
 1253
 1254
 1255
 1256
 1257
 1258
 1259
 1260
 1261
 1262
 1263
 1264
 1265
 1266
 1267
 1268
 1269
 1270
 1271
 1272
 1273
 1274
 1275
 1276
 1277
 1278
 1279
 1280
 1281
 1282
 1283
 1284
 1285
 1286
 1287
 1288
 1289
 1290
 1291
 1292
 1293
 1294
 1295
 1296
 1297
 1298
 1299
 1300
 1301
 1302
 1303
 1304
 1305
 1306
 1307
 1308
 1309
 1310
 1311
 1312
 1313
 1314
 1315
 1316
 1317
 1318
 1319
 1320
 1321
 1322
 1323
 1324
 1325
 1326
 1327
 1328
 1329
 1330
 1331
 1332
 1333
 1334
 1335
 1336
 1337
 1338
 1339
 1340
 1341
 1342
 1343
 1344
 1345
 1346
 1347
 1348
 1349
 1350
 1351
 1352
 1353
 1354
 1355
 1356
 1357
 1358
 1359
 1360
 1361
 1362
 1363
 1364
 1365
 1366
 1367
 1368
 1369
 1370
 1371
 1372
 1373
 1374
 1375
 1376
 1377
 1378
 1379
 1380
 1381
 1382
 1383
 1384
 1385
 1386
 1387
 1388
 1389
 1390
 1391
 1392
 1393
 1394
 1395
 1396
 1397
 1398
 1399
 1400
 1401
 1402
 1403
 1404
 1405
 1406
 1407
 1408
 1409
 1410
 1411
 1412
 1413
 1414
 1415
 1416
 1417
 1418
 1419
 1420
 1421
 1422
 1423
 1424
 1425
 1426
 1427
 1428
 1429
 1430
 1431
 1432
 1433
 1434
 1435
 1436
 1437
 1438
 1439
 1440
 1441
 1442
 1443
 1444
 1445
 1446
 1447
 1448
 1449
 1450
 1451
 1452
 1453
 1454
 1455
 1456
 1457
 1458
 1459
 1460
 1461
 1462
 1463
 1464
 1465

1441	1446	1451	1456	
cac aaa cct ggc agc tct act gat agt ctt tat aaa ctt tct ctg caa				4652
His Lys Pro Gly Ser Ser Thr Asp Ser Leu Tyr Lys Leu Ser Leu Gln				
1457	1462	1467	1472	
acc ctc aac gca gac att ttc tta aaa caa cgc cag acc tca ccg aca				4700
Thr Leu Asn Ala Asp Ile Phe Leu Lys Gln Arg Gln Thr Ser Pro Thr				
1473	1478	1483	1488	
cct gct tcc ccg tct ccc cca gct gcc ccc tgc ccc ttt gtg gtc cgg				4748
Pro Ala Ser Pro Ser Pro Pro Ala Ala Pro Cys Pro Phe Val Val Arg				
1489	1494	1499	1504	
ggc agc tac agc agc atc gtc aac agc agc tcc agc agt gac cct aaa				4796
Gly Ser Tyr Ser Ser Ile Val Asn Ser Ser Ser Ser Ser Asp Pro Lys				
1505	1510	1515	1520	
ata aaa cag cca aat gga agc aaa cac aag ttg aca aag gca gcc tcg				4844
Ile Lys Gln Pro Asn Gly Ser Lys His Lys Leu Thr Lys Ala Ala Ser				
1521	1526	1531	1536	
ctc ccg ggc aag aac ggc aac ccc act ttt gct gca gtc acg gct ggc				4892
Leu Pro Gly Lys Asn Gly Asn Pro Thr Phe Ala Ala Val Thr Ala Gly				
1537	1542	1547	1552	
tac gac aag agc cca ggt ggg aat ggc ttt gct aaa gtt tct tca aac				4940
Tyr Asp Lys Ser Pro Gly Gly Asn Gly Phe Ala Lys Val Ser Ser Asn				
1553	1558	1563	1568	
aaa aca ggt ttc tcc agc agc ctt ggc att tca cac gct cct gtt gac				4988
Lys Thr Gly Phe Ser Ser Ser Leu Gly Ile Ser His Ala Pro Val Asp				
1569	1574	1579	1584	
agc gat ggc tca gac agc tcg ggt ttg tgg agt ccc gtc agc aac cca				5036
Ser Asp Gly Ser Asp Ser Ser Gly Leu Trp Ser Pro Val Ser Asn Pro				
1585	1590	1595	1600	
agc agc cct gac ttc act ccc ctc aat tcg ttc tcc gcc ttt gga aac				5084
Ser Ser Pro Asp Phe Thr Pro Leu Asn Ser Phe Ser Ala Phe Gly Asn				
1601	1606	1611	1616	
tct ttt aat cta act ggt gaa gtt ttc agc aaa ctc gga tta tct cga				5132
Ser Phe Asn Leu Thr Gly Glu Val Phe Ser Lys Leu Gly Leu Ser Arg				
1617	1622	1627	1632	
tcg tgc aat cag gcc tca cag agg agc tgg aac gag ttt aat agt ggc				5180
Ser Cys Asn Gln Ala Ser Gln Arg Ser Trp Asn Glu Phe Asn Ser Gly				
1633	1638	1643	1648	
cct tca tac ctt tgg gag tcg cca gcg aca gat ccc agt cct tcc tgg				5228
Pro Ser Tyr Leu Trp Glu Ser Pro Ala Thr Asp Pro Ser Pro Ser Trp				
1649	1654	1659	1664	
cca gcc agt tcc ggc tcc ccg acc cac aca gcc aca tcg gtc ctc ggt				5276
Pro Ala Ser Ser Gly Ser Pro Thr His Thr Ala Thr Ser Val Leu Gly				
1665	1670	1675	1680	

aac acc agc ggc ctg tgg tcc acc act cca ttc agc agc tcc att tgg	5324
Asn Thr Ser Gly Leu Trp Ser Thr Thr Pro Phe Ser Ser Ser Ile Trp	
1681 1686 1691 1696	
tcc agc aac ctt agc agc gcc ctt ccc ttc acc act cca gca aac acg	5372
Ser Ser Asn Leu Ser Ser Ala Leu Pro Phe Thr Thr Pro Ala Asn Thr	
1697 1702 1707 1712	
ctg gca agc atc ggc ctc atg ggc aca gaa aac tcc cct gct cct cac	5420
Leu Ala Ser Ile Gly Leu Met Gly Thr Glu Asn Ser Pro Ala Pro His	
1713 1718 1723 1728	
gct ccc tcc acc tcc agt cca gct gac gac ttg gga cag acc tac aac	5468
Ala Pro Ser Thr Ser Ser Pro Ala Asp Asp Leu Gly Gln Thr Tyr Asn	
1729 1734 1739 1744	
ccg tgg cgg ata tgg agc ccc acg att gga aga aga agc tcg gac cct	5516
Pro Trp Arg Ile Trp Ser Pro Thr Ile Gly Arg Arg Ser Ser Asp Pro	
1745 1750 1755 1760	
tgg tct aat tcg cac ttt cct cac gag aat taa attaagca aaaaacaaac	5567
Trp Ser Asn Ser His Phe Pro His Glu Asn *	
1761 1766 1771	
aaacatagtg ggccctcgtc tagatcatga tgtgccagtt tctgagacat ctttttaagg	5627
ctcttactgc agctcccttc cccaccctcc tcttctttgc aaaacagacc caagcagggc	5687
aggctcagac cactcgcttc tttcagatct ttcttgcaat tatgataaca tgagatttgc	5747
tgttgtgctt ttagagaaaa gtctggactc agccacaaac tctaataaga cctgtacatc	5807
tgagaacctt tcccgttact gcgttttcac cacctgtctt ccccatgctt tatttatctg	5867
tatgaacaca gatttgacat tacagctaag gaaataattt gagttgatto agaaatcctg	5927
gcatgtgaca attttggttaa attaccaagt ttgggtttta ataatttctc aatattatgc	5987
gccaagatct aattttaaaa ctgtatgagg actttgtgct gaaaatagag tattttttta	6047
aagtaaggct gtcttggttt aaaagcagat tacagaaatg taagtcaact taagaacggc	6107
gaatgaatgt aaaaacattc agttgagacc atatgcattt tctgtgctgt ttgtacttga	6167
ggtatgtaac atttgtatac ctgaacttat tttaaagatg aactgaaatg cacatagcca	6227
agtcttgaga tacaagattg aatgtgtatt tcttaaaaat acaactttgt gttgtacttt	6287
gaaataaatg atgctttttt caaaaaaaaaaaa aaa	6320

<210> 136
 <211> 1085
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (250)..(1059)

<400> 136

```
cccggtgatg tatatatcta tctattcgat gatgaagata cccacacaaa cccaaaaaaa      60
gagatctctc gaggatccga attcgcggcc gcgtcgacct ttatctgaat ctattgaatt      120
gagacgatca tgtgattttt ggccttcatt ctattgatgt aacgtataac gtttagtaat      180
ttgcataatt tgaactatct ttgcattcct gggataaatc ccacttgact gtgggatatt      240
attgatttg   atg tgt tgc tgg att tgg ttt gca ggc att ttg tgc aaa      288
              Met Cys Cys Trp Ile Trp Phe Ala Gly Ile Leu Cys Lys
                1             5             10

aat ttt gcg agg cgg cat gag gac ctg cgg cag gcc ctc ttc ggc agt      336
Asn Phe Ala Arg Arg His Glu Asp Leu Arg Gln Ala Leu Phe Gly Ser
  14             19             24             29

ctc tct ggc ccg ggt tcc ctc ggc gtg cta ctg tgc gct cga tcc agc      384
Leu Ser Gly Pro Gly Ser Leu Gly Val Leu Leu Cys Ala Arg Ser Ser
  30             35             40             45

acc atg ggg aag cgg gac aat cgg gtg gcc tat atg aac cca ata gca      432
Thr Met Gly Lys Arg Asp Asn Arg Val Ala Tyr Met Asn Pro Ile Ala
  46             51             56             61

atg gcg aga tca agg ggt cca atc cag tct tca ggg cca aca ata cag      480
Met Ala Arg Ser Arg Gly Pro Ile Gln Ser Ser Gly Pro Thr Ile Gln
  62             67             72             77

gat tat ctg aat cga cca agg cct acc tgg gaa gaa gta aaa gag caa      528
Asp Tyr Leu Asn Arg Pro Arg Pro Thr Trp Glu Glu Val Lys Glu Gln
  78             83             88             93

cta gaa aag aaa aag aaa ggc tcc aag gct ttg gct gaa ttt gaa gaa      576
Leu Glu Lys Lys Lys Lys Gly Ser Lys Ala Leu Ala Glu Phe Glu Glu
  94             99             104            109

aaa atg aat gag aac tgg aag aaa gaa ctg gaa aaa cac agg gag aaa      624
Lys Met Asn Glu Asn Trp Lys Lys Glu Leu Glu Lys His Arg Glu Lys
  110            115            120            125

ttg tta agt gga agt gag agc tca tcc aaa aaa aga cag aga aag aaa      672
Leu Leu Ser Gly Ser Glu Ser Ser Ser Lys Lys Arg Gln Arg Lys Lys
  126            131            136            141

aaa gaa aag aag aaa tct ggt agg tat tca tct tct tct tca tca agc      720
Lys Glu Lys Lys Lys Ser Gly Arg Tyr Ser Ser Ser Ser Ser Ser Ser
  142            147            152            157

tct gat tct tcc agc agt tct tct gat tct gaa gat gag gat aag aaa      768
Ser Asp Ser Ser Ser Ser Ser Ser Ser Asp Ser Glu Asp Glu Asp Lys Lys
```

158	163	168	173	
caa gga aaa cgg aga aag aaa aag aag aac cgt tca cat aaa tct tct				816
Gln Gly Lys Arg Arg Lys Lys Lys Lys Asn Arg Ser His Lys Ser Ser				
174	179	184	189	
gaa agc tcc atg tca gaa act gaa tca gac agt aag gat agt tta aaa				864
Glu Ser Ser Met Ser Glu Thr Glu Ser Asp Ser Lys Asp Ser Leu Lys				
190	195	200	205	
aag aaa aag aag tca aaa gat gga act gag aaa gaa aag gat att aaa				912
Lys Lys Lys Lys Ser Lys Asp Gly Thr Glu Lys Glu Lys Asp Ile Lys				
206	211	216	221	
gga ctc agc aaa aag aga aag atg tat tct gaa gat aaa cct tta tca				960
Gly Leu Ser Lys Lys Arg Lys Met Tyr Ser Glu Asp Lys Pro Leu Ser				
222	227	232	237	
tct gag tcc ttg tca gaa tca gag tat att gag gag gtg cga gca aaa				1008
Ser Glu Ser Leu Ser Glu Ser Glu Tyr Ile Glu Glu Val Arg Ala Lys				
238	243	248	253	
aag aag aaa agc agt gaa gaa cga gaa aaa gca aca gca agt atc tct				1056
Lys Lys Lys Ser Ser Glu Glu Arg Glu Lys Ala Thr Ala Ser Ile Ser				
254	259	264	269	
taa cgtttttaca gacaatagaa taggtg				1085
*				
270				
<210> 137				
<211> 809				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> (252)..(809)				
<400> 137				
atttggccct cgaggccaag aattcggcac gagccacggt ccaggctgga cacaaccaa				60
ggcggaggac ccgtggccca cgaagctcat ctttgaactg tccccgcctt ctccgcctt				120
gacttgtgac cctaggccct ttggggcgcc tctgaccag ctagccagat cccggacca				180
aacctgttc cctgtgaagg tgaaagtgga gaaatcagag ctggagatgg ccaaagccc				240
gaaccaactg g atg ctg tct tgc agt gtc tgc tgg aga aga gtc aca tgg				290
Met Leu Ser Cys Ser Val Cys Trp Arg Arg Val Thr Trp				
1	5	10		
aca ggg agc gtc tgg atg agg aag ctg gga aaa cac cct cag aca ccc				338

Thr	Gly	Ser	Val	Trp	Met	Arg	Lys	Leu	Gly	Lys	His	Pro	Gln	Thr	Pro		
14					19					24					29		
aca	ata	aac	aca	tat	gtg	atc	aag	ctg	ttc	gac	cgg	agc	gtg	gac	ttg	386	
Thr	Ile	Asn	Thr	Tyr	Val	Ile	Lys	Leu	Phe	Asp	Arg	Ser	Val	Asp	Leu		
30					35					40					45		
gcc	cag	ttc	agc	gag	aac	acg	cca	ctg	tac	cca	atc	tgc	cgc	gcc	tgg	434	
Ala	Gln	Phe	Ser	Glu	Asn	Thr	Pro	Leu	Tyr	Pro	Ile	Cys	Arg	Ala	Trp		
46					51					56					61		
atg	cgc	aac	agc	ccc	tct	gtg	cgc	gag	cgt	gaa	tgc	tct	ccc	agc	tca	482	
Met	Arg	Asn	Ser	Pro	Ser	Val	Arg	Glu	Arg	Glu	Cys	Ser	Pro	Ser	Ser		
62					67					72					77		
ccc	ctg	ccc	ccg	ctg	cct	gag	gat	gag	gag	ggc	tca	gag	gta	acc	aac	530	
Pro	Leu	Pro	Pro	Leu	Pro	Glu	Asp	Glu	Glu	Gly	Ser	Glu	Val	Thr	Asn		
78					83					88					93		
agc	aag	agt	cgt	gat	gtg	tac	aag	ctg	ccg	cca	ccc	aca	ccc	ccg	ggg	578	
Ser	Lys	Ser	Arg	Asp	Val	Tyr	Lys	Leu	Pro	Pro	Pro	Thr	Pro	Pro	Gly		
94					99					104					109		
cca	ccc	gga	gat	gcc	tgc	aga	tcc	cgc	atc	cca	tct	cca	ctg	cag	cct	626	
Pro	Pro	Gly	Asp	Ala	Cys	Arg	Ser	Arg	Ile	Pro	Ser	Pro	Leu	Gln	Pro		
110					115					120					125		
gag	atg	cag	ggc	acc	cct	gac	gat	gag	ccc	tct	gag	ccc	gag	ccc	tca	674	
Glu	Met	Gln	Gly	Thr	Pro	Asp	Asp	Glu	Pro	Ser	Glu	Pro	Glu	Pro	Ser		
126					131					136					141		
ccc	tcc	aca	ctc	atc	tat	cgc	aac	atg	cag	cgc	tgg	aaa	cgc	atc	cgc	722	
Pro	Ser	Thr	Leu	Ile	Tyr	Arg	Asn	Met	Gln	Arg	Trp	Lys	Arg	Ile	Arg		
142					147					152					157		
cag	agg	tgg	aag	gag	gcc	tct	cat	cgg	aac	cag	ctt	cgt	tac	tca	gaa	770	
Gln	Arg	Trp	Lys	Glu	Ala	Ser	His	Arg	Asn	Gln	Leu	Arg	Tyr	Ser	Glu		
158					163					168					173		
agc	atg	aag	atc	cta	cga	gag	atg	tac	gaa	cga	cag	tga				809	
Ser	Met	Lys	Ile	Leu	Arg	Glu	Met	Tyr	Glu	Arg	Gln	*					
174					179					184							

<210> 138
 <211> 5314
 <212> DNA
 <213> Homo sapiens

 <220> |
 <221> CDS
 <222> (531) .. (4376)

 <400> 138

aattttgaag ccggtcgctt gccctaccgg tccggaattc cggggtcgac gatttcgtgg	60
ttgtttagt aaccggggaa gcagccgtcg gcggctgccc tgagccttcc tggggaagga	120
ggagggaggt aggcgcagag cgcggtccac gcctgctcgc cccgaaccat gggaagatga	180
gacaggtaaaa cgcctgcgcc cgcgcgcttc cctaccctag ggaggagcat tcccgggtcc	240
gggctggcgc ctgcagcagg acttcccgtc cagagcccgaggagtagctgt tggcttccgg	300
gcgcgcgcgc ttgaatcgcg gctgcggggg cgtcccgtcc tcccggggg gagcatctgc	360
ggacctacgt gggattgggg tgagctgggg gtggggctga gaagcaaatt cctttcggga	420
gaggagtctc cttaggaatc tgtgccatcc aaattgcttg atccagtga tctgctagga	480
aaggctctctg agggccccgt ctgctgactg catgacaaac cctaaaggaa atg cca	536
	Met Pro
	1
atc gtg atg gcc cgg gac ctg gag gaa aca gca tca tcc tca gag gat	584
Ile Val Met Ala Arg Asp Leu Glu Glu Thr Ala Ser Ser Ser Glu Asp	
3 8 13 18	
gag gag gtc ata agt caa gag gat cat cca tgc atc atg tgg act gga	632
Glu Glu Val Ile Ser Gln Glu Asp His Pro Cys Ile Met Trp Thr Gly	
19 24 29 34	
ggc tgc agg aga att cca gtt ttg gta ttc cat gcc gac gct att ctt	680
Gly Cys Arg Arg Ile Pro Val Leu Val Phe His Ala Asp Ala Ile Leu	
35 40 45 50	
aca aag gac aac aat att aga gta att gga gaa cgt tat cat ttg tct	728
Thr Lys Asp Asn Asn Ile Arg Val Ile Gly Glu Arg Tyr His Leu Ser	
51 56 61 66	
tat aag att gta cga acg gac agt cgc cta gta cgc agc att ctg aca	776
Tyr Lys Ile Val Arg Thr Asp Ser Arg Leu Val Arg Ser Ile Leu Thr	
67 72 77 82	
gcc cat gga ttt cat gaa gtt cac cca agc agc act gac tat aac cta	824
Ala His Gly Phe His Glu Val His Pro Ser Ser Thr Asp Tyr Asn Leu	
83 88 93 98	
atg tgg aca gga tcc cac ctg aag ccc ttc tta ctg cgc acc ctc tct	872
Met Trp Thr Gly Ser His Leu Lys Pro Phe Leu Leu Arg Thr Leu Ser	
99 104 109 114	
gaa gca caa aaa gtt aat cac ttt ccc agg tct tat gaa ctt acc cgg	920
Glu Ala Gln Lys Val Asn His Phe Pro Arg Ser Tyr Glu Leu Thr Arg	
115 120 125 130	
aag gac cga ctg tac aaa aac att att cga atg cag cat aca cat gga	968
Lys Asp Arg Leu Tyr Lys Asn Ile Ile Arg Met Gln His Thr His Gly	
131 136 141 146	
ttc aag gtt ttt cac atc ctc ccc cag acc ttc ctc ctg cca gct gag	1016

Phe Lys Val Phe His Ile Leu Pro Gln Thr Phe Leu Leu Pro Ala Glu	
147 152 157 162	
tac gcg gaa ttt tgt aat tca tat tcg aag gac cgg gga cct tgg ata	1064
Tyr Ala Glu Phe Cys Asn Ser Tyr Ser Lys Asp Arg Gly Pro Trp Ile	
163 168 173 178	
gta aaa cca gtg gca tct tca agg ggg cgg ggc gtc tac ctg atc aac	1112
Val Lys Pro Val Ala Ser Ser Arg Gly Arg Gly Val Tyr Leu Ile Asn	
179 184 189 194	
aat cca aac cag atc tcc ctg gaa gag aac att ttg gtc tcc cgt tac	1160
Asn Pro Asn Gln Ile Ser Leu Glu Glu Asn Ile Leu Val Ser Arg Tyr	
195 200 205 210	
att aac aac ccc ctg ctc ata gat gat ttc aag ttt gac gtg cgc ctc	1208
Ile Asn Asn Pro Leu Leu Ile Asp Asp Phe Lys Phe Asp Val Arg Leu	
211 216 221 226	
tat gtg ctc gtg act tcc tat gat cct ctt gtc atc tat ctc tat gaa	1256
Tyr Val Leu Val Thr Ser Tyr Asp Pro Leu Val Ile Tyr Leu Tyr Glu	
227 232 237 242	
gaa gga ttg gct agg ttt gca act gtg cga tat gat caa gga gcc aag	1304
Glu Gly Leu Ala Arg Phe Ala Thr Val Arg Tyr Asp Gln Gly Ala Lys	
243 248 253 258	
aac att cgg aac cag ttc atg cat ctg aca aac tac agt gtc aac aag	1352
Asn Ile Arg Asn Gln Phe Met His Leu Thr Asn Tyr Ser Val Asn Lys	
259 264 269 274	
aaa agt gga gat tac gtc agt tgt gac gat cca gaa gtg gag gat tat	1400
Lys Ser Gly Asp Tyr Val Ser Cys Asp Asp Pro Glu Val Glu Asp Tyr	
275 280 285 290	
gga aac aaa tgg agc atg agt gct atg ctt agg tac ctg aaa caa gaa	1448
Gly Asn Lys Trp Ser Met Ser Ala Met Leu Arg Tyr Leu Lys Gln Glu	
291 296 301 306	
ggc aga gat aca acc gca ttg atg gcc cat gta gaa gac ctg atc att	1496
Gly Arg Asp Thr Thr Ala Leu Met Ala His Val Glu Asp Leu Ile Ile	
307 312 317 322	
aag act ata atc tct gct gaa cta gct att gct act gcc tgt aaa acc	1544
Lys Thr Ile Ile Ser Ala Glu Leu Ala Ile Ala Thr Ala Cys Lys Thr	
323 328 333 338	
ttt gtt cct cat cgc agc agt tgt ttt gaa ctc tat ggc ttt gac gtg	1592
Phe Val Pro His Arg Ser Ser Cys Phe Glu Leu Tyr Gly Phe Asp Val	
339 344 349 354	
ctc ata gat tct act ctg aag cca tgg ttg ttg gaa gtg aat ctc tct	1640
Leu Ile Asp Ser Thr Leu Lys Pro Trp Leu Leu Glu Val Asn Leu Ser	
355 360 365 370	
cct tct ttg gcc tgt gat gcg cct ctg gac cta aag att aaa gcc agt	1688
Pro Ser Leu Ala Cys Asp Ala Pro Leu Asp Leu Lys Ile Lys Ala Ser	

371	376	381	386	
atg att tca gat atg ttc act gtt gta gga ttt gtg tgc caa gat cct				1736
Met Ile Ser Asp Met Phe Thr Val Val Gly Phe Val Cys Gln Asp Pro				
387	392	397	402	
gcc cag cgg gca tca act cgg cca att tat ccc acc ttc gag tct tcc				1784
Ala Gln Arg Ala Ser Thr Arg Pro Ile Tyr Pro Thr Phe Glu Ser Ser				
403	408	413	418	
agg cga aac cct ttc cag aaa cct cag cgt tgc cgt cca ctc tct gcc				1832
Arg Arg Asn Pro Phe Gln Lys Pro Gln Arg Cys Arg Pro Leu Ser Ala				
419	424	429	434	
agt gat gcg gaa atg aaa aac ctc gtg ggc tca gcc cgg gag aaa ggg				1880
Ser Asp Ala Glu Met Lys Asn Leu Val Gly Ser Ala Arg Glu Lys Gly				
435	440	445	450	
cca ggg aag ttg ggt ggt tct gtg ctt ggt ctg tca atg gag gag atc				1928
Pro Gly Lys Leu Gly Gly Ser Val Leu Gly Leu Ser Met Glu Glu Ile				
451	456	461	466	
aaa gtt tta cga agg gtg aag gag gag aat gat cgg cga ggt gga ttt				1976
Lys Val Leu Arg Arg Val Lys Glu Glu Asn Asp Arg Arg Gly Gly Phe				
467	472	477	482	
att cgc ata ttt cct aca tct gag aca tgg gaa ata tat ggg tcc tac				2024
Ile Arg Ile Phe Pro Thr Ser Glu Thr Trp Glu Ile Tyr Gly Ser Tyr				
483	488	493	498	
ctc gag cat aag acc tca atg aac tat atg ctg gca aca cgc ctc ttc				2072
Leu Glu His Lys Thr Ser Met Asn Tyr Met Leu Ala Thr Arg Leu Phe				
499	504	509	514	
cag gac aga atg act gct gat gga gcg cca gaa ttg aag ata gag agt				2120
Gln Asp Arg Met Thr Ala Asp Gly Ala Pro Glu Leu Lys Ile Glu Ser				
515	520	525	530	
ctg aat tca aag gcc aag ctg cat gct gca ctt tac gag agg aag ctc				2168
Leu Asn Ser Lys Ala Lys Leu His Ala Ala Leu Tyr Glu Arg Lys Leu				
531	536	541	546	
ctg tct ctg gag gtg cga aaa cgt aga cga cgg agt agc aga ttg agg				2216
Leu Ser Leu Glu Val Arg Lys Arg Arg Arg Arg Ser Ser Arg Leu Arg				
547	552	557	562	
gca atg agg cca aaa tac cca gtg att acc caa cca gct gaa atg aat				2264
Ala Met Arg Pro Lys Tyr Pro Val Ile Thr Gln Pro Ala Glu Met Asn				
563	568	573	578	
gtt aaa act gag aca gag agt gaa gag gag gaa gaa gtc gca tta gat				2312
Val Lys Thr Glu Thr Glu Ser Glu Glu Glu Glu Glu Val Ala Leu Asp				
579	584	589	594	
aat gaa gat gaa gaa cag gag gct tcc cag gag gag tct gca gga ttt				2360
Asn Glu Asp Glu Glu Gln Glu Ala Ser Gln Glu Glu Ser Ala Gly Phe				
595	600	605	610	

ctt aga gaa aat caa gcc aaa tat aca ccc tca ttg aca gct ttg gta	2408
Leu Arg Glu Asn Gln Ala Lys Tyr Thr Pro Ser Leu Thr Ala Leu Val	
611 616 621 626	
gaa aat aca ccc aaa gaa aat tcc atg aaa gtt cgt gaa tgg aat aat	2456
Glu Asn Thr Pro Lys Glu Asn Ser Met Lys Val Arg Glu Trp Asn Asn	
627 632 637 642	
aaa ggt gga cac tgc tgc aaa ctt gag act cag gag cta gag cct aaa	2504
Lys Gly Gly His Cys Cys Lys Leu Glu Thr Gln Glu Leu Glu Pro Lys	
643 648 653 658	
ttt aac ctg atg cag att ctt caa gat aat ggc aat ctt agc aaa atg	2552
Phe Asn Leu Met Gln Ile Leu Gln Asp Asn Gly Asn Leu Ser Lys Met	
659 664 669 674	
cag gcc cga ata gca ttc tct gcc tat ctc cag cat gtt caa att cgc	2600
Gln Ala Arg Ile Ala Phe Ser Ala Tyr Leu Gln His Val Gln Ile Arg	
675 680 685 690	
ctg atg aaa gac agt ggc ggt cag acg ttc agt gcc agt tgg gct gcc	2648
Leu Met Lys Asp Ser Gly Gly Gln Thr Phe Ser Ala Ser Trp Ala Ala	
691 696 701 706	
aaa gag gat gaa cag atg gag ctg gtt gtt cgt ttc ctc aag cga gca	2696
Lys Glu Asp Glu Gln Met Glu Leu Val Val Arg Phe Leu Lys Arg Ala	
707 712 717 722	
tca aat aac ctc cag cat tca ctg agg atg gta tta ccc agt cga cga	2744
Ser Asn Asn Leu Gln His Ser Leu Arg Met Val Leu Pro Ser Arg Arg	
723 728 733 738	
ttg gca ctt ctg gaa cgc aga aga atc ctg gcc cac cag ctg ggt gac	2792
Leu Ala Leu Leu Glu Arg Arg Arg Ile Leu Ala His Gln Leu Gly Asp	
739 744 749 754	
ttt atc att gta tac aac aag gaa aca gaa caa atg gct gaa aag aaa	2840
Phe Ile Ile Val Tyr Asn Lys Glu Thr Glu Gln Met Ala Glu Lys Lys	
755 760 765 770	
tca aag aag aaa gtt gag gaa gaa gag gaa gat ggg gtg aat atg gaa	2888
Ser Lys Lys Lys Val Glu Glu Glu Glu Glu Asp Gly Val Asn Met Glu	
771 776 781 786	
aac ttt cag gag ttc atc aga caa gca agt gag gct gaa ctg gag gag	2936
Asn Phe Gln Glu Phe Ile Arg Gln Ala Ser Glu Ala Glu Leu Glu Glu	
787 792 797 802	
gtg ttg act ttt tat acc caa aag aac aag tct gct agt gtc ttc ctg	2984
Val Leu Thr Phe Tyr Thr Gln Lys Asn Lys Ser Ala Ser Val Phe Leu	
803 808 813 818	
ggg act cac tct aaa att tct aag aac aac aac aat tat tct gat agt	3032
Gly Thr His Ser Lys Ile Ser Lys Asn Asn Asn Asn Tyr Ser Asp Ser	
819 824 829 834	

ggg gca aaa ggt gat cac cct gag act ata atg gaa gaa gtg aaa ata	3080
Gly Ala Lys Gly Asp His Pro Glu Thr Ile Met Glu Glu Val Lys Ile	
835 840 845 850	
aag cca cct aaa cag caa cag acg aca gaa att cat tct gat aaa tta	3128
Lys Pro Pro Lys Gln Gln Gln Thr Thr Glu Ile His Ser Asp Lys Leu	
851 856 861 866	
tct cga ttt acc act tca gca gaa aaa gag gca aaa tta gtt tat agc	3176
Ser Arg Phe Thr Thr Ser Ala Glu Lys Glu Ala Lys Leu Val Tyr Ser	
867 872 877 882	
aat tcc tcc tct ggt cct act gct act ctg cag aaa att ccc aac acc	3224
Asn Ser Ser Ser Gly Pro Thr Ala Thr Leu Gln Lys Ile Pro Asn Thr	
883 888 893 898	
cat ttg tca tct gtt aca acc tct gac ctc tct cca ggg cct tgc cac	3272
His Leu Ser Ser Val Thr Thr Ser Asp Leu Ser Pro Gly Pro Cys His	
899 904 909 914	
cat tct tct tta tct caa att cct tca gct atc ccc agc atg cct cac	3320
His Ser Ser Leu Ser Gln Ile Pro Ser Ala Ile Pro Ser Met Pro His	
915 920 925 930	
cag cca aca att tta ctg aac aca gtc tct gcc agt gct tct ccc tgc	3368
Gln Pro Thr Ile Leu Leu Asn Thr Val Ser Ala Ser Ala Ser Pro Cys	
931 936 941 946	
cta cat ccc ggg gca cag aac atc cca agc cct act ggc ctg cca cgc	3416
Leu His Pro Gly Ala Gln Asn Ile Pro Ser Pro Thr Gly Leu Pro Arg	
947 952 957 962	
tgt cga tca gga agt cac acc att ggt ccc ttt tct tcc ttc caa agt	3464
Cys Arg Ser Gly Ser His Thr Ile Gly Pro Phe Ser Ser Phe Gln Ser	
963 968 973 978	
gct gca cac atc tat agc cag aaa ctg tct cgt ccc tct tca gca aag	3512
Ala Ala His Ile Tyr Ser Gln Lys Leu Ser Arg Pro Ser Ser Ala Lys	
979 984 989 994	
gca gga tcg tgc tat cta aac aag cat cat tca gga ata gcc aaa aca	3560
Ala Gly Ser Cys Tyr Leu Asn Lys His His Ser Gly Ile Ala Lys Thr	
995 1000 1005 1010	
caa aaa gag gga gaa gat gct tct tta tat agc aaa cgg tac aac caa	3608
Gln Lys Glu Gly Glu Asp Ala Ser Leu Tyr Ser Lys Arg Tyr Asn Gln	
1011 1016 1021 1026	
agt atg gtt aca gct gaa ctt cag cgg cta gct gag aag cag gca gcg	3656
Ser Met Val Thr Ala Glu Leu Gln Arg Leu Ala Glu Lys Gln Ala Ala	
1027 1032 1037 1042	
aga cag tat tct cca tcc agc cac atc aac ctc ctc acc caa cag gta	3704
Arg Gln Tyr Ser Pro Ser Ser His Ile Asn Leu Leu Thr Gln Gln Val	
1043 1048 1053 1058	
aca aac ctg aat ttg gca act ggc atc ata aac aga agc agt gct tca	3752

Thr Asn Leu Asn Leu Ala Thr Gly Ile Ile Asn Arg Ser Ser Ala Ser	
1059 1064 1069 1074	
gct ccc cca acc ctc cga ccc atc atc agt cct agt ggc ccg aca tgg	3800
Ala Pro Pro Thr Leu Arg Pro Ile Ile Ser Pro Ser Gly Pro Thr Trp	
1075 1080 1085 1090	
tct aca cag tca gac ccc caa gct ccc gag aat cac tcc agc tct cct	3848
Ser Thr Gln Ser Asp Pro Gln Ala Pro Glu Asn His Ser Ser Ser Pro	
1091 1096 1101 1106	
gga agc agg agc ctg cag aca ggg gga ttt gcc tgg gaa gga gaa gta	3896
Gly Ser Arg Ser Leu Gln Thr Gly Gly Phe Ala Trp Glu Gly Glu Val	
1107 1112 1117 1122	
gaa aac aac gtg tac agc cag gct aca ggg gtg gtc ccc cag cac aag	3944
Glu Asn Asn Val Tyr Ser Gln Ala Thr Gly Val Val Pro Gln His Lys	
1123 1128 1133 1138	
tat cac ccc aca gca ggc agc tat cag ctt caa ttt gcc ctg cag caa	3992
Tyr His Pro Thr Ala Gly Ser Tyr Gln Leu Gln Phe Ala Leu Gln Gln	
1139 1144 1149 1154	
ctt gaa caa caa aaa ctt cag tcc cgg cag ctc ctg gac cag agt cga	4040
Leu Glu Gln Gln Lys Leu Gln Ser Arg Gln Leu Leu Asp Gln Ser Arg	
1155 1160 1165 1170	
gcc cgg cac cag gca atc ttt ggc agc cag aca cta cct aac tcc aat	4088
Ala Arg His Gln Ala Ile Phe Gly Ser Gln Thr Leu Pro Asn Ser Asn	
1171 1176 1181 1186	
tta tgg aca atg aat aat ggt gca ggt tgt aga att tcc agt gcc aca	4136
Leu Trp Thr Met Asn Asn Gly Ala Gly Cys Arg Ile Ser Ser Ala Thr	
1187 1192 1197 1202	
gct agt ggc cag aag cca acc act ctg cca caa aaa gtg gta cca cct	4184
Ala Ser Gly Gln Lys Pro Thr Thr Leu Pro Gln Lys Val Val Pro Pro	
1203 1208 1213 1218	
cca agt tct tgc gcc tcc ctg gtt ccc aaa ccc cca ccc aac cac gaa	4232
Pro Ser Ser Cys Ala Ser Leu Val Pro Lys Pro Pro Pro Asn His Glu	
1219 1224 1229 1234	
caa gtg ctc aga agg gca aca tcc cag aaa gct tcc aaa ggg tcc tcc	4280
Gln Val Leu Arg Arg Ala Thr Ser Gln Lys Ala Ser Lys Gly Ser Ser	
1235 1240 1245 1250	
gcg gaa ggg cag ctg aat gga ctc cag agc agc ctt aac cct gca gcc	4328
Ala Glu Gly Gln Leu Asn Gly Leu Gln Ser Ser Leu Asn Pro Ala Ala	
1251 1256 1261 1266	
ttt gtg ccc atc acc agc tct aca gat cct gct cac act aaa ata tga	4376
Phe Val Pro Ile Thr Ser Ser Thr Asp Pro Ala His Thr Lys Ile *	
1267 1272 1277 1282	
accacaaaca cacagagaaa caacctgttc accactcctg ggtgcatgat tgagggtgaa	4436

gcatccacca gcaattcaag ggggtccatag tatttttttt tttgctgcct caaagtcccc 4496
 aaagccttcg agcagaagtg gcagtagatg gttgccaatc agccaatgca gactttcact 4556
 gggacaacaa gaaagcagat cttctgggtt ttgatggaac ttggcagtgg ggacattcag 4616
 ctgatgcatt atataccccg tcagagcaca cttgtatott ttaccttccc ttgccccat 4676
 gccccaaaac tgcttaggtc ttctctgtcc ctttactgct gctgcacaga gatgatataa 4736
 aagaggetct ttggctatit gcatittgct tcctottott ttccagatta cagtatgaag 4796
 ctttattttc tttgtacaag cttaaaatit caacatcatc atccgcaaa gttgttcctc 4856
 ccttttcgga ggatctaggg ggaaagagga gcattcatca caagtttcct agagagagga 4916
 gacaaatcgg tgtgccattg acaacatgag ccagggtaaa ggcacccttt ggaattactg 4976
 atttcaaaga ttaataaagt aattctatit ttattttctt ttttttcct ttactaattt 5036
 cccaacaatc aatattcaca aacaggactg aagtagaacc agttttttat tttactttgt 5096
 ggctgtgcaa ttttttaaac attttagaaa tgtgagctgt aaagagatgt tttattttta 5156
 catttcattt cagcagatgg tgggtccagg ctattcccaa aggcagctcc tgcacctggg 5216
 gagcgggcat gtgcagatgt ctccgttatc agccctcgac aggcaggctc actcacagcg 5276
 tgggcctcca gtggcttgag ccctgtatcc agttgcat 5314

<210> 139
 <211> 3262
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (60)..(2279)

<400> 139
 agcgggattc gatagcatatc tcagtgtggt ggaattcgtg acttctgaca gctctctcc 59
 atg gaa gga ggc ggc ggc cgc gat gag cct tca gcc tgc cgg gca ggg 107
 Met Glu Gly Gly Gly Gly Arg Asp Glu Pro Ser Ala Cys Arg Ala Gly
 1 5 10 15
 gac gtg aac atg gat gac cct aag aag gaa gac att ctt ctt ttg gcc 155
 Asp Val Asn Met Asp Asp Pro Lys Lys Glu Asp Ile Leu Leu Leu Ala
 17 22 27 32
 gat gaa aaa ttt gac ttc gat ott tca ttg tct tct tcg agt gca aat 203
 Asp Glu Lys Phe Asp Phe Asp Leu Ser Leu Ser Ser Ser Ser Ala Asn
 33 38 43 48
 gaa gat gat gaa gtc ttc ttc gga ccc ttt gga cat aaa gaa aga tgt 251

Glu	Asp	Asp	Glu	Val	Phe	Phe	Gly	Pro	Phe	Gly	His	Lys	Glu	Arg	Cys	
49					54					59					64	
att	gct	gcc	agc	ttg	gaa	tta	aat	aat	ccg	gtt	ccc	gaa	cag	cct	ccg	299
Ile	Ala	Ala	Ser	Leu	Glu	Leu	Asn	Asn	Pro	Val	Pro	Glu	Gln	Pro	Pro	
65					70					75					80	
ttg	ccc	aca	tct	gag	agt	ccc	ttt	gcc	tgg	agc	cct	ctg	gcc	ggg	gag	347
Leu	Pro	Thr	Ser	Glu	Ser	Pro	Phe	Ala	Trp	Ser	Pro	Leu	Ala	Gly	Glu	
81					86					91					96	
aag	ttc	gtg	gag	gtg	tac	aaa	gaa	gct	cac	tta	ctg	gct	tta	cac	att	395
Lys	Phe	Val	Glu	Val	Tyr	Lys	Glu	Ala	His	Leu	Leu	Ala	Leu	His	Ile	
97					102					107					112	
gag	agc	agc	agc	cgg	aac	cag	gca	gcc	caa	gct	gcc	aag	cct	gaa	gac	443
Glu	Ser	Ser	Ser	Arg	Asn	Gln	Ala	Ala	Gln	Ala	Ala	Lys	Pro	Glu	Asp	
113					118					123					128	
cct	cgg	agc	cag	ggc	gtg	gaa	aga	ttc	ata	cag	gag	tca	aaa	tta	aaa	491
Pro	Arg	Ser	Gln	Gly	Val	Glu	Arg	Phe	Ile	Gln	Glu	Ser	Lys	Leu	Lys	
129					134					139					144	
ata	aac	ctc	ttt	gag	aaa	gaa	aag	gaa	atg	aag	aaa	agc	ccc	acg	tct	539
Ile	Asn	Leu	Phe	Glu	Lys	Glu	Lys	Glu	Met	Lys	Lys	Ser	Pro	Thr	Ser	
145					150					155					160	
ctt	aaa	agg	gag	aca	tac	tac	ctg	tca	gac	agc	ccc	ttg	ctg	ggg	ccc	587
Leu	Lys	Arg	Glu	Thr	Tyr	Tyr	Leu	Ser	Asp	Ser	Pro	Leu	Leu	Gly	Pro	
161					166					171					176	
cct	gtg	ggt	gag	cct	cgg	ctc	ttg	gcc	tcc	tcc	ccg	gcc	ctg	ccc	agc	635
Pro	Val	Gly	Glu	Pro	Arg	Leu	Leu	Ala	Ser	Ser	Pro	Ala	Leu	Pro	Ser	
177					182					187					192	
tct	ggt	gcc	cag	gcc	cgc	ctc	acc	cgg	gcg	ccg	ggg	cct	ccg	cac	tct	683
Ser	Gly	Ala	Gln	Ala	Arg	Leu	Thr	Arg	Ala	Pro	Gly	Pro	Pro	His	Ser	
193					198					203					208	
gct	cat	gct	ttg	ccc	agg	gaa	tca	tgc	act	gct	cat	gct	gca	agt	cag	731
Ala	His	Ala	Leu	Pro	Arg	Glu	Ser	Cys	Thr	Ala	His	Ala	Ala	Ser	Gln	
209					214					219					224	
gca	gcg	act	cag	agg	aag	ccc	ggg	acc	aaa	ttg	ctg	ctg	cct	cga	gcg	779
Ala	Ala	Thr	Gln	Arg	Lys	Pro	Gly	Thr	Lys	Leu	Leu	Leu	Pro	Arg	Ala	
225					230					235					240	
gcc	tct	gtt	aga	gga	aga	agc	atc	cct	ggg	gct	gcg	gag	aag	ccc	aag	827
Ala	Ser	Val	Arg	Gly	Arg	Ser	Ile	Pro	Gly	Ala	Ala	Glu	Lys	Pro	Lys	
241					246					251					256	
aaa	gag	att	cca	gct	agt	cct	tcc	agg	aca	aaa	atc	cca	gct	gag	aag	875
Lys	Glu	Ile	Pro	Ala	Ser	Pro	Ser	Arg	Thr	Lys	Ile	Pro	Ala	Glu	Lys	
257					262					267					272	
gaa	tcc	cac	cgg	gat	gtt	ctc	cct	gac	aaa	cct	gcc	ccg	ggt	gct	gtc	923
Glu	Ser	His	Arg	Asp	Val	Leu	Pro	Asp	Lys	Pro	Ala	Pro	Gly	Ala	Val	

273	278	283	288	
aat gtg ccg gcc gcc gga agc cac ttg ggc cag ggc aag cgg gcg atc				971
Asn Val Pro Ala Ala Gly Ser His Leu Gly Gln Gly Lys Arg Ala Ile				
289	294	299	304	
cct gtt cca aac aag ttg ggg ctg aag aag acc ctg tta aaa gca ccc				1019
Pro Val Pro Asn Lys Leu Gly Leu Lys Lys Thr Leu Leu Lys Ala Pro				
305	310	315	320	
ggc tct acc agc aat ctc gca agg aag tcc tcc tcg ggg cct gtt tgg				1067
Gly Ser Thr Ser Asn Leu Ala Arg Lys Ser Ser Ser Gly Pro Val Trp				
321	326	331	336	
agc ggg gca tcc agt gcg tgc aca tcc cca gca gtg ggc aaa gct aaa				1115
Ser Gly Ala Ser Ser Ala Cys Thr Ser Pro Ala Val Gly Lys Ala Lys				
337	342	347	352	
tca agt gaa ttt gca agt att cct gca aat agc tcc cgg cct ctg tca				1163
Ser Ser Glu Phe Ala Ser Ile Pro Ala Asn Ser Ser Arg Pro Leu Ser				
353	358	363	368	
aac atc agc aag tca ggc aga atg gga ccc gcc atg ctg cgg cca gct				1211
Asn Ile Ser Lys Ser Gly Arg Met Gly Pro Ala Met Leu Arg Pro Ala				
369	374	379	384	
ctg cct gca ggc cct gtg ggg gca tcc tcc tgg cag gcc aag cgg gtc				1259
Leu Pro Ala Gly Pro Val Gly Ala Ser Ser Trp Gln Ala Lys Arg Val				
385	390	395	400	
gat gtt tct gag ctg gca gcg gag cag ctc acg gca ccc ccc tca gca				1307
Asp Val Ser Glu Leu Ala Ala Glu Gln Leu Thr Ala Pro Pro Ser Ala				
401	406	411	416	
tcc ccc acc caa ccc cag act ccg gaa ggt ggc ggc cag tgg ctg aac				1355
Ser Pro Thr Gln Pro Gln Thr Pro Glu Gly Gly Gly Gln Trp Leu Asn				
417	422	427	432	
tcc agt tgc gct tgg tca gaa tct tct caa ttg aat aag act aga agt				1403
Ser Ser Cys Ala Trp Ser Glu Ser Ser Gln Leu Asn Lys Thr Arg Ser				
433	438	443	448	
atc aga cgg cga gat tcc tgt cta aat tcc aag aca aag gtt atg cct				1451
Ile Arg Arg Arg Asp Ser Cys Leu Asn Ser Lys Thr Lys Val Met Pro				
449	454	459	464	
act cct aca aat caa ttt aaa att cct aag ttt tct att ggt gac tcc				1499
Thr Pro Thr Asn Gln Phe Lys Ile Pro Lys Phe Ser Ile Gly Asp Ser				
465	470	475	480	
ccg gac agc tca aca cca aag ctt tcg cgg gca cag cgg ccg cag tcg				1547
Pro Asp Ser Ser Thr Pro Lys Leu Ser Arg Ala Gln Arg Pro Gln Ser				
481	486	491	496	
tgc acg tca gtt ggc agg gtc act gtc cac agc acc ccg gtt aga cgc				1595
Cys Thr Ser Val Gly Arg Val Thr Val His Ser Thr Pro Val Arg Arg				
497	502	507	512	

tca tct ggg cca gca cca caa agc ctg ctg agc gca cgg cgt gtg tca	1643
Ser Ser Gly Pro Ala Pro Gln Ser Leu Leu Ser Ala Arg Arg Val Ser	
513 518 523 528	
gcc ttg ccc aca ccc gcc agc cgg cgc tgc tct ggc ctt cca ccg atg	1691
Ala Leu Pro Thr Pro Ala Ser Arg Arg Cys Ser Gly Leu Pro Pro Met	
529 534 539 544	
acc ccc aaa acg atg ccc agg gcc gtg ggc tct ccc ctg tgt gtg cca	1739
Thr Pro Lys Thr Met Pro Arg Ala Val Gly Ser Pro Leu Cys Val Pro	
545 550 555 560	
gct cgg aga cgt tcc tct gag ccc cgc aag aac tct gca atg aga act	1787
Ala Arg Arg Arg Ser Ser Glu Pro Arg Lys Asn Ser Ala Met Arg Thr	
561 566 571 576	
gaa cca aca agg gag agc aac aga aag aca gat tcc agg ctg gtg gat	1835
Glu Pro Thr Arg Glu Ser Asn Arg Lys Thr Asp Ser Arg Leu Val Asp	
577 582 587 592	
gtg tcc cct gac agg ggt tct cct cct tcc cgt gtg cct cag gca ctt	1883
Val Ser Pro Asp Arg Gly Ser Pro Pro Ser Arg Val Pro Gln Ala Leu	
593 598 603 608	
aac ttt tct cca gag gaa agc gat tct act ttc tcc aaa agt act gcc	1931
Asn Phe Ser Pro Glu Glu Ser Asp Ser Thr Phe Ser Lys Ser Thr Ala	
609 614 619 624	
aca gaa gta gct cgg gag gaa gcc aag ccg ggt gga gat gca gcc cct	1979
Thr Glu Val Ala Arg Glu Glu Ala Lys Pro Gly Gly Asp Ala Ala Pro	
625 630 635 640	
agt gag gct ctt ctt gta gat atc aaa ctg gaa cca ctc gcg gtc act	2027
Ser Glu Ala Leu Leu Val Asp Ile Lys Leu Glu Pro Leu Ala Val Thr	
641 646 651 656	
cca gat gct gca agc cag ccc ctc att gac ctt cct ctc atc gac ttc	2075
Pro Asp Ala Ala Ser Gln Pro Leu Ile Asp Leu Pro Leu Ile Asp Phe	
657 662 667 672	
tgc gat acc cca gaa gca cac gtg gct gta gga tct gaa agc agg cct	2123
Cys Asp Thr Pro Glu Ala His Val Ala Val Gly Ser Glu Ser Arg Pro	
673 678 683 688	
ctg atc gac ctc atg aca aac act cca gac atg aat aaa aat gtg gcc	2171
Leu Ile Asp Leu Met Thr Asn Thr Pro Asp Met Asn Lys Asn Val Ala	
689 694 699 704	
aaa cct tca ccg gtg gtg gga cag ctc ata gac ctg agc tcc cct ctg	2219
Lys Pro Ser Pro Val Val Gly Gln Leu Ile Asp Leu Ser Ser Pro Leu	
705 710 715 720	
atc cag ctg agc cct gag gct gac aag gag aac gtg gat tcc cca ctc	2267
Ile Gln Leu Ser Pro Glu Ala Asp Lys Glu Asn Val Asp Ser Pro Leu	
721 726 731 736	

ctc aag ttc taa gcc gaaccaaadc ctttgccttg aaagaacagc cctaaagtgg 2322
 Leu Lys Phe *
 737

ttttcaaccc tcagaaacaa gcttttaggct ggtgcagtg gcttacactt gtaacccctag 2382
 aacttgggag gctgaggtgg gcggattact tgagcccagg agttcgggac cagcctggga 2442
 aatatagtga aactcctgtc cctacaaaaa atacaaaaat tagccgggtg tggtagtgca 2502
 tgctgtagt cccagctact tgggaggctg aagtgggagg atggcctgag ctcaaggaga 2562
 tgcaggctgc agtgggctgt gattgtgcca ctgcactcca gcctgggcac caatgtgaga 2622
 acctgtcttg gaaaaaaaaa aaaaaaaaaac atgttttagt agaagtttta tttgaaaaag 2682
 aaaaataagc ataaatatat tcccagtgtc ggagaggggtg ggctgagggga ctggggccag 2742
 cacggaccac ccaaggcctc tgcttcccgc cgcaccctc ctgcctgcca ttctctgggc 2802
 tggaatgtga agcctcagtc actctaaatg aagaattttc tttgaatgt tttgtatgta 2862
 aaatagcaag tggtattttt taaagttaag tttgtataaa tagttagata ttctagattt 2922
 acattaaatt gtaaaataaa tggacttatt gaagcatatc ttgattttta agcttatctt 2982
 gattttcaaa catgcatagc tattttttatc actctaataca gtaaggctac tatctagact 3042
 cgaatgcttt catacaagtg attttcaaaa attagtcaat aaaaattgat gtcagtgcag 3102
 gccaggccc gccccagat aactagtttt ctaggtctgg ggccagccta gtaattgtta 3162
 ctaggcacac aggtgatgct gactcgatgg cctgagacac accccttgag aagaagctgc 3222
 tctggggaga cgagggtatg agtggaaaga ggatgggcga 3262

<210> 140
 <211> 3061
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (60)..(2078)

<400> 140
 agcgggattc gatagcatatc tcagtgtggt ggaattcgtg acttctgaca gctctctcc 59
 atg gaa gga ggc ggc ggc cgc gat gag cct tca gcc tgc cgg gca ggg 107
 Met Glu Gly Gly Gly Gly Arg Asp Glu Pro Ser Ala Cys Arg Ala Gly
 1 5 10 15
 gac gtg aac atg gat gac cct aag aag gaa gac att ctt ctt ttg gcc 155
 Asp Val Asn Met Asp Asp Pro Lys Lys Glu Asp Ile Leu Leu Leu Ala
 17 22 27 32

gat gaa aaa ttt gac ttc gat ctt tca ttg tct tct tcg agt gca aat	203
Asp Glu Lys Phe Asp Phe Asp Leu Ser Leu Ser Ser Ser Ser Ala Asn	
33 38 43 48	
gaa gat gat gaa gtc ttc ttc gga ccc ttt gga cat aaa gaa aga tgt	251
Glu Asp Asp Glu Val Phe Phe Gly Pro Phe Gly His Lys Glu Arg Cys	
49 54 59 64	
att gct gcc agc ttg gaa tta aat aat ccg gtt ccc gaa cag cct ccg	299
Ile Ala Ala Ser Leu Glu Leu Asn Asn Pro Val Pro Glu Gln Pro Pro	
65 70 75 80	
ttg ccc aca tct gag agt ccc ttt gcc tgg agc cct ctg gcc ggg gag	347
Leu Pro Thr Ser Glu Ser Pro Phe Ala Trp Ser Pro Leu Ala Gly Glu	
81 86 91 96	
aag ttc gtg gag gtg tac aaa gaa gct cac tta ctg gct tta cac att	395
Lys Phe Val Glu Val Tyr Lys Glu Ala His Leu Leu Ala Leu His Ile	
97 102 107 112	
gag agc agc agc cgg aac cag gca gcc caa gct gcc aag cct gaa gac	443
Glu Ser Ser Ser Arg Asn Gln Ala Ala Gln Ala Ala Lys Pro Glu Asp	
113 118 123 128	
cct cgg agc cag ggc gtg gaa aga ttc ata cag gag tca aaa tta aaa	491
Pro Arg Ser Gln Gly Val Glu Arg Phe Ile Gln Glu Ser Lys Leu Lys	
129 134 139 144	
ata aac ctc ttt gag aaa gaa aag gaa atg aag aaa agc ccc acg tct	539
Ile Asn Leu Phe Glu Lys Glu Lys Glu Met Lys Lys Ser Pro Thr Ser	
145 150 155 160	
ctt aaa agg gag aca tac tac ctg tca gac agc ccc ttg ctg ggg ccc	587
Leu Lys Arg Glu Thr Tyr Tyr Leu Ser Asp Ser Pro Leu Leu Gly Pro	
161 166 171 176	
cct gtg ggt gag cct cgg ctc ttg gcc tcc tcc ccg gcc ctg ccc agc	635
Pro Val Gly Glu Pro Arg Leu Leu Ala Ser Ser Pro Ala Leu Pro Ser	
177 182 187 192	
tct ggt gcc cag gcc cgc ctc acc cgg gcg ccg ggg cct ccg cac tct	683
Ser Gly Ala Gln Ala Arg Leu Thr Arg Ala Pro Gly Pro Pro His Ser	
193 198 203 208	
gct cat gct ttg ccc agg gaa tca tgc act gct cat gct gca agt cag	731
Ala His Ala Leu Pro Arg Glu Ser Cys Thr Ala His Ala Ala Ser Gln	
209 214 219 224	
gca gcg act cag agg aag ccc ggg acc aaa ttg ctg ctg cct cga gcg	779
Ala Ala Thr Gln Arg Lys Pro Gly Thr Lys Leu Leu Leu Pro Arg Ala	
225 230 235 240	
gcc tct gtt aga gga aga agc atc cct ggg gct gcg gag aag ccc aag	827
Ala Ser Val Arg Gly Arg Ser Ile Pro Gly Ala Ala Glu Lys Pro Lys	
241 246 251 256	

aaa gag att cca gct agt cct tcc agg aca aaa atc cca gct gag aag	875
Lys Glu Ile Pro Ala Ser Pro Ser Arg Thr Lys Ile Pro Ala Glu Lys	
257 262 267 272	
 gaa tcc cac cgg gat gtt ctc cct gac aaa cct gcc ccg ggt gct gtc	923
Glu Ser His Arg Asp Val Leu Pro Asp Lys Pro Ala Pro Gly Ala Val	
273 278 283 288	
 aat gtg ccg gcc gcc gga agc cac ttg ggc cag ggc aag cgg gcg atc	971
Asn Val Pro Ala Ala Gly Ser His Leu Gly Gln Gly Lys Arg Ala Ile	
289 294 299 304	
 cct gtt cca aac aag ttg ggg ctg aag aag acc ctg tta aaa gca ccc	1019
Pro Val Pro Asn Lys Leu Gly Leu Lys Lys Thr Leu Leu Lys Ala Pro	
305 310 315 320	
 ggc tct acc agc aat ctc gca agg aag tcc tcc tcg ggg cct gtt tgg	1067
Gly Ser Thr Ser Asn Leu Ala Arg Lys Ser Ser Ser Gly Pro Val Trp	
321 326 331 336	
 agc ggg gca tcc agt gcg tgc aca tcc cca gca gtg ggc aaa gct aaa	1115
Ser Gly Ala Ser Ser Ala Cys Thr Ser Pro Ala Val Gly Lys Ala Lys	
337 342 347 352	
 tca agt gaa ttt gca agt att cct gca aat agc tcc ccg cct ctg tca	1163
Ser Ser Glu Phe Ala Ser Ile Pro Ala Asn Ser Ser Arg Pro Leu Ser	
353 358 363 368	
 aac atc agc aag tca ggc aga atg gga ccc gcc atg ctg ccg cca gct	1211
Asn Ile Ser Lys Ser Gly Arg Met Gly Pro Ala Met Leu Arg Pro Ala	
369 374 379 384	
 ctg cct gca ggc cct gtg ggg gca tcc tcc tgg cag gcc aag ccg gtc	1259
Leu Pro Ala Gly Pro Val Gly Ala Ser Ser Trp Gln Ala Lys Arg Val	
385 390 395 400	
 gat gtt tct gag ctg gca gcg gag cag ctc acg gca ccc ccc tca gca	1307
Asp Val Ser Glu Leu Ala Ala Glu Gln Leu Thr Ala Pro Pro Ser Ala	
401 406 411 416	
 tcc ccc acc caa ccc cag act ccg gaa ggt ggc ggc cag tgg ctg aac	1355
Ser Pro Thr Gln Pro Gln Thr Pro Glu Gly Gly Gly Gln Trp Leu Asn	
417 422 427 432	
 tcc agt tgc gct tgg tca gaa tct tct caa ttg aat aag act aga agt	1403
Ser Ser Cys Ala Trp Ser Glu Ser Ser Gln Leu Asn Lys Thr Arg Ser	
433 438 443 448	
 atc aga ccg cga gat tcc tgt cta aat tcc aag aca aag gtt atg cct	1451
Ile Arg Arg Arg Asp Ser Cys Leu Asn Ser Lys Thr Lys Val Met Pro	
449 454 459 464	
 act cct aca aat caa ttt aaa att cct aag ttt tct att ggt gac tcc	1499
Thr Pro Thr Asn Gln Phe Lys Ile Pro Lys Phe Ser Ile Gly Asp Ser	
465 470 475 480	
 ccg gac agc tca aca cca aag ctt tcg ccg gca cag ccg ccg cag tcg	1547

Pro Asp Ser Ser Thr	Pro Lys Leu Ser Arg	Ala Gln Arg Pro Gln Ser	
481	486	491	496
tgc acg tca gtt ggc agg gtc act gtc cac agc acc ccg gtt aga cgc			1595
Cys Thr Ser Val Gly Arg Val Thr Val His Ser Thr Pro Val Arg Arg			
497	502	507	512
tca tct ggg cca gca cca caa agc ctg ctg agc gca cgg cgt gtg tca			1643
Ser Ser Gly Pro Ala Pro Gln Ser Leu Leu Ser Ala Arg Arg Val Ser			
513	518	523	528
gcc ttg ccc aca ccc gcc agc cgg cgc tgc tct ggc ctt cca ccg atg			1691
Ala Leu Pro Thr Pro Ala Ser Arg Arg Cys Ser Gly Leu Pro Pro Met			
529	534	539	544
acc ccc aaa acg atg ccc agg gcc gtg ggc tct ccc ctg tgt gtg cca			1739
Thr Pro Lys Thr Met Pro Arg Ala Val Gly Ser Pro Leu Cys Val Pro			
545	550	555	560
gct cgg aga cgt tcc tct gag ccc cgc aag aac tct gca atg agg gct			1787
Ala Arg Arg Arg Ser Ser Glu Pro Arg Lys Asn Ser Ala Met Arg Ala			
561	566	571	576
ctt ctt gta gat atc aaa ctg gaa cca ctc gcg gtc act cca gat gct			1835
Leu Leu Val Asp Ile Lys Leu Glu Pro Leu Ala Val Thr Pro Asp Ala			
577	582	587	592
gca agc cag ccc ctc att gac ctt cct ctc atc gac ttc tgc gat acc			1883
Ala Ser Gln Pro Leu Ile Asp Leu Pro Leu Ile Asp Phe Cys Asp Thr			
593	598	603	608
cca gaa gca cac gtg gct gta gga tct gaa agc agg cct ctg atc gac			1931
Pro Glu Ala His Val Ala Val Gly Ser Glu Ser Arg Pro Leu Ile Asp			
609	614	619	624
ctc atg aca aac act cca gac atg aat aaa aat gtg gcc aaa cct tca			1979
Leu Met Thr Asn Thr Pro Asp Met Asn Lys Asn Val Ala Lys Pro Ser			
625	630	635	640
ccg gtg gtg gga cag ctc ata gac ctg agc tcc cct ctg atc cag ctg			2027
Pro Val Val Gly Gln Leu Ile Asp Leu Ser Ser Pro Leu Ile Gln Leu			
641	646	651	656
agc cct gag gct gac aag gag aac gtg gat tcc cca ctc ctc aag ttc			2075
Ser Pro Glu Ala Asp Lys Glu Asn Val Asp Ser Pro Leu Leu Lys Phe			
657	662	667	672
taa gccg aaccaaattcc ttgccttga aagaacagcc cttaaagtgg tttcaaccct			2132
*			
673			
cagaaacaag ctttaggctg gtcgcagtgg cttacacttg taaccctaga acttgggagg			2192
ctgaggtggg cggattactt gagcccagga gttcgggacc agcctgggaa atatagtga			2252
actcctgtcc ctacaaaaaa tacaaaaaatt agccgggtgt ggtagtgc at gcctgtagtc			2312

ccagctactt gggaggctga agtgggagga tggcctgagc tcaaggagat gcaggctgca 2372
gtgggctgtg attgtgccac tgcactccag cctgggcacc aatgtgagaa cctgtcttgg 2432
aaaaaaaaaa aaaaaaaca tgtttttagta gaagttttat ttgaaaaaga aaaataagca 2492
taaatatatt cccagtgtcg gagagggtgg gctgaggggac tggggccagc acggaccacc 2552
caaggcctct gcttcccgcc gccacccctcc tcgctgccat tctctgggct ggaatgtgaa 2612
gcctcagtca ctctaaatga agaattttct tttgaatgtt ttgtatgtaa aatagcaagt 2672
ggctatTTTT aaagttaagt ttgtataaat agttagatat tctagattta cattaaattg 2732
taaaataaat ggacttattg aagcatatct tgatTTTTaa gcttatcttg attttcaaac 2792
atgcatagct atttttatca ctctaatcag taaggctact atctagactc gaatgctttc 2852
atacaagtga ttttcaaaaa ttagtcaata aaaattgatg tcagtgcagg ccagggcccg 2912
ccccagata cactagtttc taggtctggg gccagcctag taattgttac taggcacaca 2972
ggtgatgtcg actcgatggc ctgagacaca ccccttgaga agaagctgct ctggggagac 3032
gagggtatga gtggaaagag gatgggcga 3061

<210> 141
<211> 5102
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (284)..(4234)

<400> 141
aggggggatt gacccttgcg gcaccgggtcc ggaattcccg ggtcgaccca cgcgtccggg 60
ttcctgcaga tagagtctgc ctccoctgcc cccttctctt ctggattcct cgctgccac 120
cctcattctc ccgggggaag cctcgcaacg aagggccgga gcgcctttc tgctcccgga 180
atgcttcacc tgtccgcagc tccgcccgcc ccacccccgg aagtgcggc gaccgcggc 240
ccctgccttt gttccgttgg gcgtccgcgg cgacggcggg aag atg gcg gcg gcg 295
Met Ala Ala Ala
1

gga gcc ctg gaa cgg agc ttc gtg gag cta agc gga gct gag cgc gaa 343
Gly Ala Leu Glu Arg Ser Phe Val Glu Leu Ser Gly Ala Glu Arg Glu
5 10 15 20

agg ccg agg cac ttt cgg gaa ttc aca gtc tgc agc att ggg act gca 391
Arg Pro Arg His Phe Arg Glu Phe Thr Val Cys Ser Ile Gly Thr Ala

21	26	31	36	
aat gcc gtg gct ggc gcc gta aaa tac agt gaa agc gcg gga ggc ttt				439
Asn Ala Val Ala Gly Ala Val Lys Tyr Ser Glu Ser Ala Gly Gly Phe				
37	42	47	52	
tac tac gtg gag agt ggc aag ttg ttc tcc gta acc aga aac agg ttc				487
Tyr Tyr Val Glu Ser Gly Lys Leu Phe Ser Val Thr Arg Asn Arg Phe				
53	58	63	68	
att cat tgg aag acc tct gga gat aca ttg gag ctg atg gag gag tca				535
Ile His Trp Lys Thr Ser Gly Asp Thr Leu Glu Leu Met Glu Glu Ser				
69	74	79	84	
ctg gac ata aat ctg ttg aat aat gcc att cgc cta aaa ttc caa aat				583
Leu Asp Ile Asn Leu Leu Asn Asn Ala Ile Arg Leu Lys Phe Gln Asn				
85	90	95	100	
tgc agt gtt tta cct gga ggg gtt tat gtc tct gag act cag aat cgt				631
Cys Ser Val Leu Pro Gly Gly Val Tyr Val Ser Glu Thr Gln Asn Arg				
101	106	111	116	
gtg ata atc ttg atg tta acc aat caa aca gtg cac agg tta ctt tta				679
Val Ile Ile Leu Met Leu Thr Asn Gln Thr Val His Arg Leu Leu Leu				
117	122	127	132	
cca cac ccc tcc cgg atg tat agg agt gag ttg gta gtt gac agt cag				727
Pro His Pro Ser Arg Met Tyr Arg Ser Glu Leu Val Val Asp Ser Gln				
133	138	143	148	
atg cag tca ata ttc act gac att gga aaa gtt gat ttc aca gat cct				775
Met Gln Ser Ile Phe Thr Asp Ile Gly Lys Val Asp Phe Thr Asp Pro				
149	154	159	164	
tgc aac tat cag tta att cca gca gta cct gga ata tct cct aat tcc				823
Cys Asn Tyr Gln Leu Ile Pro Ala Val Pro Gly Ile Ser Pro Asn Ser				
165	170	175	180	
acc gcc tct aca gcc tgg ctc agc agt gat ggg gag gcc ctg ttt gcc				871
Thr Ala Ser Thr Ala Trp Leu Ser Ser Asp Gly Glu Ala Leu Phe Ala				
181	186	191	196	
tta cca tgt gct tct ggg gga atc ttt gtt ctt aag cta cct cct tat				919
Leu Pro Cys Ala Ser Gly Gly Ile Phe Val Leu Lys Leu Pro Pro Tyr				
197	202	207	212	
gac ata cct ggt atg gtg tca gtc gtg gaa ctg aaa cag agt tca gta				967
Asp Ile Pro Gly Met Val Ser Val Val Glu Leu Lys Gln Ser Ser Val				
213	218	223	228	
atg caa cga ttg ctt aca ggc tgg atg cca aca gct atc agg ggt gac				1015
Met Gln Arg Leu Leu Thr Gly Trp Met Pro Thr Ala Ile Arg Gly Asp				
229	234	239	244	
cag tcg cct tca gat cgt ccc ctc agt ctt gct gtt cat tgt gtg gag				1063
Gln Ser Pro Ser Asp Arg Pro Leu Ser Leu Ala Val His Cys Val Glu				
245	250	255	260	

cat gat gcc ttc atc ttt gct ttg tgt cag gat cat aaa cta cga atg	1111
His Asp Ala Phe Ile Phe Ala Leu Cys Gln Asp His Lys Leu Arg Met	
261 266 271 276	
tggtcttac aag gag caa atg tgc cta atg gta gct gac atg ctg gag	1159
Trp Ser Tyr Lys Glu Gln Met Cys Leu Met Val Ala Asp Met Leu Glu	
277 282 287 292	
tat gtc cct gtg aag aaa gac ctt cgg ctt act gct gga act gga cac	1207
Tyr Val Pro Val Lys Lys Asp Leu Arg Leu Thr Ala Gly Thr Gly His	
293 298 303 308	
aaa tta cgg ctt gct tat tcc ccc acc atg gga ctc tac ctg ggg ata	1255
Lys Leu Arg Leu Ala Tyr Ser Pro Thr Met Gly Leu Tyr Leu Gly Ile	
309 314 319 324	
tac atg cat gca cca aaa cga gga cag ttc tgc att ttc cag ttg gtg	1303
Tyr Met His Ala Pro Lys Arg Gly Gln Phe Cys Ile Phe Gln Leu Val	
325 330 335 340	
agc act gag agt aat cgc tat agt ctc gat cat att tct tca ctg ttc	1351
Ser Thr Glu Ser Asn Arg Tyr Ser Leu Asp His Ile Ser Ser Leu Phe	
341 346 351 356	
act tct cag gag aca ctg att gac ttt gcc tta act tcc acg gat atc	1399
Thr Ser Gln Glu Thr Leu Ile Asp Phe Ala Leu Thr Ser Thr Asp Ile	
357 362 367 372	
tggtgcc ctgtgg cat gat gct gag aac caa aca gta gtg aaa tac atc	1447
Trp Ala Leu Trp His Asp Ala Glu Asn Gln Thr Val Val Lys Tyr Ile	
373 378 383 388	
aac ttt gaa cat aat gtt gca ggt cag tgg aat cca gtt ttt atg cag	1495
Asn Phe Glu His Asn Val Ala Gly Gln Trp Asn Pro Val Phe Met Gln	
389 394 399 404	
cct ctg cca gag gaa gag att gtc atc aga gat gat caa gac ccc aga	1543
Pro Leu Pro Glu Glu Glu Ile Val Ile Arg Asp Asp Gln Asp Pro Arg	
405 410 415 420	
gag atg tat ctg caa agt ctt ttt aca cca gga caa ttc aca aat gaa	1591
Glu Met Tyr Leu Gln Ser Leu Phe Thr Pro Gly Gln Phe Thr Asn Glu	
421 426 431 436	
gct tta tgt aag gct tta cag att ttc tgc cga gga act gag agg aat	1639
Ala Leu Cys Lys Ala Leu Gln Ile Phe Cys Arg Gly Thr Glu Arg Asn	
437 442 447 452	
ttg gat ctt tcc tgg agt gaa ctg aag aaa gaa gtt act tta gct gtt	1687
Leu Asp Leu Ser Trp Ser Glu Leu Lys Lys Glu Val Thr Leu Ala Val	
453 458 463 468	
gaa aat gag ctt caa gga agt gta aca gag tat gaa ttc tcc cag gag	1735
Glu Asn Glu Leu Gln Gly Ser Val Thr Glu Tyr Glu Phe Ser Gln Glu	
469 474 479 484	

gag ttt cga aat tta caa caa gaa ttc tgg tgc aag ttc tat gcc tgt	1783
Glu Phe Arg Asn Leu Gln Gln Glu Phe Trp Cys Lys Phe Tyr Ala Cys	
485 490 495 500	
tgt ctt cag tat caa gaa gcc ctc tct cac cct ctt gcc cta cat ttg	1831
Cys Leu Gln Tyr Gln Glu Ala Leu Ser His Pro Leu Ala Leu His Leu	
501 506 511 516	
aat cca cac aca aac atg gtg tgc ctg ctg aaa aaa ggg tac ctg tct	1879
Asn Pro His Thr Asn Met Val Cys Leu Leu Lys Lys Gly Tyr Leu Ser	
517 522 527 532	
ttc ctt att ccc tca tcc tta gtg gat cat ttg tat ctc ctg cct tat	1927
Phe Leu Ile Pro Ser Ser Leu Val Asp His Leu Tyr Leu Leu Pro Tyr	
533 538 543 548	
gag aac ctt ttg aca gaa gat gag aca acc ata tct gat gat gtg gat	1975
Glu Asn Leu Leu Thr Glu Asp Glu Thr Thr Ile Ser Asp Asp Val Asp	
549 554 559 564	
atc gct cgg gat gtc ata tgt ctt ata aaa tgc ctc cgg ctg att gaa	2023
Ile Ala Arg Asp Val Ile Cys Leu Ile Lys Cys Leu Arg Leu Ile Glu	
565 570 575 580	
gag tca gta act gtg gat atg tca gtt ata atg gaa atg agt tgt tat	2071
Glu Ser Val Thr Val Asp Met Ser Val Ile Met Glu Met Ser Cys Tyr	
581 586 591 596	
aac cta cag tct ccg gaa aag gct gca gag cag att ctg gaa gat atg	2119
Asn Leu Gln Ser Pro Glu Lys Ala Ala Glu Gln Ile Leu Glu Asp Met	
597 602 607 612	
atc act att gat gta gaa aat gtg atg gag gat att tgt agt aaa ctg	2167
Ile Thr Ile Asp Val Glu Asn Val Met Glu Asp Ile Cys Ser Lys Leu	
613 618 623 628	
caa gag att agg aac cca atc cat gca att gga cta ctt ata cgg gaa	2215
Gln Glu Ile Arg Asn Pro Ile His Ala Ile Gly Leu Leu Ile Arg Glu	
629 634 639 644	
atg gat tat gaa aca gaa gtg gaa atg gaa aag gga ttc aat cca gct	2263
Met Asp Tyr Glu Thr Glu Val Glu Met Glu Lys Gly Phe Asn Pro Ala	
645 650 655 660	
cag cct ttg aat att cga atg aat ctt acc cag ctc tat ggt agt aac	2311
Gln Pro Leu Asn Ile Arg Met Asn Leu Thr Gln Leu Tyr Gly Ser Asn	
661 666 671 676	
aca gca ggg tat att gtg tgc aga ggg gtg cat aaa atc gcc agt act	2359
Thr Ala Gly Tyr Ile Val Cys Arg Gly Val His Lys Ile Ala Ser Thr	
677 682 687 692	
cgt ttc ctg atc tgc aga gat ctt ttg atc tta cag cag ctg tta atg	2407
Arg Phe Leu Ile Cys Arg Asp Leu Leu Ile Leu Gln Gln Leu Leu Met	
693 698 703 708	
agg ctt gga gat gct gtg att tgg gga act ggt cag ctc ttt caa gct	2455

[illegible]

933	938	943	948	
gct aca tca gcc ata act gaa gca ggt gat gac tgg aaa agt cag gct				3175
Ala Thr Ser Ala Ile Thr Glu Ala Gly Asp Asp Trp Lys Ser Gln Ala				
949	954	959	964	
act cta agg aca tgt att ttc aaa cat cat ttg gat ttg ggt cac aat				3223
Thr Leu Arg Thr Cys Ile Phe Lys His His Leu Asp Leu Gly His Asn				
965	970	975	980	
agc caa gca tat gaa gcc tta acc caa att cct gat tcc agc agg caa				3271
Ser Gln Ala Tyr Glu Ala Leu Thr Gln Ile Pro Asp Ser Ser Arg Gln				
981	986	991	996	
tta gat tgt tta cgg cag ttg gtg gta gtt ctt tgt gaa cgc tca cag				3319
Leu Asp Cys Leu Arg Gln Leu Val Val Val Leu Cys Glu Arg Ser Gln				
997	1002	1007	1012	
cta cag gat ctt gta gag ttt ccc tat gtg aat ctg cat aat gag gtt				3367
Leu Gln Asp Leu Val Glu Phe Pro Tyr Val Asn Leu His Asn Glu Val				
1013	1018	1023	1028	
gtg gga ata att gag tca cgt gct aga gct gtg gac ctt atg act cac				3415
Val Gly Ile Ile Glu Ser Arg Ala Arg Ala Val Asp Leu Met Thr His				
1029	1034	1039	1044	
aat tac tat gaa ctt ctg tat gcc ttt cac atc tat cgc cac aat tac				3463
Asn Tyr Tyr Glu Leu Leu Tyr Ala Phe His Ile Tyr Arg His Asn Tyr				
1045	1050	1055	1060	
cgc aag gct ggc aca gtg atg ttt gag tat gga atg cgg ctt ggc aga				3511
Arg Lys Ala Gly Thr Val Met Phe Glu Tyr Gly Met Arg Leu Gly Arg				
1061	1066	1071	1076	
gaa gtt cga act ctc cgg gga ctt gag aaa caa ggc aac tgt tat ctg				3559
Glu Val Arg Thr Leu Arg Gly Leu Glu Lys Gln Gly Asn Cys Tyr Leu				
1077	1082	1087	1092	
gct gct ctc aat tgt tta cga ctt att cgt cca gaa tat gcg tgg att				3607
Ala Ala Leu Asn Cys Leu Arg Leu Ile Arg Pro Glu Tyr Ala Trp Ile				
1093	1098	1103	1108	
gtg cag cca gtg tct ggt gca gtg tat gat cgc cct gga gca tcc cct				3655
Val Gln Pro Val Ser Gly Ala Val Tyr Asp Arg Pro Gly Ala Ser Pro				
1109	1114	1119	1124	
aag agg aat cat gat gga gaa tgc aca gct gcc ccc aca aat cga caa				3703
Lys Arg Asn His Asp Gly Glu Cys Thr Ala Ala Pro Thr Asn Arg Gln				
1125	1130	1135	1140	
att gaa atc ctg gaa ctg gaa gat ctg gag aaa gag tgt tcc ttg gct				3751
Ile Glu Ile Leu Glu Leu Glu Asp Leu Glu Lys Glu Cys Ser Leu Ala				
1141	1146	1151	1156	
cgc atc cgc ctc act ttg gct cag cat gat cca tca gcg gtt gca gtt				3799
Arg Ile Arg Leu Thr Leu Ala Gln His Asp Pro Ser Ala Val Ala Val				
1157	1162	1167	1172	

gct gga agt tca tca gca gag gaa atg gtc act ctc ttg gtt cag gcg	3847
Ala Gly Ser Ser Ser Ala Glu Glu Met Val Thr Leu Leu Val Gln Ala	
1173 1178 1183 1188	
ggc ctc ttt gac act gcc ata tca ctc tgt cag act ttt aag ctt ccc	3895
Gly Leu Phe Asp Thr Ala Ile Ser Leu Cys Gln Thr Phe Lys Leu Pro	
1189 1194 1199 1204	
tta acg cca gtc ttt gaa ggg ctt gcc ttc aaa tgc atc aaa ttg caa	3943
Leu Thr Pro Val Phe Glu Gly Leu Ala Phe Lys Cys Ile Lys Leu Gln	
1205 1210 1215 1220	
ttt gga gga gag gca gca caa gca gaa gcc tgg gcc tgg cta gca gcc	3991
Phe Gly Gly Glu Ala Ala Gln Ala Glu Ala Trp Ala Trp Leu Ala Ala	
1221 1226 1231 1236	
aat cag ctc tca tct gtc atc act act aag gag tct agt gct aca gat	4039
Asn Gln Leu Ser Ser Val Ile Thr Thr Lys Glu Ser Ser Ala Thr Asp	
1237 1242 1247 1252	
gaa gca tgg cga cta tta tcc act tac ctg gag agg tac aaa gtc cag	4087
Glu Ala Trp Arg Leu Leu Ser Thr Tyr Leu Glu Arg Tyr Lys Val Gln	
1253 1258 1263 1268	
aat aac ttg tat cac cac tgt gta atc aac aag ctc ttg tct cat gga	4135
Asn Asn Leu Tyr His His Cys Val Ile Asn Lys Leu Leu Ser His Gly	
1269 1274 1279 1284	
gtg cct ctg cct aat tgg ctt ata aac agt cac aac atc gca ctg tcc	4183
Val Pro Leu Pro Asn Trp Leu Ile Asn Ser His Asn Ile Ala Leu Ser	
1285 1290 1295 1300	
caa aaa gtt gat aag gca aca cgg gat tta tta tat cgt cgg acc ttg	4231
Gln Lys Val Asp Lys Ala Thr Arg Asp Leu Leu Tyr Arg Arg Thr Leu	
1301 1306 1311 1316	
tga tttg gattgtcacc tagcctttgt aaccgcttgg tgccctcttag gacttaagac	4288
*	
1317	
taccctacag gaaccctgta ctcaaggccg atttttgtaa ctgtaaatga tgtgtacaac	4348
attcaagtct gcattctgca caagatagga gggcggaaga gtcagaggac cctgtgcttg	4408
ctgggtggtgc taacacaatt tctggtgttc aaccttggtc tcaaatagct gcttttgtat	4468
atgattcacg agctttttta gagttttatat ttttttaaac taccgaagac attcattatc	4528
tgcaaattaa gactcacctt cactttccaa aatagctgag gggtgttggtc ttgttgtagc	4588
tgaccaccaa aagcagtcac tgcaaatctt ttaattcttc cctatcacct tttgtatttt	4648
aatgcaatta ttttgggtcca gaactgacct gtattttctg tattgtacac aaaagctaat	4708
aattttgtgt actttttatt tattttggag gttttatatg atottcaatt gagtattaaa	4768

taatttgcct agattaagcc taaaatgatg accagctaata taaagaagat attttgaatc 4828
 tggttctgag ctaaagttga gtaaattctt agctaagaaa aaattggaaa tccatcatct 4888
 atattagcaa cagattctca gagtaaattg ttaacttcta tgatttatga taatcaagct 4948
 ggacttgatc atacaagtta gtctcataat gtattggacc aaaatgtaaa cttcattgggt 5008
 cagatttaga agcattcatg ctcacaagtt ttgggaaagt gaaaaataat aaaatcatct 5068
 tggattttat tctgtatatt aaaatttatc tttt 5102

<210> 142
 <211> 1510
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (60)..(884)

<400> 142
 atttggccct cgaggccaag aattcggcac gaggaccact ctgctcccc gcctaagcc 59
 atg cac ctc tgt ggg agc aat ggg ctg ctg acc cag aca gac ccc aag 107
 Met His Leu Cys Gly Ser Asn Gly Leu Leu Thr Gln Thr Asp Pro Lys
 1 5 10 15
 gag caa caa agg cag ctg aag aag cag aag aac cgg gca gcc gcc cag 155
 Glu Gln Gln Arg Gln Leu Lys Lys Gln Lys Asn Arg Ala Ala Ala Gln
 17 22 27 32
 cga agc cgg cag aag cac aca gac aag gca gac gcc ctg cac cag cag 203
 Arg Ser Arg Gln Lys His Thr Asp Lys Ala Asp Ala Leu His Gln Gln
 33 38 43 48
 cac gag tct ctg gaa aaa gac aac ctc gcc ctg cgg aag gag atc cag 251
 His Glu Ser Leu Glu Lys Asp Asn Leu Ala Leu Arg Lys Glu Ile Gln
 49 54 59 64
 tcc ctg cag gcc gag ctg gcg tgg tgg agc cgg acc ctg cac gtg cat 299
 Ser Leu Gln Ala Glu Leu Ala Trp Trp Ser Arg Thr Leu His Val His
 65 70 75 80
 gag cgc ctg tgc ccc atg gat tgt gcc tcc tgc tca gct cca ggg ctc 347
 Glu Arg Leu Cys Pro Met Asp Cys Ala Ser Cys Ser Ala Pro Gly Leu
 81 86 91 96
 ctg ggc tgc tgg gac cag gct gag ggg ctc ctg ggc cct ggc cca cag 395
 Leu Gly Cys Trp Asp Gln Ala Glu Gly Leu Leu Gly Pro Gly Pro Gln
 97 102 107 112
 gga caa cat ggc tgc cgg gag cag ctg gag ctg ttc cag acc ccg ggt 443
 Gly Gln His Gly Cys Arg Glu Gln Leu Glu Leu Phe Gln Thr Pro Gly
 113 118 123 128

tcc tgt tac cca gct cag ccg ctc tct cca ggt cca cag cct cat gat	491
Ser Cys Tyr Pro Ala Gln Pro Leu Ser Pro Gly Pro Gln Pro His Asp	
129 134 139 144	
tct ccc agc ctc ctc cag tgc ccc ctg ccc tca ctg tcc ctt ggc ccc	539
Ser Pro Ser Leu Leu Gln Cys Pro Leu Pro Ser Leu Ser Leu Gly Pro	
145 150 155 160	
gct gtg gtt gct gaa cct cct gtc cag ctg tcc ccc agc cct ctc ctg	587
Ala Val Val Ala Glu Pro Pro Val Gln Leu Ser Pro Ser Pro Leu Leu	
161 166 171 176	
ttt gcc tcg cac act ggt tcc agc ctg cag ggg tct tcc tct aag ctc	635
Phe Ala Ser His Thr Gly Ser Ser Leu Gln Gly Ser Ser Ser Lys Leu	
177 182 187 192	
agt gcc ctc cag ccc agc ctc acg gcc caa act gcc cct cca cag ccc	683
Ser Ala Leu Gln Pro Ser Leu Thr Ala Gln Thr Ala Pro Pro Gln Pro	
193 198 203 208	
ctc gag ctg gag cat ccc acc aga ggg aag ctg ggg tcc tct ccc gac	731
Leu Glu Leu Glu His Pro Thr Arg Gly Lys Leu Gly Ser Ser Pro Asp	
209 214 219 224	
aac cct tcc tct gcc ctg ggg ctt gca cgt ctg cag agc agg gag cac	779
Asn Pro Ser Ser Ala Leu Gly Leu Ala Arg Leu Gln Ser Arg Glu His	
225 230 235 240	
aaa cct gct ctc tca gca gcc act tgg caa ggg ctg gtt gtg gat ccc	827
Lys Pro Ala Leu Ser Ala Ala Thr Trp Gln Gly Leu Val Val Asp Pro	
241 246 251 256	
agc cct cac cct ctc ctg gcc ttt cct ctg ctc tcc tct gct caa gtc	875
Ser Pro His Pro Leu Leu Ala Phe Pro Leu Leu Ser Ser Ala Gln Val	
257 262 267 272	
cac ttc taa cctggtc ttoggagctg gggtggcccc ttctttgggc tcaggaagca	931
His Phe *	
273	
gccttagcac acgggcctct cctccctcac tactgggtgc tgccctgcgt ggctgaccag	991
ctggcccagg atttcacagt cgaaaaggaa gccaccactg atgcctccca ctgtgacagg	1051
ccctgtcacc accaatatct tatttcaacc tcacagttga cctgagaaat cgagattatc	1111
actccacttt ttcagacaag gaaactgagg ctgaggaag ccaagtgaca agtccaaggt	1171
cacgaagact ttcttgagc ccgaaacacc accctctgct cctccttctc ctgtcctggg	1231
cccaggcatc ctaggggctg aaatcctgga aaaccctggg ggccttgggt ggttgaaaaa	1291
aaggggtttt gccaatggcc tccaagaagg ccaagaaaaa aaaggggggt ttctttcccc	1351
ccactggttt tgtgattcca agggcccaga gccatgccag tccccagaaa accccaacct	1411

taaacttggg gcaagtccca gagtccaagc ccctggtggg gtaagaggcc aaagcaagaa 1471
gacctgaagt gggactcttt gcttccccta agaaggggt 1510

<210> 143
<211> 2995
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (285)..(2351)

<400> 143
gcgtgttgta tataactatc tattcgatga tgaagatacc ccaccaaacc caaaaaaaga 60
gatctctcga ggatccgaat tcgcggccgc gtcgaccgcg gccgcgtcga cagaagattg 120
tgggtgtagt ggccacagcc ttacaggcag gcaggggtgg ttggtgtcaa caggggggcc 180
aacaggggtac cagagccaag accctcggcc tcttcccccg ccgccttcct gcagatctgc 240
ttggctttga ggaagagtgg cagtactgcc tcaactgcata aggg atg gga tca gag 296
Met Gly Ser Glu
1
aac agt gct tta aag agc tat aca ctg aga gaa cca cca ttt acc tta 344
Asn Ser Ala Leu Lys Ser Tyr Thr Leu Arg Glu Pro Pro Phe Thr Leu
5 10 15 20
ccc tct gga ctt gct gtt tat ccc gct gta ctg caa gat ggc aaa ttt 392
Pro Ser Gly Leu Ala Val Tyr Pro Ala Val Leu Gln Asp Gly Lys Phe
21 26 31 36
gct tca gtt ttt gtg tat aag aga gaa aat gaa gac aag gtt aat aaa 440
Ala Ser Val Phe Val Tyr Lys Arg Glu Asn Glu Asp Lys Val Asn Lys
37 42 47 52
gct gcc aag cat ttg aag aca ctt cgt cac cct tgc ttg cta aga ttt 488
Ala Ala Lys His Leu Lys Thr Leu Arg His Pro Cys Leu Leu Arg Phe
53 58 63 68
tta tct tgt act gtg gaa gcg gat ggc att cat ctt gtc act gag cga 536
Leu Ser Cys Thr Val Glu Ala Asp Gly Ile His Leu Val Thr Glu Arg
69 74 79 84
gta cag ccc ctg gaa gtg gct ttg gaa aca ttg tct tct gca gag gtc 584
Val Gln Pro Leu Glu Val Ala Leu Glu Thr Leu Ser Ser Ala Glu Val
85 90 95 100
tgt gct ggg atc tat gac ata ttg ctg gct ctt atc ttc ctt cat gac 632
Cys Ala Gly Ile Tyr Asp Ile Leu Leu Ala Leu Ile Phe Leu His Asp
101 106 111 116

aga gga cac cta aca cac aat aat gtc tgt tta tca tct gtg ttt gtg	680
Arg Gly His Leu Thr His Asn Asn Val Cys Leu Ser Ser Val Phe Val	
117 122 127 132	
agt gaa gat gga cac tgg aag cta gga gga atg gaa act gtt tgt aaa	728
Ser Glu Asp Gly His Trp Lys Leu Gly Gly Met Glu Thr Val Cys Lys	
133 138 143 148	
gtt tct cag gcc aca cca gag ttt ctg agg agt att cag tca ata aga	776
Val Ser Gln Ala Thr Pro Glu Phe Leu Arg Ser Ile Gln Ser Ile Arg	
149 154 159 164	
gac cca gca tct atc cct cct gaa gag atg tct cca gaa ttc aca act	824
Asp Pro Ala Ser Ile Pro Pro Glu Glu Met Ser Pro Glu Phe Thr Thr	
165 170 175 180	
ctc cca gag tgt cat gga cat gcc cgg gat gcc ttt tca ttt gga aca	872
Leu Pro Glu Cys His Gly His Ala Arg Asp Ala Phe Ser Phe Gly Thr	
181 186 191 196	
ttg gtg gaa agt ttg ctc aca atc tta aat gaa cag gtt tca gcg gat	920
Leu Val Glu Ser Leu Leu Thr Ile Leu Asn Glu Gln Val Ser Ala Asp	
197 202 207 212	
gtt ctc tcc agc ttt caa cag acc ttg cac tca act ttg ctg aat ccc	968
Val Leu Ser Ser Phe Gln Gln Thr Leu His Ser Thr Leu Leu Asn Pro	
213 218 223 228	
att cca aaa tgt cgg cca gcg ctc tgc acc tta cta tct cat gac ttc	1016
Ile Pro Lys Cys Arg Pro Ala Leu Cys Thr Leu Leu Ser His Asp Phe	
229 234 239 244	
ttc aga aat gat ttt ctg gaa gtt gtg aat ttc ttg aaa agt tta aca	1064
Phe Arg Asn Asp Phe Leu Glu Val Val Asn Phe Leu Lys Ser Leu Thr	
245 250 255 260	
ttg aag agt gaa gag gag aaa acg gaa ttc ttt aaa ttt ctg ctg gac	1112
Leu Lys Ser Glu Glu Glu Lys Thr Glu Phe Phe Lys Phe Leu Leu Asp	
261 266 271 276	
aga gtc agc tgc ttg tca gag gaa ttg ata gct tca agg ttg gtg cct	1160
Arg Val Ser Cys Leu Ser Glu Glu Leu Ile Ala Ser Arg Leu Val Pro	
277 282 287 292	
ctt ctg ctt aat cag ttg gtg ttt gca gag cca gtg gct gtt aag agt	1208
Leu Leu Leu Asn Gln Leu Val Phe Ala Glu Pro Val Ala Val Lys Ser	
293 298 303 308	
ttt ctt cct tat ctg ctt ggc ccc aaa aaa gat cat gcg cag gga gaa	1256
Phe Leu Pro Tyr Leu Leu Gly Pro Lys Lys Asp His Ala Gln Gly Glu	
309 314 319 324	
act cct tgc ttg ctc tca cca gcc ctg ttc cag tca cgg gtg atc ccc	1304
Thr Pro Cys Leu Leu Ser Pro Ala Leu Phe Gln Ser Arg Val Ile Pro	
325 330 335 340	
gtg ctt ctc cag ttg ttt gaa gtt cat gaa gag cat gtg cgg atg gtg	1352

Val	Leu	Leu	Gln	Leu	Phe	Glu	Val	His	Glu	Glu	His	Val	Arg	Met	Val	
341					346					351					356	
ctg	ctg	tct	cac	atc	gag	gcc	tac	gtg	gag	cac	ttc	act	cag	gag	cag	1400
Leu	Leu	Ser	His	Ile	Glu	Ala	Tyr	Val	Glu	His	Phe	Thr	Gln	Glu	Gln	
357					362					367					372	
ctg	aag	aaa	gtc	atc	ttg	cca	cag	gtt	ttg	ctg	ggc	ctg	cgt	gat	act	1448
Leu	Lys	Lys	Val	Ile	Leu	Pro	Gln	Val	Leu	Leu	Gly	Leu	Arg	Asp	Thr	
373					378					383					388	
agc	gat	tcc	att	gtg	gca	att	act	ctg	cat	agc	cta	gca	gtg	ctg	gtc	1496
Ser	Asp	Ser	Ile	Val	Ala	Ile	Thr	Leu	His	Ser	Leu	Ala	Val	Leu	Val	
389					394					399					404	
tct	ctg	ctt	gga	cca	gag	gtg	gtt	gtg	gga	gga	gaa	cga	acc	aag	atc	1544
Ser	Leu	Leu	Gly	Pro	Glu	Val	Val	Val	Gly	Gly	Glu	Arg	Thr	Lys	Ile	
405					410					415					420	
ttc	aaa	cgc	act	gcc	cca	agt	ttt	act	aaa	aat	act	gac	ctt	tct	cta	1592
Phe	Lys	Arg	Thr	Ala	Pro	Ser	Phe	Thr	Lys	Asn	Thr	Asp	Leu	Ser	Leu	
421					426					431					436	
gaa	ggc	gat	cca	ttt	tct	cag	cct	att	aaa	ttt	ccc	ata	aat	gga	ctc	1640
Glu	Gly	Asp	Pro	Phe	Ser	Gln	Pro	Ile	Lys	Phe	Pro	Ile	Asn	Gly	Leu	
437					442					447					452	
tca	gat	gta	aaa	aat	act	tcg	gag	gac	agt	gaa	aac	ttc	cca	tca	agt	1688
Ser	Asp	Val	Lys	Asn	Thr	Ser	Glu	Asp	Ser	Glu	Asn	Phe	Pro	Ser	Ser	
453					458					463					468	
tct	aaa	aag	tct	gag	gag	tgg	cct	gac	tgg	agt	gaa	cct	gag	gag	cct	1736
Ser	Lys	Lys	Ser	Glu	Glu	Trp	Pro	Asp	Trp	Ser	Glu	Pro	Glu	Glu	Pro	
469					474					479					484	
gaa	aat	caa	act	gtc	aac	ata	cag	att	tgg	cct	aga	gaa	cct	tgt	gat	1784
Glu	Asn	Gln	Thr	Val	Asn	Ile	Gln	Ile	Trp	Pro	Arg	Glu	Pro	Cys	Asp	
485					490					495					500	
gat	gtc	aag	tcc	cag	tgc	act	acc	ttg	gat	gtg	gaa	gag	tca	tct	tgg	1832
Asp	Val	Lys	Ser	Gln	Cys	Thr	Thr	Leu	Asp	Val	Glu	Glu	Ser	Ser	Trp	
501					506					511					516	
gat	gac	tgc	gag	ccc	agc	agc	tta	gat	act	aaa	gta	aac	cca	gga	ggt	1880
Asp	Asp	Cys	Glu	Pro	Ser	Ser	Leu	Asp	Thr	Lys	Val	Asn	Pro	Gly	Gly	
517					522					527					532	
gga	atc	act	gct	aca	aaa	cct	gtt	acc	tca	ggg	gag	cag	aag	cct	att	1928
Gly	Ile	Thr	Ala	Thr	Lys	Pro	Val	Thr	Ser	Gly	Glu	Gln	Lys	Pro	Ile	
533					538					543					548	
cct	gct	ttg	ctt	tca	ctc	act	gaa	gag	tct	atg	cct	tgg	aaa	tca	agc	1976
Pro	Ala	Leu	Leu	Ser	Leu	Thr	Glu	Glu	Ser	Met	Pro	Trp	Lys	Ser	Ser	
549					554					559					564	
tta	ccc	cga	aag	att	agc	ctt	gta	caa	agg	ggg	gat	gac	gca	gac	caa	2024
Leu	Pro	Arg	Lys	Ile	Ser	Leu	Val	Gln	Arg	Gly	Asp	Asp	Ala	Asp	Gln	

565	570	575	580	
atc gag ccg cca aaa gta tca tca caa gaa agg ccc ctt aag gtt cca				2072
Ile Glu Pro Pro Lys Val Ser Ser Gln Glu Arg Pro Leu Lys Val Pro				
581	586	591	596	
tca gaa ctt ggt tta gga gag gaa ttc acc att caa gta aaa aag aag				2120
Ser Glu Leu Gly Leu Gly Glu Glu Phe Thr Ile Gln Val Lys Lys Lys				
597	602	607	612	
cca gta aaa gat cct gag atg gat tgg ttt gct gat atg atc cca gaa				2168
Pro Val Lys Asp Pro Glu Met Asp Trp Phe Ala Asp Met Ile Pro Glu				
613	618	623	628	
att aag cct tct gct gct ttt ctt ata tta cct gaa ctg agg aca gaa				2216
Ile Lys Pro Ser Ala Ala Phe Leu Ile Leu Pro Glu Leu Arg Thr Glu				
629	634	639	644	
atg gtc cca aaa aag gat gat gtc tcc cca gtg atg cag ttt tcc tca				2264
Met Val Pro Lys Lys Asp Asp Val Ser Pro Val Met Gln Phe Ser Ser				
645	650	655	660	
aaa ttt gct gca gca gaa att act gag gga gag gct gaa ggc tgg gaa				2312
Lys Phe Ala Ala Ala Glu Ile Thr Glu Gly Glu Ala Glu Gly Trp Glu				
661	666	671	676	
gaa gaa ggg gag ctg aac tgg gaa gat aat aac tgg tga caatagatgt				2361
Glu Glu Gly Glu Leu Asn Trp Glu Asp Asn Asn Trp *				
677	682	687		
gagttaaact ttaggaaaaa ggattccctt tttttaaaaa aaatcaatac ctcaaaagca				2421
ggctttggga caagaaaacc ccaaagtggc ctgcttttcc catcccagga gctcattatc				2481
cagtctgtgc caactgaagt aggagactga ctgtgagtgc tggctaaaag ccctgggtgg				2541
tgaggctcac agtactggtt tccaggagga agagcctttg tgcatttgac tgaggccagt				2601
ttctatgaag agcaagtagc tgaggagagg tcgaatttac tgctttttcc aggacaattc				2661
tggaagtaaa gaaaatgtaa ttcaagctgg ttagcttaat tttgtgccat tcttttcttt				2721
aacataagag taagctctat tatgaaatac aactttaaaa aatttttagct ataaattata				2781
taaagatttt taaattgctg aggttttctt aggcagctta tttatttggt tacagttaga				2841
ctatctgagt aaatggttct ttgtggacct aggcagttcc tgactgttcc acatgtagta				2901
cattgtacca aagttcttaa taagaatatt cccacaatc ctgttctcta aatgtcaaat				2961
aaagattatt ttcactagat tcaaaaaaaaaaaaa				2995

<210> 144
<211> 1031

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (138)..(950)

<220>
<221> misc_feature
<222> (1)...(1031)
<223> n = a,t,c or g

<400> 144
atttggccct cgaggccaag aattcggcac gagagggggg atcgctggga gcggttgagg 60
cgtgcgggga gctgagttat agctgtgact tctgccctgc caggccgcac acaagctggc 120
tgacccggtt tgtaaaa atg gaa ttt caa gca gta gtg atg gca gta ggt 170
Met Glu Phe Gln Ala Val Val Met Ala Val Gly
1 5
gga gga tct cgg atg aca gac cta act tcc agc att ccc aaa cct ctg 218
Gly Gly Ser Arg Met Thr Asp Leu Thr Ser Ser Ile Pro Lys Pro Leu
12 17 22 27
ctt cca gtt ggg aac aaa cct tta att tgg tac cca ttg aac ctg ctt 266
Leu Pro Val Gly Asn Lys Pro Leu Ile Trp Tyr Pro Leu Asn Leu Leu
28 33 38 43
gag cgt gtt gga ttt gaa gaa gtc att gtg gtt aca acc agg gat gtt 314
Glu Arg Val Gly Phe Glu Glu Val Ile Val Val Thr Thr Arg Asp Val
44 49 54 59
caa aag gct cta tgt gca gaa ttc aag atg aaa atg aag cca gat att 362
Gln Lys Ala Leu Cys Ala Glu Phe Lys Met Lys Met Lys Pro Asp Ile
60 65 70 75
gtg tgt att cct gat gac gct gac atg gga act gca gat tct ttg cgc 410
Val Cys Ile Pro Asp Asp Ala Asp Met Gly Thr Ala Asp Ser Leu Arg
76 81 86 91
tac ata tat cca aaa ctt aag aca gat gtg ctg gtg ctg agc tgt gat 458
Tyr Ile Tyr Pro Lys Leu Lys Thr Asp Val Leu Val Leu Ser Cys Asp
92 97 102 107
ctg ata aca gac gtt gcc tta cat gag gtt gtg gac ctg ttt aga gct 506
Leu Ile Thr Asp Val Ala Leu His Glu Val Val Asp Leu Phe Arg Ala
108 113 118 123
tat gat gca tca ctt gct atg ttg atg aga aaa ggc caa gat agc ata 554
Tyr Asp Ala Ser Leu Ala Met Leu Met Arg Lys Gly Gln Asp Ser Ile
124 129 134 139
gaa cct gtt ccc ggt caa aag ggg aaa aaa aaa gca gtg gag cag cgt 602
Glu Pro Val Pro Gly Gln Lys Gly Lys Lys Lys Ala Val Glu Gln Arg
140 145 150 155

gac ttc att gga gtg gac agc aca gga aag agg ctg ctc ttc atg gct	650
Asp Phe Ile Gly Val Asp Ser Thr Gly Lys Arg Leu Leu Phe Met Ala	
156 161 166 171	
aat gaa gca gac ttg gat gaa gag ctg gtc att aag gga tcc atc cta	698
Asn Glu Ala Asp Leu Asp Glu Glu Leu Val Ile Lys Gly Ser Ile Leu	
172 177 182 187	
cag aag cat cct aga ata cgt ttc cac acg ggt ctt gtg gat gcc cac	746
Gln Lys His Pro Arg Ile Arg Phe His Thr Gly Leu Val Asp Ala His	
188 193 198 203	
ctc tac tgt ttg aaa aaa tac atc gtg gat ttc cta atg gaa aat ggg	794
Leu Tyr Cys Leu Lys Lys Tyr Ile Val Asp Phe Leu Met Glu Asn Gly	
204 209 214 219	
tca ata act tct atc cgg agt gaa ctg att cca tat tta gtg aga aaa	842
Ser Ile Thr Ser Ile Arg Ser Glu Leu Ile Pro Tyr Leu Val Arg Lys	
220 225 230 235	
cag ttt tcc tca gct tcc tca caa cag ggg aca agg aag gaa aaa gag	890
Gln Phe Ser Ser Ala Ser Ser Gln Gln Gly Thr Arg Lys Glu Lys Glu	
236 241 246 251	
gga ggg tct aaa gga aaa agg ggc ttg aag tcc ttt agg ata tct tac	938
Gly Gly Ser Lys Gly Lys Arg Gly Leu Lys Ser Phe Arg Ile Ser Tyr	
252 257 262 267	
agt ttt tat taa aag gaagccaatt aactggaac cggggctccc tatggatggc	993
Ser Phe Tyr *	
268	
ctgctgggga ttgcctgttc gagggnggac ggttgggg	1031

<210> 145
 <211> 2130
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (184)..(1236)

<400> 145	
gttttctcca catggaaact tattggcggt tgccctgcga gacagaaccg tgagactctg	60
gattcctgat aagagaggaa aattctcata atttaaagct catacagctc cagttogaag	120
tggagacttt tcacctgatg gccagtttct agctacagct tctgaagaca aatccataat	180
agt atg gag cat gta tcg cca gcg ctt cct gta ttc ctt gga tcg aca	228
Met Glu His Val Ser Pro Ala Leu Pro Val Phe Leu Gly Ser Thr	
1 5 10	

tac aca ctg tgt acg ctg tgc cca att gta ccc gat gga aga cta att	276
Tyr Thr Leu Cys Thr Leu Cys Pro Ile Val Pro Asp Gly Arg Leu Ile	
16 21 26 31	
gtg tca tgt agt gag gat aaa act att aaa att tgg gat acc aca aat	324
Val Ser Cys Ser Glu Asp Lys Thr Ile Lys Ile Trp Asp Thr Thr Asn	
32 37 42 47	
aag caa tgt gtt aat aac ttc tca gat tcc gtt gga ttt gca aat ttt	372
Lys Gln Cys Val Asn Asn Phe Ser Asp Ser Val Gly Phe Ala Asn Phe	
48 53 58 63	
gtg gac ttt aac cct agt ggt aca tgc ata gct tca gca ggt tct gat	420
Val Asp Phe Asn Pro Ser Gly Thr Cys Ile Ala Ser Ala Gly Ser Asp	
64 69 74 79	
caa act gtg aaa gtc tgg gat gta aga gtg aac aaa tta cta cag cat	468
Gln Thr Val Lys Val Trp Asp Val Arg Val Asn Lys Leu Leu Gln His	
80 85 90 95	
tac caa gtt cac agc ggt gga gtt aat tgc ata tca ttc cat cct tcg	516
Tyr Gln Val His Ser Gly Gly Val Asn Cys Ile Ser Phe His Pro Ser	
96 101 106 111	
ggt aac tat ctc atc aca gct tct tca gat ggt acc ctt aag att ctg	564
Gly Asn Tyr Leu Ile Thr Ala Ser Ser Asp Gly Thr Leu Lys Ile Leu	
112 117 122 127	
gac ctc tta gaa gga agg ctc atc tat aca ctt caa gga cat acg gga	612
Asp Leu Leu Glu Gly Arg Leu Ile Tyr Thr Leu Gln Gly His Thr Gly	
128 133 138 143	
cct gtc ttt act gtt tca ttt tca aaa ggt gga gag cta ttt gca tca	660
Pro Val Phe Thr Val Ser Phe Ser Lys Gly Gly Glu Leu Phe Ala Ser	
144 149 154 159	
gga ggt gca gac aca cag gtc tta tta tgg agg act aac ttt gat gaa	708
Gly Gly Ala Asp Thr Gln Val Leu Leu Trp Arg Thr Asn Phe Asp Glu	
160 165 170 175	
ttg cat tgt aaa ggt ctt acc aaa aga aat ctc aaa aga tta cat ttt	756
Leu His Cys Lys Gly Leu Thr Lys Arg Asn Leu Lys Arg Leu His Phe	
176 181 186 191	
gat tca cca cca cat ctt ctt gat atc tac cca aga aca cca cat ccc	804
Asp Ser Pro Pro His Leu Leu Asp Ile Tyr Pro Arg Thr Pro His Pro	
192 197 202 207	
cat gag gaa aaa gtt gag act gta gaa att aat cca aag ctt gag gta	852
His Glu Glu Lys Val Glu Thr Val Glu Ile Asn Pro Lys Leu Glu Val	
208 213 218 223	
atc gat ttg cag atc tct act ccc cct gtt atg gat atc ctt tct ttt	900
Ile Asp Leu Gln Ile Ser Thr Pro Pro Val Met Asp Ile Leu Ser Phe	
224 229 234 239	
gat tct acc aca aca aca gaa acc agt ggt agg act ctg cca gac aag	948

Asp Ser Thr Thr Thr Thr Glu Thr Ser Gly Arg Thr Leu Pro Asp Lys	
240 245 250 255	
ggt gaa gag gcc tgt gga tat ttc ttg aac cct tcc tta atg tca cca	996
Gly Glu Glu Ala Cys Gly Tyr Phe Leu Asn Pro Ser Leu Met Ser Pro	
256 261 266 271	
gaa tgt ttg cca aca acc acg aaa aag aaa aca gaa gac atg agt gac	1044
Glu Cys Leu Pro Thr Thr Thr Lys Lys Lys Thr Glu Asp Met Ser Asp	
272 277 282 287	
ctc ccc tgt gaa agt caa agg agc ata cct ctc gct gtg act gat gct	1092
Leu Pro Cys Glu Ser Gln Arg Ser Ile Pro Leu Ala Val Thr Asp Ala	
288 293 298 303	
tta gag cat att atg gaa caa ctc aat gtt ttg aca cag act gtt tca	1140
Leu Glu His Ile Met Glu Gln Leu Asn Val Leu Thr Gln Thr Val Ser	
304 309 314 319	
atc ttg gag cag cga ctg act ttg aca gag gat aag ctg aaa gac tgc	1188
Ile Leu Glu Gln Arg Leu Thr Leu Thr Glu Asp Lys Leu Lys Asp Cys	
320 325 330 335	
ctt gaa aat cag caa aag ctt ttc agt gct gtc caa cag aaa agc tga	1236
Leu Glu Asn Gln Gln Lys Leu Phe Ser Ala Val Gln Gln Lys Ser *	
336 341 346 351	
ataaaaaatt catttttcatt tggtgggcag agggccaata aatgaacaaa tgtacataca	1296
ctcaggaagg tagtacaaga tactccatac aacacaacca tgtgctatatt atcatggcat	1356
ttcttaaaag ggtgagcaac agaacaaaag gcagaaaagg catacctaag gactaattta	1416
aacacatatc aatgtgaagg actaatttaa attactatca tttatgattg cagtaataaa	1476
gtgataagca ttcaagcaac tctgtatttt ccccatatta ttttaaagt ccattttcat	1536
ttataggcca aatcctgccca ggaaagtaac ccagatctct ggatttcact gttaagtcac	1596
ttcagattga ccatattcag acagtcattg ggtgaaataa ttcacttacc tccaaaatag	1656
catcctatat ggccaataat gagttattga totgactagt tgtatgtctt tctgttcaaa	1716
atagaaatta tcctttctta ctaatgcctt gaaagaatga acaataaaaa attcccagac	1776
cacagaattt ccacagcaag aatacactta ttttaattaa caatagcaca gatatagcat	1836
agggcagtgg gtttttttagt taatttatgg ccgactttgt ttatccattg gccaacctga	1896
aggaaatgaa actcacctat ctttctatca cagatgaatg cgctagatga atgatttggg	1956
ctggatctga ccattggttca cacaatttat gtcagggtgg ttagtgacg gtaaattgtct	2016
gagtgattcg agagtgattt ttatcatcct attccactgt aggggcactt gctcgagaaa	2076
tattgctgtt atgctgactt cggctgcttt tcgtatctcc ttttataatc ttctg	2130

<210> 146
 <211> 4515
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (44) .. (1381)

<400> 146

```

cggaattgcc ggaccgacga tttcgtgtag aggcggcggc aaa  atg gcg gcg cct      55
                                         Met Ala Ala Pro
                                         1

gag gag cgg gat cta acc cag gag cag aca gag aag ctg ctg cag ttt      103
Glu Glu Arg Asp Leu Thr Gln Glu Gln Thr Glu Lys Leu Leu Gln Phe
  5              10              15              20

cag gat ctc act ggc atc gaa tct atg gat cag tgt cgc cat acc ttg      151
Gln Asp Leu Thr Gly Ile Glu Ser Met Asp Gln Cys Arg His Thr Leu
  21              26              31              36

gaa cag cat aac tgg aac ata gag gct gct gta cag gac aga ttg aat      199
Glu Gln His Asn Trp Asn Ile Glu Ala Ala Val Gln Asp Arg Leu Asn
  37              42              47              52

gag caa gag ggc gta cct agt gtt ttc aac cca cct cca tca cga ccc      247
Glu Gln Glu Gly Val Pro Ser Val Phe Asn Pro Pro Pro Ser Arg Pro
  53              58              63              68

ctg cag gtt aat aca gct gac cac agg atc tac agc tat gtt gtc tca      295
Leu Gln Val Asn Thr Ala Asp His Arg Ile Tyr Ser Tyr Val Val Ser
  69              74              79              84

aga cct caa cca agg ggg ctg ctt gga tgg ggt tat tac ttg ata atg      343
Arg Pro Gln Pro Arg Gly Leu Leu Gly Trp Gly Tyr Tyr Leu Ile Met
  85              90              95              100

ctt cca ttc cgg ttt acc tat tac acg ata ctt gat ata ttt agg ttt      391
Leu Pro Phe Arg Phe Thr Tyr Tyr Thr Ile Leu Asp Ile Phe Arg Phe
  101             106             111             116

gct ctt cgt ttt ata cgg cct gac cct cgc agc cgg gtc act gac ccc      439
Ala Leu Arg Phe Ile Arg Pro Asp Pro Arg Ser Arg Val Thr Asp Pro
  117             122             127             132

gtt ggg gac att gtt tca ttt atg cac tct ttt gaa gag aaa tat ggg      487
Val Gly Asp Ile Val Ser Phe Met His Ser Phe Glu Glu Lys Tyr Gly
  133             138             143             148

agg gca cac cct gtc ttc tac cag gga acg tac agc cag gca ctt aac      535
Arg Ala His Pro Val Phe Tyr Gln Gly Thr Tyr Ser Gln Ala Leu Asn
  149             154             159             164

```

gat gcc aaa agg gag ctt cgc ttt ctt ttg gtt tat ctt cat gga gat	583
Asp Ala Lys Arg Glu Leu Arg Phe Leu Leu Val Tyr Leu His Gly Asp	
165 170 175 180	
gat cac cag gac tct gat gag ttt tgt cgc aac aca ctc tgt gca cct	631
Asp His Gln Asp Ser Asp Glu Phe Cys Arg Asn Thr Leu Cys Ala Pro	
181 186 191 196	
gaa gtt att tca cta ata aac act agg atg ctc ttc tgg gca tgc tct	679
Glu Val Ile Ser Leu Ile Asn Thr Arg Met Leu Phe Trp Ala Cys Ser	
197 202 207 212	
aca aac aaa cct gag gga tac agg gtc tca cag gct tta cga gag aac	727
Thr Asn Lys Pro Glu Gly Tyr Arg Val Ser Gln Ala Leu Arg Glu Asn	
213 218 223 228	
acc tat cca ttc ctg gcc atg att atg ctg aag gat cga agg atg act	775
Thr Tyr Pro Phe Leu Ala Met Ile Met Leu Lys Asp Arg Arg Met Thr	
229 234 239 244	
gtg gtg gga cgg cta gaa ggc ctc att caa cct gat gac ctc att aac	823
Val Val Gly Arg Leu Glu Gly Leu Ile Gln Pro Asp Asp Leu Ile Asn	
245 250 255 260	
caa ctg aca ttt atc atg gat gct aac cag act tac ctg gtg tca gaa	871
Gln Leu Thr Phe Ile Met Asp Ala Asn Gln Thr Tyr Leu Val Ser Glu	
261 266 271 276	
cgc cta gaa agg gaa gaa aga aac cag acc caa gtg ctg aga caa cag	919
Arg Leu Glu Arg Glu Glu Arg Asn Gln Thr Gln Val Leu Arg Gln Gln	
277 282 287 292	
cag gat gag gcc tac ctg gcc tct ctc aga gct gac cag gag aaa gaa	967
Gln Asp Glu Ala Tyr Leu Ala Ser Leu Arg Ala Asp Gln Glu Lys Glu	
293 298 303 308	
aga aag aaa cgg gag gag cgg gag cgt aag cgg cgg aag gag gag gag	1015
Arg Lys Lys Arg Glu Glu Arg Glu Arg Lys Arg Arg Lys Glu Glu Glu	
309 314 319 324	
gtg caa cag caa aag ttg gca gag gag aga cgg cgg cag aat tta cag	1063
Val Gln Gln Gln Lys Leu Ala Glu Glu Arg Arg Arg Gln Asn Leu Gln	
325 330 335 340	
gag gaa aag gaa agg aag ttg gaa tgc ctg ccc cct gaa cct tcc cct	1111
Glu Glu Lys Glu Arg Lys Leu Glu Cys Leu Pro Pro Glu Pro Ser Pro	
341 346 351 356	
gat gac cct gaa agt gtc aag atc atc ttc aaa tta cct aat gat tct	1159
Asp Asp Pro Glu Ser Val Lys Ile Ile Phe Lys Leu Pro Asn Asp Ser	
357 362 367 372	
cga gta gag aga cga ttc cac ttt tca cag tct cta aca gta atc cac	1207
Arg Val Glu Arg Arg Phe His Phe Ser Gln Ser Leu Thr Val Ile His	
373 378 383 388	
gac ttc tta ttc tcc ttg aag gaa agc cca gaa aag ttt cag att gaa	1255

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

gttgagttaa tggtaatggg tacatgggtc aggccatgta ttaacagatg ccagtgcgct 2722
ctgacaagta ttccaaagtg ttccgtagct agactgggtc aggcctggtg taccactgca 2782
accgactgac gttactgtag ttccctagaat gctgtgaggg cgggggggtc agatcaacat 2842
aaagcctaac ttgctggagt tgtagtctca aggccttctc tcttgcttaa ctaaaccta 2902
aggaccactg tttttggtag caattatatg gttactatcc actgcagtcc tcagttgttg 2962
gggtaaatcc cacatggcag agtaaggcac cccacagaaa ttaacttga gagcctgaga 3022
aattcccagt ggccctggca tagctgtcta gaacaccatc tctaggaaaa ttttaattctg 3082
tccctggcca gctattgttc ttccacttcg ttttctgctg tcccaaggcc agatgagtgg 3142
aatcaccatc tgactgttgt cagtaaaatg tatctggcgt gaacagcagg ataaccatg 3202
ttctccacat aaggataacc ttacgtgaaa ccttcctgct gacaaccatg cagaggaatt 3262
ttttccactt aagtcagagc cttcctcccc atctggaatt cacagctgtt ccctgggcag 3322
cacacaggag ggtattaagg acctttgtga ggctaggtac actgtccaca cctctttggg 3382
gaagttacga tttttttttt ccatacataat tcagtctctt cttattctac agtgtgcact 3442
ttatgcctct cgcccttttga taatagttgt tcagtgaagg aagtcagctg ccagaatatt 3502
aagaagggtc tcccttttatg tcagtacaac tggttagggcg gccttcccat ttactttagg 3562
tttcaagagg attcaccgga agcacatgcc ccggtctagt cccatttgaa acagttctgc 3622
tttactgaga ccctaggccg gtctccttgc tgaccctagc gctgctgcct aggtgccatt 3682
tcctttcctc ctcagtcaaa tacaggctgc acattttgtc acttaatgcc agtacaatct 3742
gtgttactcc taaggacttt tgggattttg atgagacctg cgaggagaa gacactgaga 3802
agccagtgat ctgcaagcat ttgctcttgt ttccacatca cctctgggat atttcagctg 3862
ttgtttccaa atggcaaata atcaactaaa agcacttggt tcaagttttg ttctgcactc 3922
ccacgactga agttgtagat tgagctgaat aaccatggga agtgaccaag caaagacact 3982
cgattggagt cagttgaata tttgtaccct cagtggagcc cttctggtct tttcttcac 4042
ttctgcagaa tttcctctag caaatacttc tttctccttg cttgcctcca ccatgatatt 4102
tgaataagag atggccagag gataacactt gtctcttaaa aactaagcta aaaagaacct 4162
agaaccttca attgagcagt tgtgaaaatt gctaattggt ccaaggccaa gcaaagagtt 4222
tcagaaatg actgagaagg agcgataacc cccagaatgc aaaatcaggg gcatcattat 4282
ccggtgcttg aacaaggagc tccgctctac aactggtttt tttaggactt gtgaggaaca 4342
cagcaacgga aatccatcca caaaggatgc agtgcccaa cttgtactgc gcctgaatag 4402

tcatgtgata atttactgaa gaaatctagt gtactttaaa tttttttcat aaaagtttac 4462
attgtattgt aggttaacat taaatgtttt atagcaaaaaa cttcaaaaaa aaa 4515

<210> 147
<211> 5761
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (168)..(2885)

<400> 147
tttcgtcagg aatttccctt caaggtagca ggagatgaac gcgtgctgct ccaggatttt 60
acagaactga ttctgcagca aagacaaatg ttgcctgtat ttgccagata gtataaacag 120
gagcaaaaagt tgcacagcta aaccaggggc tcattcccag gacagac atg cag tta 176
Met Gln Leu
1
tgg att ccg aaa gac aag tca agg aca ctg atg aca ttg aaa gtc cta 224
Trp Ile Pro Lys Asp Lys Ser Arg Thr Leu Met Thr Leu Lys Val Leu
4 9 14 19
aac gca gta tcc gag aca gtg gct aca tcg act gct ggg att ccg agc 272
Asn Ala Val Ser Glu Thr Val Ala Thr Ser Thr Ala Gly Ile Pro Ser
20 25 30 35
gca gcg act ccc tct ctc ctc ctc gcc acg gca gag atg att cct tcg 320
Ala Ala Thr Pro Ser Leu Leu Leu Ala Thr Ala Glu Met Ile Pro Ser
36 41 46 51
aca gcc tgg att cct ttg gct ctc gct cgt cgg cag acg cct tca cca 368
Thr Ala Trp Ile Pro Leu Ala Leu Ala Arg Arg Gln Thr Pro Ser Pro
52 57 62 67
gat gta gtc ctc agg gga agc agc gat ggg aga gga agc gac tct gaa 416
Asp Val Val Leu Arg Gly Ser Ser Asp Gly Arg Gly Ser Asp Ser Glu
68 73 78 83
tcc gac ttg cct cat cgg aag ctg cca gat gtg aag aag gat gac atg 464
Ser Asp Leu Pro His Arg Lys Leu Pro Asp Val Lys Lys Asp Asp Met
84 89 94 99
tct gca cgg cgg act tcc cat ggt gag cgg aaa tca gca gtg cct ttt 512
Ser Ala Arg Arg Thr Ser His Gly Glu Pro Lys Ser Ala Val Pro Phe
100 105 110 115
aac cag tac ctc ccg aac aaa agc aat cag acg gcc tac gtc ccc gcg 560
Asn Gln Tyr Leu Pro Asn Lys Ser Asn Gln Thr Ala Tyr Val Pro Ala
116 121 126 131

cct ctg aga aag aag aaa gca gag aga gag gaa tac cgc aag agc tgg	608
Pro Leu Arg Lys Lys Lys Ala Glu Arg Glu Glu Tyr Arg Lys Ser Trp	
132 137 142 147	
agt acc gcc acc tcc ccg ctg ggt ggg gag agg ccc ttc aga tac ggt	656
Ser Thr Ala Thr Ser Pro Leu Gly Gly Glu Arg Pro Phe Arg Tyr Gly	
148 153 158 163	
ccg aga act cct gtg tct gat gac gca gag agc acc agc atg ttt gac	704
Pro Arg Thr Pro Val Ser Asp Asp Ala Glu Ser Thr Ser Met Phe Asp	
164 169 174 179	
atg cgg tgt gag gag gag gcc gcg gtg cag ccg cac agc agg gcc cgc	752
Met Arg Cys Glu Glu Glu Ala Ala Val Gln Pro His Ser Arg Ala Arg	
180 185 190 195	
cag gag cag ctg cag ctg ata aat aac cag ctg agg gaa gag gac gac	800
Gln Glu Gln Leu Gln Leu Ile Asn Asn Gln Leu Arg Glu Glu Asp Asp	
196 201 206 211	
aaa tgg caa gat gac ctg gct cgt tgg aag agt cgt aga aga agt gtt	848
Lys Trp Gln Asp Asp Leu Ala Arg Trp Lys Ser Arg Arg Arg Ser Val	
212 217 222 227	
tct cag gac tta atc aag aaa gag gaa gaa agg aaa aaa atg gag aag	896
Ser Gln Asp Leu Ile Lys Lys Glu Glu Glu Arg Lys Lys Met Glu Lys	
228 233 238 243	
tta ctg gct gga gaa gat ggg aca agt gaa cga agg aaa agc atc aaa	944
Leu Leu Ala Gly Glu Asp Gly Thr Ser Glu Arg Arg Lys Ser Ile Lys	
244 249 254 259	
acc tac aga gaa att gtt caa gaa aaa gag cgg aga gag aga gag ctg	992
Thr Tyr Arg Glu Ile Val Gln Glu Lys Glu Arg Arg Glu Arg Glu Leu	
260 265 270 275	
cat gaa gca tat aag aac gct cgg tcc cag gag gag gca gag ggg atc	1040
His Glu Ala Tyr Lys Asn Ala Arg Ser Gln Glu Glu Ala Glu Gly Ile	
276 281 286 291	
ctt caa cag tac att gag agg ttc acc atc agt gag gct gtt ctc gaa	1088
Leu Gln Gln Tyr Ile Glu Arg Phe Thr Ile Ser Glu Ala Val Leu Glu	
292 297 302 307	
cgc ttg gag atg cca aaa att ctg gaa aga agc cat tca aca gag cca	1136
Arg Leu Glu Met Pro Lys Ile Leu Glu Arg Ser His Ser Thr Glu Pro	
308 313 318 323	
aat tta tcc tcc ttc ctg aat gac ccc aat ccc atg aaa tac ctg cgg	1184
Asn Leu Ser Ser Phe Leu Asn Asp Pro Asn Pro Met Lys Tyr Leu Arg	
324 329 334 339	
caa cag tca ctg cct cca ccc aaa ttc act gcc act gtt gaa acc acc	1232
Gln Gln Ser Leu Pro Pro Pro Lys Phe Thr Ala Thr Val Glu Thr Thr	
340 345 350 355	

att gct cgt gcc agt gtt ctg gat acc agc atg tca gca ggc agt ggg Ile Ala Arg Ala Ser Val Leu Asp Thr Ser Met Ser Ala Gly Ser Gly 356 361 366 371	1280
tct cca agc aaa act gtc act ccc aaa gca gtg cct atg ctg aca ccc Ser Pro Ser Lys Thr Val Thr Pro Lys Ala Val Pro Met Leu Thr Pro 372 377 382 387	1328
aag cct tac tcc cag ccc aaa aat tct caa gat gtt ctg aag acc ttt Lys Pro Tyr Ser Gln Pro Lys Asn Ser Gln Asp Val Leu Lys Thr Phe 388 393 398 403	1376
aag gta gac ggg aaa gtc agt gtg aat gga gag acg gtt cat aga gag Lys Val Asp Gly Lys Val Ser Val Asn Gly Glu Thr Val His Arg Glu 404 409 414 419	1424
gag gag aag gaa aga gag tgt ccc acg gtg gca cct gcc cac tcc tta Glu Glu Lys Glu Arg Glu Cys Pro Thr Val Ala Pro Ala His Ser Leu 420 425 430 435	1472
acc aaa tcc cag atg ttt gaa ggt gtg gcc aga gtg cac ggg tct cca Thr Lys Ser Gln Met Phe Glu Gly Val Ala Arg Val His Gly Ser Pro 436 441 446 451	1520
ctg gag ctg aaa caa gac aac ggt agc atc gag atc aac ata aag aag Leu Glu Leu Lys Gln Asp Asn Gly Ser Ile Glu Ile Asn Ile Lys Lys 452 457 462 467	1568
cca aac tct gtt ccc caa gag ctc gca gca acc act gag aaa acg gaa Pro Asn Ser Val Pro Gln Glu Leu Ala Ala Thr Thr Glu Lys Thr Glu 468 473 478 483	1616
ccg aat agt caa gag gac aag aat gat ggt gga aaa tca aga aaa ggg Pro Asn Ser Gln Glu Asp Lys Asn Asp Gly Gly Lys Ser Arg Lys Gly 484 489 494 499	1664
aat ata gaa ctt gcc tca tca gaa cca cag cat ttt aca aca act gtg Asn Ile Glu Leu Ala Ser Ser Glu Pro Gln His Phe Thr Thr Thr Val 500 505 510 515	1712
act cga tgc agc ccg acc gtg gcc ttt gtg gaa ttt ccc tcc agc ccc Thr Arg Cys Ser Pro Thr Val Ala Phe Val Glu Phe Pro Ser Ser Pro 516 521 526 531	1760
cag ctg aag aat gat gtg tcg gaa gaa aaa gac cag aag aaa cca gaa Gln Leu Lys Asn Asp Val Ser Glu Glu Lys Asp Gln Lys Lys Pro Glu 532 537 542 547	1808
aat gaa atg agt gga aag gtg gag ttg gtg ctg tca caa aag gtg gta Asn Glu Met Ser Gly Lys Val Glu Leu Val Leu Ser Gln Lys Val Val 548 553 558 563	1856
aag cca aaa tct cca gaa ccc gaa gca acg ctg aca ttt cca ttt ctg Lys Pro Lys Ser Pro Glu Pro Glu Ala Thr Leu Thr Phe Pro Phe Leu 564 569 574 579	1904
gac aaa atg cct gaa gcc aac caa cta cat ttg cca aat ctc aat tct	1952

Asp	Lys	Met	Pro	Glu	Ala	Asn	Gln	Leu	His	Leu	Pro	Asn	Leu	Asn	Ser	
580					585					590					595	
caa	gtg	gat	tct	cca	agc	agt	gag	aag	tca	cct	gtt	acg	aca	cct	ttt	2000
Gln	Val	Asp	Ser	Pro	Ser	Ser	Glu	Lys	Ser	Pro	Val	Thr	Thr	Pro	Phe	
596					601					606					611	
aag	ttc	tgg	gca	tgg	gac	cca	gaa	gag	gag	cgc	agg	cga	cag	gaa	aaa	2048
Lys	Phe	Trp	Ala	Trp	Asp	Pro	Glu	Glu	Glu	Arg	Arg	Arg	Gln	Glu	Lys	
612					617					622					627	
tgg	caa	cag	gaa	cag	gaa	cgt	ttg	ctc	cag	gag	aga	tac	cag	aag	gag	2096
Trp	Gln	Gln	Glu	Gln	Glu	Arg	Leu	Leu	Gln	Glu	Arg	Tyr	Gln	Lys	Glu	
628					633					638					643	
cag	gac	aag	ctg	aaa	gaa	gag	tgg	gaa	aag	gcc	caa	aag	gag	gtg	gaa	2144
Gln	Asp	Lys	Leu	Lys	Glu	Glu	Trp	Glu	Lys	Ala	Gln	Lys	Glu	Val	Glu	
644					649					654					659	
gag	gaa	gaa	cgc	aga	tac	tat	gag	gag	gag	cgt	aag	ata	att	gaa	gac	2192
Glu	Glu	Glu	Arg	Arg	Tyr	Tyr	Glu	Glu	Glu	Arg	Lys	Ile	Ile	Glu	Asp	
660					665					670					675	
act	gtg	gtt	cca	ttt	act	gtt	tct	tca	agt	tcc	gct	gac	cag	ctg	tct	2240
Thr	Val	Val	Pro	Phe	Thr	Val	Ser	Ser	Ser	Ser	Ala	Asp	Gln	Leu	Ser	
676					681					686					691	
acc	tct	tcc	tcc	atg	act	gaa	ggc	agt	ggg	aca	atg	aat	aag	ata	gac	2288
Thr	Ser	Ser	Ser	Met	Thr	Glu	Gly	Ser	Gly	Thr	Met	Asn	Lys	Ile	Asp	
692					697					702					707	
ctg	gga	aac	tgt	caa	gat	gaa	aaa	caa	gac	aga	aga	tgg	aag	aaa	tca	2336
Leu	Gly	Asn	Cys	Gln	Asp	Glu	Lys	Gln	Asp	Arg	Arg	Trp	Lys	Lys	Ser	
708					713					718					723	
ttc	cag	gga	gat	gac	agt	gac	tta	ttg	ctg	aag	act	agg	gaa	agt	gat	2384
Phe	Gln	Gly	Asp	Asp	Ser	Asp	Leu	Leu	Leu	Lys	Thr	Arg	Glu	Ser	Asp	
724					729					734					739	
cga	ctg	gag	gag	aag	ggc	agc	cta	act	gaa	ggg	gcc	ttg	gct	cat	tct	2432
Arg	Leu	Glu	Glu	Lys	Gly	Ser	Leu	Thr	Glu	Gly	Ala	Leu	Ala	His	Ser	
740					745					750					755	
ggg	aac	cct	gta	tca	aaa	gga	gtc	cat	gaa	gac	cat	cag	ctg	gat	acc	2480
Gly	Asn	Pro	Val	Ser	Lys	Gly	Val	His	Glu	Asp	His	Gln	Leu	Asp	Thr	
756					761					766					771	
gag	gct	ggg	gcc	cca	cac	tgt	gga	aca	aac	cca	cag	ctt	gct	cag	gat	2528
Glu	Ala	Gly	Ala	Pro	His	Cys	Gly	Thr	Asn	Pro	Gln	Leu	Ala	Gln	Asp	
772					777					782					787	
cca	tcc	cag	aat	cag	cag	aca	tca	aat	cca	acg	cac	agt	tca	gaa	gat	2576
Pro	Ser	Gln	Asn	Gln	Gln	Thr	Ser	Asn	Pro	Thr	His	Ser	Ser	Glu	Asp	
788					793					798					803	
gtg	aag	cca	aaa	acc	ctc	ccg	ctg	gat	aaa	agc	att	aac	cat	cag	atc	2624
Val	Lys	Pro	Lys	Thr	Leu	Pro	Leu	Asp	Lys	Ser	Ile	Asn	His	Gln	Ile	

804	809	814	819	
gag tct ccc agt gaa agg cgg aag tct ata agt gga aag aag ctg tgc				2672
Glu Ser Pro Ser Glu Arg Arg Lys Ser Ile Ser Gly Lys Lys Leu Cys				
820	825	830	835	
tct tcc tgt ggg ctt cct ttg ggt aaa gga gct gca atg atc atc gag				2720
Ser Ser Cys Gly Leu Pro Leu Gly Lys Gly Ala Ala Met Ile Ile Glu				
836	841	846	851	
acc ctc aat ctc tat ttt cac atc cag tgt ttc agg tgt gga att tgt				2768
Thr Leu Asn Leu Tyr Phe His Ile Gln Cys Phe Arg Cys Gly Ile Cys				
852	857	862	867	
aaa ggc cag ctt gga gat gca gtg agt ggg acg gat gtt agg att cga				2816
Lys Gly Gln Leu Gly Asp Ala Val Ser Gly Thr Asp Val Arg Ile Arg				
868	873	878	883	
aat ggt ctc ctg aac tgt aat gat tgc tac atg cga tcc aga agt gcc				2864
Asn Gly Leu Leu Asn Cys Asn Asp Cys Tyr Met Arg Ser Arg Ser Ala				
884	889	894	899	
ggg cag cct aca aca ttg tga ca cggttttcaa gcttccggat cactcaccat				2917
Gly Gln Pro Thr Thr Leu *				
900	905			
ttctttactg agagtgtccc ctggcaactg cttaacaaaa tcccaagctc aggggcttct				2977
caccattttac ctaattttctg aaaggctctt ctgaaagggtg gtatctgttc tttcgtagca				3037
cagtgtttat gtttttctg tttattgttt tgggtttttt ttttttttg catttgca				3097
gtatacacia aagaatatgg ggttgtaatg atcctgaata gctcaaaaaa ggtttttagca				3157
tggtcaaaca ggcttatggg ttaaaatgtg ttattctctt ctttggggaat tagctaaatg				3217
atgcaataaa cctgttttgt tttagaatgt ctaggaatta aacactttat gtttacagaa				3277
ttgagctgca gaaagtgcaa gacatgccaa tttgagacac acggtcttct aagactgaag				3337
gataaattta atgcatttca gaaactaaac atcacagcaa gctctatctc tgagctataa				3397
tttggtttta atgcaaagac actagtttga taatatatac tgtaatcctg aaacatttgt				3457
gttacttacc tttggaggta gaaattatac caataaatta ttgcaccgtt agtattagat				3517
tctgtgtacc ttggaagtta tgtcattaat ataggctggg tcatcaaata aagcaaaacc				3577
ttgcaatata agctagattt acactccggg acgttgccca aaggtaggaa gaaagcagag				3637
ggaaatattt cagtcatcat ttccaaagtc attatcaaaa tctgtgagga agtttaattct				3697
tccaaagagt caatgtcaga catcaggcct ctgttgctg cttctctoga ggcactagat				3757
taggagtctt caataagaga cttaacatga ggtatatgga agatgaggca ccgagataag				3817
ttcatcatta ggtgtgagca ctgctcacc ttgctggcaa gttctcctta agggccctga				3877

agcacagggtg	tccaaagaaa	agcgttaagt	ccatcttaat	agaatctatg	tggtatatga	3937
tgtggggtcag	cccctgggtc	tgtgatcagc	aagaacctac	agcacagatt	atgccctgcc	3997
cacttcaatg	aatacctact	ctcctccatt	ctccatcact	ttttttgctg	tcaagaactc	4057
cggaccttgc	ccatggagaa	gtttagagag	gaactcttgt	ggagagctgg	tttattttct	4117
gcccctgtgc	gacgagtttc	agctggccaa	gaaaggagtc	aagttattaa	aaagcatcac	4177
aatgtagatc	tccaggctgg	ttttttgttt	tttgttgtta	agactgggga	aagggggact	4237
atttattctg	ccttaaatca	atggcaaata	agtcaagatg	acattttgtg	aatgtagact	4297
atggatacac	tcctaataka	ttgatgtagt	cataaaaggg	ggtcaagtag	atgtttttct	4357
gttatgtaag	caataatttt	tccgtgtctt	attgagtatg	gctagcgatt	atttattaca	4417
tgctagatgg	gttctttgca	tgtgggttcc	atatagggtg	agaaatttcc	tcagccactg	4477
gagggatttc	gaccatattt	gtcatttgga	tgagctgtta	ttagattgaa	atctacacat	4537
catttcatta	aaaattgtgc	cttagaaaac	gcaaagctgt	tgccatggc	gataaattat	4597
ggatgcagta	cattgaagag	agatgaagtc	acttccaagt	ttccaagact	tctcatggag	4657
gtgtttgctg	ttttacagga	aaaaataaaa	ataaaaaaag	aaaaaaagaa	aaaattaaaa	4717
agaaaaattg	ttttgaaaat	gtacagatca	agtccaatat	tttgattatc	cacctgcatg	4777
ttttattaaa	tattttgata	atgtggatgt	ttacactttg	catgatatta	gcagagtacc	4837
actagtaatg	cacaaacatg	tacaatatgg	tcattcataa	ccgattttta	tagaataactt	4897
tttacatgtg	caactccatc	cgttatgtaa	ggattacatg	aatattgcac	attcccttct	4957
ggtttcacaa	accattttat	acatattttct	tagtgagggt	cattgtacat	gtattgaagc	5017
tagaatcgag	tcaagaaaaa	taaagcccca	ttctccaact	gcaaaatgtg	ctttcccata	5077
atgaacacta	gtcaccagca	cagaataatc	tccaacattt	tctaaattct	aattgccaac	5137
tggtttctat	ttatatttga	tttatatttc	atttgaggtc	tgttacatgg	cagcttaagc	5197
agactagatc	ttgttttttc	caatgcagca	taatgagtat	gatctatttc	ttttcaaata	5257
atctttgaga	tcccaggaaa	aaaaaaatgc	tctgtcccat	tgagctataa	tgtaaagtgtg	5317
tttgtttaaa	aaacaggtga	ggcaagtgtg	tgatttattg	ttcctgagga	agtatatctg	5377
attttttttc	tcataactcca	aaagctagtc	cctactcttt	aataaaaata	atgggtaact	5437
ttttgttttt	cactagcgaa	cttccatgac	atttcctttc	tatgtagtgt	gattaatgca	5497
atacatatta	tagttatcta	tacacagtgt	aagatttaac	aaactgaaat	gatccaccto	5557

atatgtgagt ccggtccaaaa gatgttactg ctctgggtgg gccagtgttc tatatcggtt 5617
 atactaactt tcattttaaag tattttattct aaaatgcctc tgagaaacag taaaaataaa 5677
 aaacaacaag ttgtctaaaa tgcaacagct tttatagtaa atgtacattt ataaataaaa 5737
 tactcaaatac aaaaaaaaaa aaaa 5761

<210> 148
 <211> 2622
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (336) .. (1799)

<400> 148
 gcaagttcct gagagccggg aagaactgta ggaatagtca cagcttgaca accgaacaca 60
 acctgagtgt gctgagaact catggcgttg accacctgag ctataatgag ctatgccaac 120
 tcttgtttca gaacgacccc tggcttttgc cagaaatttg ccaacattac aacaaaggag 180
 atggacccca cggctcttgt gcctttcaaa agcagtgcac caagctccat atctgccagt 240
 attttttaca gggggaatgc aagtttggca ctagctgtaa gagatcccat gattttctcta 300
 attctgagaa tctggaaaaa ttggagaagt tgggt atg agc tca gac ctg gtg 353
 Met Ser Ser Asp Leu Val
 1
 agc agg ctg cct acc att tat aga aat gca cat gac atc aag aat aag 401
 Ser Arg Leu Pro Thr Ile Tyr Arg Asn Ala His Asp Ile Lys Asn Lys
 7 12 17 22
 agc tct gcc ccc agc aga gtg cct cct ctt ttt gtc cca cag ggg act 449
 Ser Ser Ala Pro Ser Arg Val Pro Pro Leu Phe Val Pro Gln Gly Thr
 23 28 33 38
 tct gaa aga aaa gac agt tca ggt tct gtg tcc cca aac act ctt agc 497
 Ser Glu Arg Lys Asp Ser Ser Gly Ser Val Ser Pro Asn Thr Leu Ser
 39 44 49 54
 cag gag gag ggt gat cag atc tgt ttg tac cat atc cgg aaa agt tgt 545
 Gln Glu Glu Gly Asp Gln Ile Cys Leu Tyr His Ile Arg Lys Ser Cys
 55 60 65 70
 agc ttt caa gat aag tgc cat aga gtt cat ttc cat ttg ccg tat cga 593
 Ser Phe Gln Asp Lys Cys His Arg Val His Phe His Leu Pro Tyr Arg
 71 76 81 86
 /
 tgg caa ttc ttg gat aga ggc aaa tgg gag gat ttg gac aac atg gaa 641
 Trp Gln Phe Leu Asp Arg Gly Lys Trp Glu Asp Leu Asp Asn Met Glu

87	92	97	102	
ctt att gaa gag gca tat tgc aat ccc aaa ata gaa agg atc ctg tgc				689
Leu Ile Glu Glu Ala Tyr Cys Asn Pro Lys Ile Glu Arg Ile Leu Cys				
103	108	113	118	
tct gag tca gcc agt acc ttt cac tct cat tgt ctg aac ttt aac gcc				737
Ser Glu Ser Ala Ser Thr Phe His Ser His Cys Leu Asn Phe Asn Ala				
119	124	129	134	
atg act tac ggt gct acc cag gct cgc cgc ctc tcc acg gcc tcc tct				785
Met Thr Tyr Gly Ala Thr Gln Ala Arg Arg Leu Ser Thr Ala Ser Ser				
135	140	145	150	
gtc acc aaa cct cca cac ttc atc ctc acc act gac tgg att tgg tac				833
Val Thr Lys Pro Pro His Phe Ile Leu Thr Thr Asp Trp Ile Trp Tyr				
151	156	161	166	
tgg agt gat gag ttt ggt tct tgg cag gaa tat gga aga cag ggc acg				881
Trp Ser Asp Glu Phe Gly Ser Trp Gln Glu Tyr Gly Arg Gln Gly Thr				
167	172	177	182	
gtg cac cct gtg acc act gtc agc agt agc gac gtg gag aag gcc tac				929
Val His Pro Val Thr Thr Val Ser Ser Ser Asp Val Glu Lys Ala Tyr				
183	188	193	198	
ctg gcc tac tgt aca ccg ggg tct gac ggc cag gca gcc acc ttg aag				977
Leu Ala Tyr Cys Thr Pro Gly Ser Asp Gly Gln Ala Ala Thr Leu Lys				
199	204	209	214	
ttc cag gcc gga aag cac aac tac gag tta gat ttc aaa gcc ttc gtt				1025
Phe Gln Ala Gly Lys His Asn Tyr Glu Leu Asp Phe Lys Ala Phe Val				
215	220	225	230	
cag aaa aac ctg gtc tat ggc aca act aaa aag gtt tgc cgc aga ccc				1073
Gln Lys Asn Leu Val Tyr Gly Thr Thr Lys Lys Val Cys Arg Arg Pro				
231	236	241	246	
aaa tac gtg tct ccc cag gat gtg acg acc atg caa acc tgc aat acc				1121
Lys Tyr Val Ser Pro Gln Asp Val Thr Thr Met Gln Thr Cys Asn Thr				
247	252	257	262	
aag ttt cca ggc ccg aag agc atc cca gac tat tgg gac tcc tct gcc				1169
Lys Phe Pro Gly Pro Lys Ser Ile Pro Asp Tyr Trp Asp Ser Ser Ala				
263	268	273	278	
ctg cca gac cca ggc ttt cag aag atc acc ctt agt tct tcc tcg gaa				1217
Leu Pro Asp Pro Gly Phe Gln Lys Ile Thr Leu Ser Ser Ser Ser Glu				
279	284	289	294	
gag tat cag aag gtc tgg aac ctc ttt aac cgc acg ctg cct ttc tac				1265
Glu Tyr Gln Lys Val Trp Asn Leu Phe Asn Arg Thr Leu Pro Phe Tyr				
295	300	305	310	
ttt gtt cag aag att gag cga gta cag aac ctg gcc ctc tgg gaa gtc				1313
Phe Val Gln Lys Ile Glu Arg Val Gln Asn Leu Ala Leu Trp Glu Val				
311	316	321	326	

tac cag tgg caa aaa gga cag atg cag aag cag aac gga ggg aag gcc	1361
Tyr Gln Trp Gln Lys Gly Gln Met Gln Lys Gln Asn Gly Gly Lys Ala	
327 332 337 342	
gtg gac gag cgg cag ctg ttc cac ggc acc agc gcc att ttt gtg gac	1409
Val Asp Glu Arg Gln Leu Phe His Gly Thr Ser Ala Ile Phe Val Asp	
343 348 353 358	
gcc atc tgc cag cag aac ttt gac tgg cgg gtc tgt ggt gtt cat gcc	1457
Ala Ile Cys Gln Gln Asn Phe Asp Trp Arg Val Cys Gly Val His Gly	
359 364 369 374	
act tcc tac ggc aag ggg agc tac ttt gcc cga gat gct gca tat tcc	1505
Thr Ser Tyr Gly Lys Gly Ser Tyr Phe Ala Arg Asp Ala Ala Tyr Ser	
375 380 385 390	
cac cac tac agc aaa tcc gac acg cag acc cac acg atg ttc ctg gcc	1553
His His Tyr Ser Lys Ser Asp Thr Gln Thr His Thr Met Phe Leu Ala	
391 396 401 406	
cgg gtg ctg gtg ggc gag ttc gtc agg ggc aat gcc tcc ttt gtc cgt	1601
Arg Val Leu Val Gly Glu Phe Val Arg Gly Asn Ala Ser Phe Val Arg	
407 412 417 422	
ccg ccg gcc aag gag ggc tgg agc aac gcc ttc tat gat agc tgc gtg	1649
Pro Pro Ala Lys Glu Gly Trp Ser Asn Ala Phe Tyr Asp Ser Cys Val	
423 428 433 438	
aac agt gtg tcc gac ccc tcc atc ttt gtg atc ttt gag aaa cac cag	1697
Asn Ser Val Ser Asp Pro Ser Ile Phe Val Ile Phe Glu Lys His Gln	
439 444 449 454	
gtc tac cca gag tat gtc atc cag tac acc acc tcc tcc aag ccc tcg	1745
Val Tyr Pro Glu Tyr Val Ile Gln Tyr Thr Thr Ser Ser Lys Pro Ser	
455 460 465 470	
gtc aca ccc tcc atc ctg ctg gcc ttg ggc tcc ctg ttc agc agc cga	1793
Val Thr Pro Ser Ile Leu Leu Ala Leu Gly Ser Leu Phe Ser Ser Arg	
471 476 481 486	
cag tga gcgcacagga gtgttccagg cctttcacct gctotgcctt gaaatggcta	1849
Gln *	
487	
tttgggcctt toctttttctt tttaaacaga aacttttaat gaactgttct cttaacattg	1909
acctctcaat gaagttatgt tcttaatctc ttgctaataa tgattttttac ttttaagtca	1969
cttttgggtt cactagtgga ttaaccagaa gtgattgtag ttgagtccag ttttgctttt	2029
taataatgtg ttgaagtttt agtttttact ctttggtgac tttgctgctt attggcacca	2089
gggacagagt ttctagatac aatttttatgg attggtttta atttttatga gtttgtctct	2149
gcagtgatcc ggtttctcag agtctcatgg catcatagtt tttccagaat gacacagtag	2209

ccaccggtgg atgacagccc acgggcgga cagtcacttc tgccgtgtgc tctgacacca 2269
 acccaggcag ctctgctgtg gcttctctctg ggctctggca ttagttggtc tgtgtcacat 2329
 tgtcagaaca ggtggtctgt gtgtggtgcc atcgagtcct tgctggttcc ccttgtctctg 2389
 ggagggtcac ccattgccc aggaagtgc tccacctggc aggtgacctg gaggagtagc 2449
 ttccccgagg acccccaggc ttggcctgtg attgcgcaaa cccacatttc ctaagcacac 2509
 tggacaccct tcgagtgtgg gttttaacat ccctgtgaga ttgaatactt gtgccacaca 2569
 tgtcacaaaa gagtatggaa ataaaaggaa atttatccga aaaaaaaaaa aaa 2622

<210> 149
 <211> 4285
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (346) .. (3285)

<400> 149
 taagcttgcg gccgctctgc ctgcgcgctg ctctgtctct gctacctgaa tgttgtacca 60
 tctttgggta ggcagacttc cctgacgaca tcagtgtac ccaaagctga gcagagcgtg 120
 gottacaaag actttattta ttttactgtc tttgaaggaa acgttcgcaa cgtttctgaa 180
 gtctcggttg agtatttatg ctctcagcct tgtgttgtca atttgggaagc agttgtttca 240
 tctgagttca gaagtagcat tcccggtgtac aaaaaaaggc ggaagaatga gaaacatctt 300
 cacaccagca ggacacaaat agtacatgtg aaatttccaa gcatt atg gtt tac 354
 Met Val Tyr
 1

aga gat gat tat ttc atc aga cat tcc atc tct gta tct gca gtg ata 402
 Arg Asp Asp Tyr Phe Ile Arg His Ser Ile Ser Val Ser Ala Val Ile
 4 9 14 19
 gta cgc gcc tgg att act cac aaa tac agt ggc aga gac tgg aat gtt 450
 Val Arg Ala Trp Ile Thr His Lys Tyr Ser Gly Arg Asp Trp Asn Val
 20 25 30 35
 aaa tgg gag gaa aac ttg ctc cat gct gta gca aag aat tat acc ctc 498
 Lys Trp Glu Glu Asn Leu Leu His Ala Val Ala Lys Asn Tyr Thr Leu
 36 41 46 51
 ctg cag acc atc ccg cct ttt gaa cgc cct ttc aaa gat cat caa gtg 546
 Leu Gln Thr Ile Pro Pro Phe Glu Arg Pro Phe Lys Asp His Gln Val
 52 57 62 67

tgc ctt gag tgg aac atg ggt tat att tgg aac ctt cgg gca aac agg	594
Cys Leu Glu Trp Asn Met Gly Tyr Ile Trp Asn Leu Arg Ala Asn Arg	
68 73 78 83	
att cca cag tgt cct ctg gaa aat gat gtg gtt gcc ctg ctt ggc ttt	642
Ile Pro Gln Cys Pro Leu Glu Asn Asp Val Val Ala Leu Leu Gly Phe	
84 89 94 99	
cct tat gcc tcc agt gga gaa aac aca ggc att gtc aag aag ttc cgg	690
Pro Tyr Ala Ser Ser Gly Glu Asn Thr Gly Ile Val Lys Lys Phe Pro	
100 105 110 115	
agg ttt cgg aac cga gag ctg gag gcc act cga cgc cag agg atg gat	738
Arg Phe Arg Asn Arg Glu Leu Glu Ala Thr Arg Arg Gln Arg Met Asp	
116 121 126 131	
tac cca gtg ttt act gtt tca ttg tgg ctt tat tta ctc cat tat tgc	786
Tyr Pro Val Phe Thr Val Ser Leu Trp Leu Tyr Leu Leu His Tyr Cys	
132 137 142 147	
aag gcc aac ctc tgt ggg att ctg tac ttt gtt gac tct aat gag atg	834
Lys Ala Asn Leu Cys Gly Ile Leu Tyr Phe Val Asp Ser Asn Glu Met	
148 153 158 163	
tac ggc aca cct tct gta ttt ctt acg gaa gag ggc tat ttg cat att	882
Tyr Gly Thr Pro Ser Val Phe Leu Thr Glu Glu Gly Tyr Leu His Ile	
164 169 174 179	
cag atg cat ctt gtc aaa ggg gaa gac ctt gct gta aaa act aaa ttc	930
Gln Met His Leu Val Lys Gly Glu Asp Leu Ala Val Lys Thr Lys Phe	
180 185 190 195	
atc ata cct ttg aag gag tgg ttt cga ctg gat atc tct ttt aac gga	978
Ile Ile Pro Leu Lys Glu Trp Phe Arg Leu Asp Ile Ser Phe Asn Gly	
196 201 206 211	
ggc cag ata gta gta acc act agc att gga cag gat ttg aaa agc tac	1026
Gly Gln Ile Val Val Thr Thr Ser Ile Gly Gln Asp Leu Lys Ser Tyr	
212 217 222 227	
cac aat cag acc att agc ttc cgg gag gat ttc cat tat aat gac aca	1074
His Asn Gln Thr Ile Ser Phe Arg Glu Asp Phe His Tyr Asn Asp Thr	
228 233 238 243	
gct ggg tac ttc att att gga ggg agc agg tat gtg gct ggc att gaa	1122
Ala Gly Tyr Phe Ile Ile Gly Gly Ser Arg Tyr Val Ala Gly Ile Glu	
244 249 254 259	
ggg ttt ttt gga ccc ctg aag tac tat cgc ctt cgc agt ctg cac tca	1170
Gly Phe Phe Gly Pro Leu Lys Tyr Tyr Arg Leu Arg Ser Leu His Ser	
260 265 270 275	
gcc ctg att ttt aat ccc ctc ctt gag aag caa ctt gct gaa caa atc	1218
Ala Leu Ile Phe Asn Pro Leu Leu Glu Lys Gln Leu Ala Glu Gln Ile	
276 281 286 291	
aag tta tat tat gaa agg tgt gct gag gtt caa gaa ata gta tct gtg	1266

Lys	Leu	Tyr	Tyr	Glu	Arg	Cys	Ala	Glu	Val	Gln	Glu	Ile	Val	Ser	Val		
292					297					302					307		
tat	gca	tct	gca	gca	aag	cac	ggg	ggc	gag	aga	caa	gaa	gca	tgc	cac		1314
Tyr	Ala	Ser	Ala	Ala	Lys	His	Gly	Gly	Glu	Arg	Gln	Glu	Ala	Cys	His		
308					313					318					323		
ctc	cac	aac	tcc	tac	ctg	gac	ctc	cag	cgc	agg	tat	ggg	aga	ccc	tcg		1362
Leu	His	Asn	Ser	Tyr	Leu	Asp	Leu	Gln	Arg	Arg	Tyr	Gly	Arg	Pro	Ser		
324					329					334					339		
atg	tgc	aga	gcc	ttc	ccc	tgg	gag	aag	gag	ctg	aaa	gac	aaa	cac	ccc		1410
Met	Cys	Arg	Ala	Phe	Pro	Trp	Glu	Lys	Glu	Leu	Lys	Asp	Lys	His	Pro		
340					345					350					355		
agc	ttg	ttc	cag	gca	ttg	ctg	gag	atg	gat	ctg	ctg	acc	gtg	cca	agg		1458
Ser	Leu	Phe	Gln	Ala	Leu	Leu	Glu	Met	Asp	Leu	Leu	Thr	Val	Pro	Arg		
356					361					366					371		
aac	caa	aat	gaa	tct	gta	tca	gaa	atc	ggg	ggg	aag	ata	ttt	gag	aag		1506
Asn	Gln	Asn	Glu	Ser	Val	Ser	Glu	Ile	Gly	Gly	Lys	Ile	Phe	Glu	Lys		
372					377					382					387		
gct	gta	aag	aga	ctc	tct	agc	att	gat	ggg	ctt	cac	caa	att	agc	tct		1554
Ala	Val	Lys	Arg	Leu	Ser	Ser	Ile	Asp	Gly	Leu	His	Gln	Ile	Ser	Ser		
388					393					398					403		
atc	gtc	ccc	ttt	ctg	acg	gat	tcc	agc	tgc	tgt	gga	tac	cat	aaa	gca		1602
Ile	Val	Pro	Phe	Leu	Thr	Asp	Ser	Ser	Cys	Cys	Gly	Tyr	His	Lys	Ala		
404					409					414					419		
tcc	tac	tac	ctt	gca	gtc	ttt	tat	gag	act	gga	tta	aat	gtt	cct	cgg		1650
Ser	Tyr	Tyr	Leu	Ala	Val	Phe	Tyr	Glu	Thr	Gly	Leu	Asn	Val	Pro	Arg		
420					425					430					435		
gat	cag	ctg	cag	ggc	atg	ttg	tat	agt	ttg	gtt	gga	ggc	cag	ggg	agt		1698
Asp	Gln	Leu	Gln	Gly	Met	Leu	Tyr	Ser	Leu	Val	Gly	Gly	Gln	Gly	Ser		
436					441					446					451		
gag	agg	ctg	tct	tca	atg	aat	ctt	ggg	tat	aaa	cac	tac	cag	ggg	att		1746
Glu	Arg	Leu	Ser	Ser	Met	Asn	Leu	Gly	Tyr	Lys	His	Tyr	Gln	Gly	Ile		
452					457					462					467		
gac	aac	tac	ccc	ctg	gac	tgg	gaa	ctg	tgc	tat	gcc	tac	tac	agc	aac		1794
Asp	Asn	Tyr	Pro	Leu	Asp	Trp	Glu	Leu	Ser	Tyr	Ala	Tyr	Tyr	Ser	Asn		
468					473					478					483		
att	gcc	acc	aag	aca	ccc	ctt	gac	cag	cac	aca	ctg	caa	gga	gat	cag		1842
Ile	Ala	Thr	Lys	Thr	Pro	Leu	Asp	Gln	His	Thr	Leu	Gln	Gly	Asp	Gln		
484					489					494					499		
gca	tat	gtt	gaa	aca	att	aga	cta	aaa	gat	gat	gaa	ata	ctc	aag	gta		1890
Ala	Tyr	Val	Glu	Thr	Ile	Arg	Leu	Lys	Asp	Asp	Glu	Ile	Leu	Lys	Val		
500					505					510					515		
caa	acc	aaa	gaa	gat	gga	gat	gtc	ttt	atg	tgg	ttg	aag	cat	gaa	gct		1938
Gln	Thr	Lys	Glu	Asp	Gly	Asp	Val	Phe	Met	Trp	Leu	Lys	His	Glu	Ala		

516		521		526		531	
acc cga ggc aat gca gca gct cag caa cga ttg gcc cag atg ctg ttc							1986
Thr Arg Gly Asn Ala Ala Ala Gln Gln Arg Leu Ala Gln Met Leu Phe							
532		537		542		547	
tggtggg cag caa ggt gtgtgcc aag aat ccc gaagca gca att gag tgg							2034
Trp Gly Gln Gln Gly Val Ala Lys Asn Pro Glu Ala Ala Ile Glu Trp							
548		553		558		563	
tac gcc aag ggc gcc ctgtgag acg gag gat cct gcgtta atc tat gac							2082
Tyr Ala Lys Gly Ala Leu Glu Thr Glu Asp Pro Ala Leu Ile Tyr Asp							
564		569		574		579	
tat gcc att gtgtcta ttc aag ggt caa gga gta aaa aag aac aga cgg							2130
Tyr Ala Ile Val Leu Phe Lys Gly Gln Gly Val Lys Lys Asn Arg Arg							
580		585		590		595	
ctt gcc tta gag ctgtatg aag aaa gca gct tcc aag gga ttgtcat cag							2178
Leu Ala Leu Glu Leu Met Lys Lys Ala Ala Ser Lys Gly Leu His Gln							
596		601		606		611	
gca gtc aat ggc ctggga tgg tat tac cac aaa ttc aag aaa aat tac							2226
Ala Val Asn Gly Leu Gly Trp Tyr Tyr His Lys Phe Lys Lys Asn Tyr							
612		617		622		627	
gcc aaa gca gca aag tactgg tta aaa gca gaagaatg ggg aac cca							2274
Ala Lys Ala Ala Lys Tyr Trp Leu Lys Ala Glu Glu Met Gly Asn Pro							
628		633		638		643	
gat gcgtcat tac aat ctt gga gtc ctgtcat ttgtgat ggc atc ttc cct							2322
Asp Ala Ser Tyr Asn Leu Gly Val Leu His Leu Asp Gly Ile Phe Pro							
644		649		654		659	
gga gtt cct gga aggaat caa act tta gct ggt gaatat ttc cat aag							2370
Gly Val Pro Gly Arg Asn Gln Thr Leu Ala Gly Glu Tyr Phe His Lys							
660		665		670		675	
gct gcg caa ggt gga cac atg gaagg acc ttgtgtgt tct ctc tac							2418
Ala Ala Gln Gly Gly His Met Glu Gly Thr Leu Trp Cys Ser Leu Tyr							
676		681		686		691	
tat atc aca ggc aacctgt gag aca ttc cct aga gat cct gag aaa gct							2466
Tyr Ile Thr Gly Asn Leu Glu Thr Phe Pro Arg Asp Pro Glu Lys Ala							
692		697		702		707	
gtt gta tgg gca aaa cat gta gct gag aaa aat ggc tac ttgtggc cat							2514
Val Val Trp Ala Lys His Val Ala Glu Lys Asn Gly Tyr Leu Gly His							
708		713		718		723	
gtc atc cgc aaa ggc ctc aat gcc tac ctgtgaagggt tca tgg cat gaa							2562
Val Ile Arg Lys Gly Leu Asn Ala Tyr Leu Glu Gly Ser Trp His Glu							
724		729		734		739	
gct ttgtctgtat tatgtt tta gca gca gaactgga att gaa gtgtca							2610
Ala Leu Leu Tyr Tyr Val Leu Ala Ala Glu Thr Gly Ile Glu Val Ser							
740		745		750		755	

cag	aca	aat	tta	gca	cac	atc	tgt	gag	gag	agg	cca	gac	ctg	gcc	agg	2658
Gln	Thr	Asn	Leu	Ala	His	Ile	Cys	Glu	Glu	Arg	Pro	Asp	Leu	Ala	Arg	
756					761					766					771	
aga	tac	ttg	ggt	gtt	aac	tgt	gtt	tgg	aga	tac	tat	aat	ttc	tct	gtt	2706
Arg	Tyr	Leu	Gly	Val	Asn	Cys	Val	Trp	Arg	Tyr	Tyr	Asn	Phe	Ser	Val	
772					777					782					787	
ttt	caa	atc	gat	gct	cct	tcc	ttt	gca	tat	ttg	aag	atg	gga	gac	ctt	2754
Phe	Gln	Ile	Asp	Ala	Pro	Ser	Phe	Ala	Tyr	Leu	Lys	Met	Gly	Asp	Leu	
788					793					798					803	
tac	tac	tat	ggc	cac	caa	aac	cag	tca	caa	gac	ctg	gag	ttg	tct	gtg	2802
Tyr	Tyr	Tyr	Gly	His	Gln	Asn	Gln	Ser	Gln	Asp	Leu	Glu	Leu	Ser	Val	
804					809					814					819	
cag	atg	tac	gcc	caa	gcc	gcc	ctg	gat	gga	gac	tcc	cag	gga	ttt	ttt	2850
Gln	Met	Tyr	Ala	Gln	Ala	Ala	Leu	Asp	Gly	Asp	Ser	Gln	Gly	Phe	Phe	
820					825					830					835	
aac	ctg	gcc	ctg	cta	atc	gag	gaa	ggt	acg	ata	atc	cca	cac	cat	atc	2898
Asn	Leu	Ala	Leu	Leu	Ile	Glu	Glu	Gly	Thr	Ile	Ile	Pro	His	His	Ile	
836					841					846					851	
ttg	gat	ttc	ttg	gaa	att	gac	tca	act	ctc	cat	tct	aat	aac	atc	tcc	2946
Leu	Asp	Phe	Leu	Glu	Ile	Asp	Ser	Thr	Leu	His	Ser	Asn	Asn	Ile	Ser	
852					857					862					867	
att	ctc	cag	gaa	ctg	tac	gaa	agg	tgc	tgg	agc	cac	agt	aac	gag	gag	2994
Ile	Leu	Gln	Glu	Leu	Tyr	Glu	Arg	Cys	Trp	Ser	His	Ser	Asn	Glu	Glu	
868					873					878					883	
tcc	ttc	agc	ccc	tgc	tcc	ttg	gcc	tgg	ctt	tac	ctg	cac	ttg	cgg	ctt	3042
Ser	Phe	Ser	Pro	Cys	Ser	Leu	Ala	Trp	Leu	Tyr	Leu	His	Leu	Arg	Leu	
884					889					894					899	
ctc	tgg	ggt	gct	atc	ctg	cac	tca	gcc	ctg	atc	tac	ttt	ctg	gga	acc	3090
Leu	Trp	Gly	Ala	Ile	Leu	His	Ser	Ala	Leu	Ile	Tyr	Phe	Leu	Gly	Thr	
900					905					910					915	
ttt	ctg	cta	tcc	ata	ttg	atc	gcc	tgg	act	gtg	cag	tat	ttc	cag	tct	3138
Phe	Leu	Leu	Ser	Ile	Leu	Ile	Ala	Trp	Thr	Val	Gln	Tyr	Phe	Gln	Ser	
916					921					926					931	
gtc	tca	gca	agc	gat	ccc	cct	cca	aga	cca	tcc	cag	gcc	tcc	cca	gac	3186
Val	Ser	Ala	Ser	Asp	Pro	Pro	Pro	Arg	Pro	Ser	Gln	Ala	Ser	Pro	Asp	
932					937					942					947	
act	gcc	acg	tcc	act	gca	agt	cca	gct	gtg	act	cca	gct	gca	gat	gcc	3234
Thr	Ala	Thr	Ser	Thr	Ala	Ser	Pro	Ala	Val	Thr	Pro	Ala	Ala	Asp	Ala	
948					953					958					963	
tct	gac	caa	gac	cag	ccc	aca	gta	act	aat	aac	ccg	gag	cca	cgt	ggg	3282
Ser	Asp	Gln	Asp	Gln	Pro	Thr	Val	Thr	Asn	Asn	Pro	Glu	Pro	Arg	Gly	
964					969					974					979	

tga actg tgcactccag ttctctccag atgagagaga atcttttcaa cagctggat	3339
*	
980	
tggaagctg gggccagggc atgacctga taaacacctt aaatgtcttg tcaactggat	3399
gcaaattttg caattggtgt cttttttttt aaagtcaa atacaaggaag taccagatc	3459
aggcagtggg aataccaaag gtcacaaac acatacaagg aacatcttga tcatagggca	3519
tgtggggaag ttactgggc catcacagac ttttgttcta gtgattgtat gtattaggag	3579
tcatagcatg ccctacggca gatctggatt cttatacact aagatgtgtc ttaagaatca	3639
cagtgcgtgc ttcacccctt tattgaagaa cagaaaatta tgactactct acaaggtgga	3699
taatattttg gtacctgtgc ttgccacagc cctgttctc aaagctgaat tgatagattt	3759
ctctttgact tccaagacct agcagttata aggcaccttg aaataaattg tttgtgcctg	3819
gaaatgcagg gagggcaata gctttgtaaa ttggtttaca tttttctcct tgaatttttc	3879
tagggtccta gtgcttccga atcattta atgcattgtcg gatattttt acatttcaat	3939
tgcaatccat gaaattacat ttagaagatt cttagtactt aactgtagtc ttctccatga	3999
attacacgtt agaatagact ggcagcaact gaatatgcag caagtaagcc tctagcttat	4059
agtttcatcc ctaccctca tgctgcgtg agtctgtaca gggatatgtg tgtgtgtgtg	4119
tgtgtgtgtg tgtagagag gaagaggaag agcagaatgt ctgtatacta catgctgcta	4179
aggtagtgaa taaatcagta atgcaatatt gtgggtccaa actactctt gcactactt	4239
atttacagta gtaaataaaa ttatttttat acaaaaaaaaa aaaaaa	4285

<210> 150
 <211> 4618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (282)..(4043)

<400> 150	
cggaattccc gggctcgacga ttctgtcttc gcttgacgat ttcgtagggg aggaggccga	60
gtgtttcctg ggcgattccc ggccagcccg agtgactcac tcggccaagg aaactcccag	120
ggccccgcca ggacccccaa gccgccgagg acgcagaatg tggtcagct gccctggtc	180
ccatcccagg gcagagctcc tcttgagtac ccttgagact ggagcagatt cagcagaagg	240

cagattgccc cctctccctg gagctggctc tgaagcccag g	atg gcg gcc cag	293
	Met Ala Ala Gln	
	1	
gtg act ctg gag gac gcg ctg tcc aac gtg gac ctc ctg gag gag ctg		341
Val Thr Leu Glu Asp Ala Leu Ser Asn Val Asp Leu Leu Glu Glu Leu		
5 10 15 20		
ccc ctg ccc gac cag cag ccc tgc atc gag ccc ccg cca tcc tcc ctg		389
Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro Pro Ser Ser Leu		
21 26 31 36		
ctc tac cag cca aat ttc aac act aac ttt gaa gac aga aat gca ttt		437
Leu Tyr Gln Pro Asn Phe Asn Thr Asn Phe Glu Asp Arg Asn Ala Phe		
37 42 47 52		
gtt act ggc atc gca aga tac att gaa caa gcc acc gtc cac tct agc		485
Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala Thr Val His Ser Ser		
53 58 63 68		
atg aac gag atg ctg gag gag ggc caa gaa tat gct gtc atg ctg tac		533
Met Asn Glu Met Leu Glu Glu Gly Gln Glu Tyr Ala Val Met Leu Tyr		
69 74 79 84		
acc tgg agg agc tgc tcc cgg gcc atc cca cag gtg aaa tgt aac gag		581
Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln Val Lys Cys Asn Glu		
85 90 95 100		
cag cct aac aga gtg gaa atc tac gag aaa acc gtg gag gtt ctg gag		629
Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr Val Glu Val Leu Glu		
101 106 111 116		
cct gag gtc aca aaa ctg atg aat ttc atg tac ttc cag aga aat gcc		677
Pro Glu Val Thr Lys Leu Met Asn Phe Met Tyr Phe Gln Arg Asn Ala		
117 122 127 132		
att gag cgt ttc tgc ggg gaa gtg agg cgc ctg tgc cat gcc gag agg		725
Ile Glu Arg Phe Cys Gly Glu Val Arg Arg Leu Cys His Ala Glu Arg		
133 138 143 148		
agg aag gac ttc gtg tca gaa gcc tac ctg atc aca ctg ggc aaa ttc		773
Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Ile Thr Leu Gly Lys Phe		
149 154 159 164		
atc aac atg ttc gct gtg ctg gac gag ctg aag aac atg aag tgc agt		821
Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys Asn Met Lys Cys Ser		
165 170 175 180		
gtg aag aac gac cac tca gcg tac aag agg gcc gct cag ttt tta cgt		869
Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala Ala Gln Phe Leu Arg		
181 186 191 196		
aaa atg gca gat cca cag tcc atc cag gaa tcc cag aat ctg tcc atg		917
Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser Gln Asn Leu Ser Met		
197 202 207 212		
ttc ctg gcc aat cat aac aag atc aca cag tct ctg cag cag cag ctc		965

Phe	Leu	Ala	Asn	His	Asn	Lys	Ile	Thr	Gln	Ser	Leu	Gln	Gln	Gln	Leu	
213					218					223					228	
gaa	gtg	att	tct	ggc	tac	gaa	gag	ctc	ctg	gca	gat	att	gtg	aat	ctg	1013
Glu	Val	Ile	Ser	Gly	Tyr	Glu	Glu	Leu	Leu	Ala	Asp	Ile	Val	Asn	Leu	
229					234					239					244	
tgt	gtg	gat	tac	tac	gag	aac	agg	atg	tat	ttg	acg	ccc	agt	gag	aaa	1061
Cys	Val	Asp	Tyr	Tyr	Glu	Asn	Arg	Met	Tyr	Leu	Thr	Pro	Ser	Glu	Lys	
245					250					255					260	
cac	atg	ctt	ctc	aaa	gtc	atg	gga	ttt	ggc	ctg	tac	ctg	atg	gat	ggg	1109
His	Met	Leu	Leu	Lys	Val	Met	Gly	Phe	Gly	Leu	Tyr	Leu	Met	Asp	Gly	
261					266					271					276	
agt	gtc	agt	aac	atc	tat	aag	ttg	gat	gcc	aag	aaa	aga	ata	aac	tta	1157
Ser	Val	Ser	Asn	Ile	Tyr	Lys	Leu	Asp	Ala	Lys	Lys	Arg	Ile	Asn	Leu	
277					282					287					292	
tcc	aaa	atc	gac	aag	tac	ttc	aag	caa	ctc	cag	gtg	gtt	cca	cta	ttt	1205
Ser	Lys	Ile	Asp	Lys	Tyr	Phe	Lys	Gln	Leu	Gln	Val	Val	Pro	Leu	Phe	
293					298					303					308	
ggg	gac	atg	caa	ata	gaa	ctg	gca	aga	tat	atc	aag	acc	agc	gcc	cac	1253
Gly	Asp	Met	Gln	Ile	Glu	Leu	Ala	Arg	Tyr	Ile	Lys	Thr	Ser	Ala	His	
309					314					319					324	
tac	gag	gaa	aat	aaa	tct	cga	tgg	acg	tgc	aca	tcc	tcc	ggc	agc	agc	1301
Tyr	Glu	Glu	Asn	Lys	Ser	Arg	Trp	Thr	Cys	Thr	Ser	Ser	Gly	Ser	Ser	
325					330					335					340	
cct	cag	tac	aac	atc	tgc	gag	cag	atg	atc	cag	atc	cgc	gag	gac	cac	1349
Pro	Gln	Tyr	Asn	Ile	Cys	Glu	Gln	Met	Ile	Gln	Ile	Arg	Glu	Asp	His	
341					346					351					356	
atg	cgc	ttc	att	tcg	gag	ctg	gcg	cgc	tac	agc	aac	agc	gag	gtg	gtc	1397
Met	Arg	Phe	Ile	Ser	Glu	Leu	Ala	Arg	Tyr	Ser	Asn	Ser	Glu	Val	Val	
357					362					367					372	
acg	ggc	tcg	ggc	cgc	cag	gag	gcc	cag	aag	acg	gac	gcg	gag	tac	cgc	1445
Thr	Gly	Ser	Gly	Arg	Gln	Glu	Ala	Gln	Lys	Thr	Asp	Ala	Glu	Tyr	Arg	
373					378					383					388	
aag	ctc	ttc	gac	ctg	gcg	ctg	cag	ggc	ctg	cag	ctg	ttg	tcg	cag	tgg	1493
Lys	Leu	Phe	Asp	Leu	Ala	Leu	Gln	Gly	Leu	Gln	Leu	Leu	Ser	Gln	Trp	
389					394					399					404	
agc	gcg	cac	gtg	atg	gaa	gtg	tat	tcc	tgg	aag	ctt	gtg	cac	ccc	acc	1541
Ser	Ala	His	Val	Met	Glu	Val	Tyr	Ser	Trp	Lys	Leu	Val	His	Pro	Thr	
405					410					415					420	
gac	aag	tac	tcc	aac	aag	gac	tgc	ccc	gac	agc	gct	gaa	gag	tac	gag	1589
Asp	Lys	Tyr	Ser	Asn	Lys	Asp	Cys	Pro	Asp	Ser	Ala	Glu	Glu	Tyr	Glu	
421					426					431					436	
cgt	gcc	acg	cgc	tac	aac	tac	acc	agc	gag	gag	aag	ttt	gcc	cta	gtg	1637
Arg	Ala	Thr	Arg	Tyr	Asn	Tyr	Thr	Ser	Glu	Glu	Lys	Phe	Ala	Leu	Val	

437	442	447	452	
gag gtg atc gcc atg atc aaa ggc ctg cag	gtg ctg atg ggc agg atg	1685		
Glu Val Ile Ala Met Ile Lys Gly Leu Gln	Val Leu Met Gly Arg Met			
453	458	463	468	
gag agc gtg ttc aac cac gcc atc cgg cac	acc gtc tat gcc gca ctg	1733		
Glu Ser Val Phe Asn His Ala Ile Arg His	Thr Val Tyr Ala Ala Leu			
469	474	479	484	
cag gac ttc tcc cag gtg acc ctt agg gag	cgc ctg cgg cag gcc atc	1781		
Gln Asp Phe Ser Gln Val Thr Leu Arg Glu	Pro Leu Arg Gln Ala Ile			
485	490	495	500	
aag aag aag aag aac gtc atc cag agt gtc	ctg cag gcc atc agg aag	1829		
Lys Lys Lys Lys Asn Val Ile Gln Ser Val	Leu Gln Ala Ile Arg Lys			
501	506	511	516	
acc gtg tgt gac tgg gag acg ggg cat gag	ccc ttc aat gac cca gcc	1877		
Thr Val Cys Asp Trp Glu Thr Gly His Glu	Pro Phe Asn Asp Pro Ala			
517	522	527	532	
ttg cgg ggc gag aag gac ccc aag agc ggc	ttc gac ata aaa gta cca	1925		
Leu Arg Gly Glu Lys Asp Pro Lys Ser Gly	Phe Asp Ile Lys Val Pro			
533	538	543	548	
cgc cgc gcc gtg gga ccc tcc agc act cag	ctt tac atg gtg aga acc	1973		
Arg Arg Ala Val Gly Pro Ser Ser Thr Gln	Leu Tyr Met Val Arg Thr			
549	554	559	564	
atg cta gag tcc ctc att gca gac aaa agt	ggt tcc aag aaa acc ttg	2021		
Met Leu Glu Ser Leu Ile Ala Asp Lys Ser	Gly Ser Lys Lys Thr Leu			
565	570	575	580	
aga agt agc ctt gag ggg ccc acc ata ttg	gac ata gaa aaa ttt cat	2069		
Arg Ser Ser Leu Glu Gly Pro Thr Ile Leu	Asp Ile Glu Lys Phe His			
581	586	591	596	
cga gag tca ttc ttc tac act cac ttg ata	aat ttc agt gaa acg ctg	2117		
Arg Glu Ser Phe Phe Tyr Thr His Leu Ile	Asn Phe Ser Glu Thr Leu			
597	602	607	612	
cag cag tgc tgt gac ctt tcg cag ctg tgg	ttc cga gag ttc ttc ctg	2165		
Gln Gln Cys Cys Asp Leu Ser Gln Leu Trp	Phe Arg Glu Phe Phe Leu			
613	618	623	628	
gag ctg acc atg ggc agg agg atc cag ttc	ccc att gag atg tcg atg	2213		
Glu Leu Thr Met Gly Arg Arg Ile Gln Phe	Pro Ile Glu Met Ser Met			
629	634	639	644	
ccc tgg atc ctg acg gac cac atc ctg gag	acc aag gag gca tcg atg	2261		
Pro Trp Ile Leu Thr Asp His Ile Leu Glu	Thr Lys Glu Ala Ser Met			
645	650	655	660	
atg gag tac gtg ctc tac tcc ctg tac ctg	tac aat gac agc gcc cac	2309		
Met Glu Tyr Val Leu Tyr Ser Leu Tyr Leu	Tyr Asn Asp Ser Ala His			
661	666	671	676	

tac gcg ctc acc agg ttc aac aag cag ttc ctg tac gac gaa att gag	2357
Tyr Ala Leu Thr Arg Phe Asn Lys Gln Phe Leu Tyr Asp Glu Ile Glu	
677 682 687 692	
gcc gag gtg aat cta tgt ttt gac caa ttt gtt tac aag cta gca gac	2405
Ala Glu Val Asn Leu Cys Phe Asp Gln Phe Val Tyr Lys Leu Ala Asp	
693 698 703 708	
cag ata ttt gcc tat tat aag gtt atg gca gga agt ttg ctt ctt gat	2453
Gln Ile Phe Ala Tyr Tyr Lys Val Met Ala Gly Ser Leu Leu Leu Asp	
709 714 719 724	
aaa cgg tta cga tca gaa tgc aag aat cag gga gcc acg atc cac ctc	2501
Lys Arg Leu Arg Ser Glu Cys Lys Asn Gln Gly Ala Thr Ile His Leu	
725 730 735 740	
ccg ccg tct aac cgc tac gag acg ctg ctg aag cag agg cat gtg cag	2549
Pro Pro Ser Asn Arg Tyr Glu Thr Leu Leu Lys Gln Arg His Val Gln	
741 746 751 756	
ctc ctc ggc aga tca ata gac ctc aat cgt ctg atc acc cag cgc gtc	2597
Leu Leu Gly Arg Ser Ile Asp Leu Asn Arg Leu Ile Thr Gln Arg Val	
757 762 767 772	
tca gca gcc atg tat aag tcc cta gaa ctg gcg att gga cga ttt gaa	2645
Ser Ala Ala Met Tyr Lys Ser Leu Glu Leu Ala Ile Gly Arg Phe Glu	
773 778 783 788	
agt gaa gat ttg acc tcc ata gtt gag ctg gat ggc ctg ttg gaa atc	2693
Ser Glu Asp Leu Thr Ser Ile Val Glu Leu Asp Gly Leu Leu Glu Ile	
789 794 799 804	
aac cgc atg acc cac aag ctg ctg agc cgg tac ctg acg ctg gac ggc	2741
Asn Arg Met Thr His Lys Leu Leu Ser Arg Tyr Leu Thr Leu Asp Gly	
805 810 815 820	
ttc gac gcc atg ttc cgg gag gcc aac cac aac gtg tca gcg ccc tac	2789
Phe Asp Ala Met Phe Arg Glu Ala Asn His Asn Val Ser Ala Pro Tyr	
821 826 831 836	
ggg agg atc acc ctg cac gtc ttc tgg gag ctc aac tat gac ttc ctg	2837
Gly Arg Ile Thr Leu His Val Phe Trp Glu Leu Asn Tyr Asp Phe Leu	
837 842 847 852	
ccc aac tac tgc tac aac ggc tct acc aac cgg ttt gtt cgg aca gtg	2885
Pro Asn Tyr Cys Tyr Asn Gly Ser Thr Asn Arg Phe Val Arg Thr Val	
853 858 863 868	
tta cca ttt tct cag gaa ttt caa aga gat aag cag cct aat gca cag	2933
Leu Pro Phe Ser Gln Glu Phe Gln Arg Asp Lys Gln Pro Asn Ala Gln	
869 874 879 884	
cct cag tat ctg cat gga tcc aag gct ttg aac ttg gcc tac tcc agc	2981
Pro Gln Tyr Leu His Gly Ser Lys Ala Leu Asn Leu Ala Tyr Ser Ser	
885 890 895 900	

att tac ggc agc tac cgg aac ttc gtg gga cct cca cac ttt caa gtc	3029
Ile Tyr Gly Ser Tyr Arg Asn Phe Val Gly Pro Pro His Phe Gln Val	
901 906 911 916	
atc tgc cgg ctt ctc ggc tac cag ggt atc gcc gtg gtc atg gag gag	3077
Ile Cys Arg Leu Leu Gly Tyr Gln Gly Ile Ala Val Val Met Glu Glu	
917 922 927 932	
ctg ctg aag gtc gtc aag agc ctg ctg caa ggc aca atc ctg cag tac	3125
Leu Leu Lys Val Val Lys Ser Leu Leu Gln Gly Thr Ile Leu Gln Tyr	
933 938 943 948	
gtg aag acg ctg atg gag gtg atg ccc aag atc tgc cgc ctg ccc cgg	3173
Val Lys Thr Leu Met Glu Val Met Pro Lys Ile Cys Arg Leu Pro Arg	
949 954 959 964	
cac gag tac ggc tct cct ggt atc ctg gag ttc ttc cac cac cag ctg	3221
His Glu Tyr Gly Ser Pro Gly Ile Leu Glu Phe Phe His His Gln Leu	
965 970 975 980	
aag gac atc gtg gag tac gca gag ctg aag acg gtg tgc ttc cag aac	3269
Lys Asp Ile Val Glu Tyr Ala Glu Leu Lys Thr Val Cys Phe Gln Asn	
981 986 991 996	
ctg cgg gag gtg ggg aac gcc atc ctc ttc tgc ctg ctc atc gag cag	3317
Leu Arg Glu Val Gly Asn Ala Ile Leu Phe Cys Leu Leu Ile Glu Gln	
997 1002 1007 1012	
agc ctg tct tta gaa gaa gtg tgt gac ctg ctg cac gcg gct cct ttc	3365
Ser Leu Ser Leu Glu Glu Val Cys Asp Leu Leu His Ala Ala Pro Phe	
1013 1018 1023 1028	
cag aac atc ttg ccg cga gtc cat gtg aaa gag ggg gag aga ctt gat	3413
Gln Asn Ile Leu Pro Arg Val His Val Lys Glu Gly Glu Arg Leu Asp	
1029 1034 1039 1044	
gcc aaa atg aaa aga cta gaa tca aag tac gcc ccg ctg cat ctt gtc	3461
Ala Lys Met Lys Arg Leu Glu Ser Lys Tyr Ala Pro Leu His Leu Val	
1045 1050 1055 1060	
cca ctg att gaa aga ctg ggg acc cct cag caa att gcc atc gca aga	3509
Pro Leu Ile Glu Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg	
1061 1066 1071 1076	
gag ggg gac ctg ctg aca aag gag cgc ctc tgc tgc ggc ctg tcc atg	3557
Glu Gly Asp Leu Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met	
1077 1082 1087 1092	
ttt gag gtc atc ctg aca cgg atc cgg agc ttt ctg gat gac ccc atc	3605
Phe Glu Val Ile Leu Thr Arg Ile Arg Ser Phe Leu Asp Asp Pro Ile	
1093 1098 1103 1108	
tgg cgc ggg cct ctg ccc agc aat ggg gtc atg cat gtg gac gag tgt	3653
Trp Arg Gly Pro Leu Pro Ser Asn Gly Val Met His Val Asp Glu Cys	
1109 1114 1119 1124	
gtg gag ttt cac aga ctg tgg agt gcc atg cag ttt gtc tac tgc att	3701

<211> 4244
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (230) .. (2311)

<400> 151

```
gcacgagccc tgccgggtgg aaccgaggcg gcggcggccg tggcgcgggcg tgggtggcgga      60
gggacgggtgg agacggctgc cctagtggga gaggcggcgc ggcgcgagtg aggaggaggg      120
tgaagcggcg gcgtcgaagg agaatgcttg gacagaagag atgagtacta tttccactaa      180
ggcctataat tgccctactgt acaaatagtc ctgatcaggc aatatacga      atg gcc      235
                                     Met Ala
                                     1

caa gga agc cac caa att gat ttt cag gtt tta cat gac ctg cga caa      283
Gln Gly Ser His Gln Ile Asp Phe Gln Val Leu His Asp Leu Arg Gln
  3                               8                               13                               18

aaa ttc cct gaa gta cct gaa gtt gtt gta tcc agg tgc atg tta cag      331
Lys Phe Pro Glu Val Pro Glu Val Val Val Ser Arg Cys Met Leu Gln
  19                               24                               29                               34

aat aat aat aac ctg gat gcc tgc tgt gct gtt ctc tct cag gag agt      379
Asn Asn Asn Asn Leu Asp Ala Cys Cys Ala Val Leu Ser Gln Glu Ser
  35                               40                               45                               50

aca aga tat ctt tat ggt gaa gga gac ttg aat ttt tca gat gat tct      427
Thr Arg Tyr Leu Tyr Gly Glu Gly Asp Leu Asn Phe Ser Asp Asp Ser
  51                               56                               61                               66

gga att tct ggt cta cgc aat cac atg act tct ctc aac ttg gac ttg      475
Gly Ile Ser Gly Leu Arg Asn His Met Thr Ser Leu Asn Leu Asp Leu
  67                               72                               77                               82

caa tca cag aac att tac cac cat gga aga gaa ggg agt agg atg aat      523
Gln Ser Gln Asn Ile Tyr His His Gly Arg Glu Gly Ser Arg Met Asn
  83                               88                               93                               98

gga agt agg act cta acg cac agc att agt gat gga caa ctt caa ggt      571
Gly Ser Arg Thr Leu Thr His Ser Ile Ser Asp Gly Gln Leu Gln Gly
  99                               104                               109                               114

ggc cag tcc aat agt gaa cta ttt cag cag gag cca cag aca gca cca      619
Gly Gln Ser Asn Ser Glu Leu Phe Gln Gln Glu Pro Gln Thr Ala Pro
  115                               120                               125                               130

gct caa gtt cct caa ggc ttt aat gtt ttt gga atg tcc agt tcc tct      667
Ala Gln Val Pro Gln Gly Phe Asn Val Phe Gly Met Ser Ser Ser Ser
  131                               136                               141                               146

ggt gct tca aat tca gca cca cat ctt gga ttt cac tta ggc agc aaa      715
Gly Ala Ser Asn Ser Ala Pro His Leu Gly Phe His Leu Gly Ser Lys
```

147	152	157	162	
gga aca tct agc ctt tct caa caa act ccc aga ttt aat ccc att atg				763
Gly Thr Ser Ser Leu Ser Gln Gln Thr Pro Arg Phe Asn Pro Ile Met				
163	168	173	178	
gta act tta gcc cca aat atc cag act ggt cgt aat act cct aca tct				811
Val Thr Leu Ala Pro Asn Ile Gln Thr Gly Arg Asn Thr Pro Thr Ser				
179	184	189	194	
ttg cac ata cat ggt gta cct cca cct gta ctt aac agt cca cag gga				859
Leu His Ile His Gly Val Pro Pro Pro Val Leu Asn Ser Pro Gln Gly				
195	200	205	210	
aat tct atc tat att agg cct tac att aca act cct ggt ggt aca act				907
Asn Ser Ile Tyr Ile Arg Pro Tyr Ile Thr Thr Pro Gly Gly Thr Thr				
211	216	221	226	
cga cag aca caa cag cat tct ggc tgg gta tct cag ttt aat ccc atg				955
Arg Gln Thr Gln Gln His Ser Gly Trp Val Ser Gln Phe Asn Pro Met				
227	232	237	242	
aac cct cag caa gtt tat cag cct tca cag cct ggt ccc tgg act act				1003
Asn Pro Gln Gln Val Tyr Gln Pro Ser Gln Pro Gly Pro Trp Thr Thr				
243	248	253	258	
tgt cct gca tct aat cct ctg tca cat acc tca tct caa cag cca aat				1051
Cys Pro Ala Ser Asn Pro Leu Ser His Thr Ser Ser Gln Gln Pro Asn				
259	264	269	274	
cag caa ggc cac cag acc tct cat gtc tac atg cca atc agt tca cct				1099
Gln Gln Gly His Gln Thr Ser His Val Tyr Met Pro Ile Ser Ser Pro				
275	280	285	290	
act act tca caa cca cca acc att cat tca tct ggt agc tca cag tct				1147
Thr Thr Ser Gln Pro Pro Thr Ile His Ser Ser Gly Ser Ser Gln Ser				
291	296	301	306	
tct gcc cat agc caa tat aac att cag aat att tca aca gga cct cga				1195
Ser Ala His Ser Gln Tyr Asn Ile Gln Asn Ile Ser Thr Gly Pro Arg				
307	312	317	322	
aaa aac cag att gaa atc aaa ctt gaa ccc cca caa aga aat aat tct				1243
Lys Asn Gln Ile Glu Ile Lys Leu Glu Pro Pro Gln Arg Asn Asn Ser				
323	328	333	338	
tca aaa ctg cgt tct tct gga cct cga acc tcc agc act tcc tct tca				1291
Ser Lys Leu Arg Ser Ser Gly Pro Arg Thr Ser Ser Thr Ser Ser Ser				
339	344	349	354	
gtc aat agc cag acc tta aac aga aat cag ccc act gtt tac ata gct				1339
Val Asn Ser Gln Thr Leu Asn Arg Asn Gln Pro Thr Val Tyr Ile Ala				
355	360	365	370	
gcc agc ccc cca aat acg gat gag ctg atg tcc cgt agt caa cct aag				1387 /
Ala Ser Pro Pro Asn Thr Asp Glu Leu Met Ser Arg Ser Gln Pro Lys				
371	376	381	386	

gtc tat att tca gcg aat gct gcc aca gga gat gaa cag gtc atg cgg	1435
Val Tyr Ile Ser Ala Asn Ala Ala Thr Gly Asp Glu Gln Val Met Arg	
387 392 397 402	
aat cag ccc aca ctc ttc ata tcc aca aac tct gga gca tct gct gcc	1483
Asn Gln Pro Thr Leu Phe Ile Ser Thr Asn Ser Gly Ala Ser Ala Ala	
403 408 413 418	
tcc agg aac atg tct ggg caa gtg agc atg ggt cct gcc ttt att cat	1531
Ser Arg Asn Met Ser Gly Gln Val Ser Met Gly Pro Ala Phe Ile His	
419 424 429 434	
cac cat cct ccc aaa agt cga gca ata ggc aat aac tct gca acc tct	1579
His His Pro Pro Lys Ser Arg Ala Ile Gly Asn Asn Ser Ala Thr Ser	
435 440 445 450	
cct cga gtg gta gtc act cag ccc aat acg aaa tac act ttc aaa att	1627
Pro Arg Val Val Val Thr Gln Pro Asn Thr Lys Tyr Thr Phe Lys Ile	
451 456 461 466	
aca gtc tct ccc aat aag ccc cct gca gtt tca cca ggg gtg gtg tcc	1675
Thr Val Ser Pro Asn Lys Pro Pro Ala Val Ser Pro Gly Val Val Ser	
467 472 477 482	
cct acc ttt gaa ctt aca aat ctt ctt aat cat cct gat cat tat gta	1723
Pro Thr Phe Glu Leu Thr Asn Leu Leu Asn His Pro Asp His Tyr Val	
483 488 493 498	
gaa acc gag aat att cag cac ctc acg gac cct aca tta gca cat gtg	1771
Glu Thr Glu Asn Ile Gln His Leu Thr Asp Pro Thr Leu Ala His Val	
499 504 509 514	
gat aga ata agt gaa aca cgg aaa ctg agt atg gga tct gat gat gct	1819
Asp Arg Ile Ser Glu Thr Arg Lys Leu Ser Met Gly Ser Asp Asp Ala	
515 520 525 530	
gcc tac aca caa gct ctt ttg gta cac cag aag gcc aga atg gaa cga	1867
Ala Tyr Thr Gln Ala Leu Leu Val His Gln Lys Ala Arg Met Glu Arg	
531 536 541 546	
ctt caa aga gaa ctt gag att caa aag aaa aag ctg gat aaa tta aaa	1915
Leu Gln Arg Glu Leu Glu Ile Gln Lys Lys Lys Leu Asp Lys Leu Lys	
547 552 557 562	
tct gag gtt aat gaa atg gaa aat aat cta act cga agg cgc ctg aaa	1963
Ser Glu Val Asn Glu Met Glu Asn Asn Leu Thr Arg Arg Arg Leu Lys	
563 568 573 578	
aga tca aat tct ata tcc cag ata cct tcc ctt gaa gaa atg cag cag	2011
Arg Ser Asn Ser Ile Ser Gln Ile Pro Ser Leu Glu Glu Met Gln Gln	
579 584 589 594	
ctg aga agt tgt aat aga caa ctc cag att gac att gac tgc tta acc	2059
Leu Arg Ser Cys Asn Arg Gln Leu Gln Ile Asp Ile Asp Cys Leu Thr	
595 600 605 610	

aaa gaa att gat ctt ttt caa gcc cga gga cca cat ttt aac ccc agc	2107
Lys Glu Ile Asp Leu Phe Gln Ala Arg Gly Pro His Phe Asn Pro Ser	
611 616 621 626	
gct att cat aac ttt tat gac aat att gga ttt gta ggt cct gtg cca	2155
Ala Ile His Asn Phe Tyr Asp Asn Ile Gly Phe Val Gly Pro Val Pro	
627 632 637 642	
cca aaa ccc aaa gat caa agg tcc atc atc aaa aca cca aag act caa	2203
Pro Lys Pro Lys Asp Gln Arg Ser Ile Ile Lys Thr Pro Lys Thr Gln	
643 648 653 658	
gac aca gaa gat gat gag gga gct cag tgg aat tgt acc gcc tgt act	2251
Asp Thr Glu Asp Asp Glu Gly Ala Gln Trp Asn Cys Thr Ala Cys Thr	
659 664 669 674	
ttt ttg aac cat cca gcc tta att cgc tgt gaa cag tgt gag atg cca	2299
Phe Leu Asn His Pro Ala Leu Ile Arg Cys Glu Gln Cys Glu Met Pro	
675 680 685 690	
agg cat ttc tga gcc aaatggccct gtatcttctc taaaaccaca tctaaagtcc	2354
Arg His Phe *	
691	
aagaaactag tctgtcatcg ggaaaaagtt tcactgctac ataggatttt gtcaaattga	2414
aggtgtgaca agatggtggt ctgctaattgt taaatgtcag cccacagagc taataatacc	2474
tcagtataat gtcattgagca gttgaaattc atcacatgaa aagtaattctg ctgaaagact	2534
tggttgccca ctgcctaact gtgtacagtg ttaccagtgt cccattatgg ataattctca	2594
atatgttaac acctaggtgt tcccaatacc tttttccct catgtcacta ctgaattttg	2654
acaggaggaa ggaatagaat gatagcttgt tttatttgta aagctttcag tgaaacacta	2714
catacacgaa gaaaaggaa aaggtttaac tatttaagaa ccatttgctg ccgcatagt	2774
ccattggata gggaagaact tcagaaatct gtggtactct tggccttgctc tttgtcttcc	2834
ctgaacgtgt ctccactctg tgaagccagc atctaggggc taaagatgca aaggaaagca	2894
gcatgcattg tctgtacaaa tgtgcagcga aatacccca agcttttcct actgtacaga	2954
tctctcgagt ctgctttaag tgatttcttt tcttcttgat tattttctta tatttctata	3014
tgtatagtgt aatagccttt tggttaactaa ttttcttttt tccttttagt aattaagcac	3074
gatcatgtcc ctttttaagc cttacctgag aggaacaatg ccttaaaata aaaaagcatt	3134
aatgagatga aagtatgcac agaataactt tcctctactt attctgtact ttgccctcat	3194
gagttccaat gttgtgtgaa gacaggcaga tgctgcacag tgaattgcag atgatattac	3254
agaagtgatg tctgtaggctc acattaaata ctgacttgag cagtgggtga cacaacacag	3314
tgtttgtctt ccacagggaa gcttaaaaca aaagatatatt ttaaccact gacagaacaa	3374

caagggttaag cttcatctgc ttggtgtccc acagaacttg cacaagcagt tgttattggg	3434
aaagtacagt ctcaaaacca gcaacagcag cagtacctac agcccttttt ttggagagaa	3494
gtttaaatgc tttactgttg gggcagtcca tttctaatacc tgacttggtg acagtatcat	3554
gtgtatttat aaaacaaggc tagccatatt taggacaact gaagaaaagc tggaaaaaaa	3614
aacaagcaaa cttgaacact gaagcaacct caagcatctc tttattttga tgatatattt	3674
ttgtaaggaa aatattcaga tgatcaggaa tgtatataac tgaaatcaag aaaaagaaca	3734
gtatgcattt aaaaagacag aattatgaaa ttatatgagt gcttagaatg gggctaaggg	3794
aagtgctgaa atagagcaaa ggatggaaga taatatagac taccaccacac tgtaaatgtt	3854
tgcaagtggc tgtgttttaa atgggattat tacagttgat ctctatgaat gtcagagccc	3914
taactttcag gctttgcatt ttgtatatgg gaagaaatat gacaatccta ggtaattaaa	3974
ccatagaccc aaagccctta cgtttgatgc aatttatttt taaaataggc cttgtttttc	4034
agcttcatct gcagttctat gtgaagattg ataaatcagt ttttacttgt tttattaata	4094
aaacgtaatt tggatatctt gagttgatgg ttttgtgatt tagctgggta aactatcttt	4154
gtaacagata agttatttat aaaaattaaa aaacttatat tctaaaaaaa aaaaaaaaaa	4214
aaaaaaaaaa aaaagggcgg cccaagctta	4244

<210> 152
 <211> 2703
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (398) .. (2329)

<400> 152	
atttggccct cgaggccaag aattcggcac gagccgtagg ctcccttcagg gctgagccat	60
cctgcgtgtc ttgcgctcgg tggaaatgcc cagccgaggg acgcgaccag aggacagctc	120
tgtgctgata cccaccgaca attcgacccc acacaaggag gatctaagca gcaagattaa	180
agaacaaaaa attgtgggtg atgaactttc taaccttaag aagaatagga aagtatatag	240
gcaacaacag aacagcaata tattctttct tgcagaccga acagaaatgc tgtctgagag	300
caagaatata ttggatgaac tgaaaaaaga ataccaagaa atagaaaact tagacaagac	360
caaatcaag aaatagtcaa cctgatttca cataaca atg tgt ggc att tgt tgt	415

Met Cys Gly Ile Cys Cys

1

tct gta aac ttt tct gct gag cat ttc agt caa gat tta aaa gag gac	463
Ser Val Asn Phe Ser Ala Glu His Phe Ser Gln Asp Leu Lys Glu Asp	
7 12 17 22	
tta cta tat aat ctt aaa cag cgg gga ccc aat agt agt aaa caa ttg	511
Leu Leu Tyr Asn Leu Lys Gln Arg Gly Pro Asn Ser Ser Lys Gln Leu	
23 28 33 38	
tta aag tct gat gtt aac tac cag tgt tta ttt tct gct cac gtc cta	559
Leu Lys Ser Asp Val Asn Tyr Gln Cys Leu Phe Ser Ala His Val Leu	
39 44 49 54	
cac ttg agg ggt gtt ttg act acc cag cct gtg gaa gat gaa aga ggc	607
His Leu Arg Gly Val Leu Thr Thr Gln Pro Val Glu Asp Glu Arg Gly	
55 60 65 70	
aat gtg ttt cta tgg aat gga gaa att ttt agt gga ata aag gtt gaa	655
Asn Val Phe Leu Trp Asn Gly Glu Ile Phe Ser Gly Ile Lys Val Glu	
71 76 81 86	
gct gaa gag aat gac act caa att ttg ttt aat tat ctt tcc tcc tgt	703
Ala Glu Glu Asn Asp Thr Gln Ile Leu Phe Asn Tyr Leu Ser Ser Cys	
87 92 97 102	
aag aat gaa tct gag att ttg tca ctc ttc tca gaa gta caa ggt ccc	751
Lys Asn Glu Ser Glu Ile Leu Ser Leu Phe Ser Glu Val Gln Gly Pro	
103 108 113 118	
tgg tca ttt ata tat tat caa gca tct agt cat tat tta tgg ttt ggt	799
Trp Ser Phe Ile Tyr Tyr Gln Ala Ser Ser His Tyr Leu Trp Phe Gly	
119 124 129 134	
agg gat ttt ttt ggt cgc cgt agc ttg ctt tgg cat ttt agt aat ttg	847
Arg Asp Phe Phe Gly Arg Arg Ser Leu Leu Trp His Phe Ser Asn Leu	
135 140 145 150	
ggc aag agt ttc tgc ctc tct tca gtt ggc acc caa aca tct gga ttg	895
Gly Lys Ser Phe Cys Leu Ser Ser Val Gly Thr Gln Thr Ser Gly Leu	
151 156 161 166	
gca aat cag tgg caa gaa gtt cca gca tct gga ctt ttc aga att gat	943
Ala Asn Gln Trp Gln Glu Val Pro Ala Ser Gly Leu Phe Arg Ile Asp	
167 172 177 182	
ctt aag tct act gtc att tcc aga tgc att att tta caa ctg tat cct	991
Leu Lys Ser Thr Val Ile Ser Arg Cys Ile Ile Leu Gln Leu Tyr Pro	
183 188 193 198	
tgg aaa tat att tct agg gag aat att att gaa gaa aat gtt aat agc	1039
Trp Lys Tyr Ile Ser Arg Glu Asn Ile Ile Glu Glu Asn Val Asn Ser	
199 204 209 214	
ctg agt caa att tca gca gac tta cca gca ttt gta tca gtg gta gca	1087
Leu Ser Gln Ile Ser Ala Asp Leu Pro Ala Phe Val Ser Val Val Ala	

215	220	225	230	
aat gaa gcc aaa ctg	tat ctt gaa aaa cct	gtt gtt cct tta aat atg		1135
Asn Glu Ala Lys Leu	Tyr Leu Glu Lys Pro	Val Val Pro Leu Asn Met		
231	236	241	246	
atg ttg cca caa gct	gca ttg gag act cat	tgc agt aat att tcc aat		1183
Met Leu Pro Gln Ala	Ala Leu Glu Thr His	Cys Ser Asn Ile Ser Asn		
247	252	257	262	
gtg cca cct aca aga	gag ata ctt caa gtc	ttt ctt act gat gta cac		1231
Val Pro Pro Thr Arg	Glu Ile Leu Gln Val	Phe Leu Thr Asp Val His		
263	268	273	278	
atg aag gaa gta att	cag cag ttc att gat	gtc ctg agt gta gca gtc		1279
Met Lys Glu Val Ile	Gln Gln Phe Ile Asp	Val Leu Ser Val Ala Val		
279	284	289	294	
aag aaa cgt gtc ttg	tgt tta cct agg gat	gaa aac ctg aca gca aat		1327
Lys Lys Arg Val Leu	Cys Leu Pro Arg Asp	Glu Asn Leu Thr Ala Asn		
295	300	305	310	
gaa gtt ttg aaa acg	tgt gat agg aaa gca	aat gtt gca atc ctg ttt		1375
Glu Val Leu Lys Thr	Cys Asp Arg Lys Ala	Asn Val Ala Ile Leu Phe		
311	316	321	326	
tct ggg ggc att gat	tcc atg gtt att gca	acc ctt gct gac cgt cat		1423
Ser Gly Gly Ile Asp	Ser Met Val Ile Ala	Thr Leu Ala Asp Arg His		
327	332	337	342	
att cct tta gat gaa	cca att gat ctt ctt	aat gta gct ttc ata gct		1471
Ile Pro Leu Asp Glu	Pro Ile Asp Leu Leu	Asn Val Ala Phe Ile Ala		
343	348	353	358	
gaa gaa aag acc atg	cca act acc ttt aac	aga gaa ggg aat aaa cag		1519
Glu Glu Lys Thr Met	Pro Thr Thr Phe Asn	Arg Glu Gly Asn Lys Gln		
359	364	369	374	
aaa aat aaa tgt gaa	ata cct tca gaa gaa	ttc tct aaa gat gtt gct		1567
Lys Asn Lys Cys Glu	Ile Pro Ser Glu Glu	Phe Ser Lys Asp Val Ala		
375	380	385	390	
gct gct gct gct gac	agt cct aat aaa cat	gtc agt gta cca gat cga		1615
Ala Ala Ala Ala Asp	Ser Pro Asn Lys His	Val Ser Val Pro Asp Arg		
391	396	401	406	
atc aca gga agg gcg	gga cta aag gaa cta	caa gct gtt agc cct tcc		1663
Ile Thr Gly Arg Ala	Gly Leu Lys Glu Leu	Gln Ala Val Ser Pro Ser		
407	412	417	422	
cga att tgg aat ttt	ggt gaa att aat gtt	tct atg gaa gaa ctg cag		1711
Arg Ile Trp Asn Phe	Val Glu Ile Asn Val	Ser Met Glu Glu Leu Gln		
423	428	433	438	
aaa tta aga aga act	cga ata tgt cac tta	att cgg cca ttg gat aca		1759
Lys Leu Arg Arg Thr	Arg Ile Cys His Leu	Ile Arg Pro Leu Asp Thr		
439	444	449	454	

gtt ttg gat gat agc att ggc tgt gca gtc tgg ttt gct tct aga gga	1807
Val Leu Asp Asp Ser Ile Gly Cys Ala Val Trp Phe Ala Ser Arg Gly	
455 460 465 470	
att ggt tgg tta gtg gcc cag gaa gga gtg aaa tcc tat cag agc aat	1855
Ile Gly Trp Leu Val Ala Gln Glu Gly Val Lys Ser Tyr Gln Ser Asn	
471 476 481 486	
gca aag gta gtt ctc act gga att ggt gca gat gag caa ctt gca ggt	1903
Ala Lys Val Val Leu Thr Gly Ile Gly Ala Asp Glu Gln Leu Ala Gly	
487 492 497 502	
tat tct cgt cat cgt gtc cgc ttt cag tcg cat ggg ctg gaa gga ttg	1951
Tyr Ser Arg His Arg Val Arg Phe Gln Ser His Gly Leu Glu Gly Leu	
503 508 513 518	
aat aag gaa ata atg atg gaa ctg ggt cga att tct tct aga aat ctt	1999
Asn Lys Glu Ile Met Met Glu Leu Gly Arg Ile Ser Ser Arg Asn Leu	
519 524 529 534	
ggt cgt gat gac aga gtt att ggt gat cat gga aaa gaa gca aga ttt	2047
Gly Arg Asp Asp Arg Val Ile Gly Asp His Gly Lys Glu Ala Arg Phe	
535 540 545 550	
cct ttc ctg gat gaa aat gtt gtc tcc ttt cta aat tct ctg ccg att	2095
Pro Phe Leu Asp Glu Asn Val Val Ser Phe Leu Asn Ser Leu Pro Ile	
551 556 561 566	
tgg gaa aaa gca aac ttg act tta ccc cga gga att ggt gaa aaa tta	2143
Trp Glu Lys Ala Asn Leu Thr Leu Pro Arg Gly Ile Gly Glu Lys Leu	
567 572 577 582	
ctt tta cgc ctt gca gct gtg gaa ctt ggt ctt aca gcc tct gct ctt	2191
Leu Leu Arg Leu Ala Ala Val Glu Leu Gly Leu Thr Ala Ser Ala Leu	
583 588 593 598	
ctg ccc aaa cgg gcc atg cag ttt gga tca aga att gca aaa atg gaa	2239
Leu Pro Lys Arg Ala Met Gln Phe Gly Ser Arg Ile Ala Lys Met Glu	
599 604 609 614	
aaa att aat gaa aag gca tct gat aaa tgt gga cgg ctc caa atc atg	2287
Lys Ile Asn Glu Lys Ala Ser Asp Lys Cys Gly Arg Leu Gln Ile Met	
615 620 625 630	
tcc tta gaa aat ctt tct att gaa aag gag act aaa ttg taa tgtgatt	2336
Ser Leu Glu Asn Leu Ser Ile Glu Lys Glu Thr Lys Leu *	
631 636 641	
cacaatgtaa caatataaaa ataagttttt atataattat ataaaagtaa gatactctgc	2396
tgctttacta ttgtataata tagtagtttt aaagttcatt tggttgaatt ttcatttttt	2456
cctgtcacag agcttctaaa accatggaat ttccttagtg atagggaata tcttttgttg	2516
ttcataataa gccccttttg atcacacctg agtttatgct aatgcggtga cttagggtga	2576

ggctctctaaa tagccttttaa cacctgcagc ttgggaggcc aaggcagagg gatctcttga 2636
gtccaggagt ttgagaacag cctgggcaac atgatgaaac ctcatctcta ccaaaaaaaaa 2696
aaaaaaa 2703

<210> 153
<211> 5092
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (455)..(4195)

<400> 153
ctcagaacaa cgacagcggc cgcctcttgt gtttgactca atagcatccg gggatgaaac 60
aggagaactt ttctgttact gtttcaacac aaaagacagc gcccgcctct ttatataacc 120
caggacgatt ttctgtctta cttgctcacc tcatcatgaa gatttagtag ccattggcta 180
caaggatggc atagtgggtga taattgacat cagtaagaaa ggagaagtta ttcataggct 240
tcgaggccat gatgatgaaa tccactccat agcctggtgt cccctgcctg gtgaagattg 300
tttatctata aaccaagagg aaacttcaga agaagctgaa attaccaacg ggaatgctgt 360
agcacaagct ccagtaacaa aagggttgcta cttagccact ggaagcaaag atcaaaccat 420
tcgaatctgg agctgttcta gaggccgagg ggtg atg att ttg aaa ttg ccc 472
Met Ile Leu Lys Leu Pro
1
ttt ctg aag aga aga gga ggg ggt ata gac cca act gtt aaa gag cgc 520
Phe Leu Lys Arg Arg Gly Gly Gly Ile Asp Pro Thr Val Lys Glu Arg
7 12 17 22
ctt tgg ttg aca ctc cat tgg ccc agc aat caa cca aca cag ctg gta 568
Leu Trp Leu Thr Leu His Trp Pro Ser Asn Gln Pro Thr Gln Leu Val
23 28 33 38
tct agc tgt ttt gga ggt gaa ctg ttg caa tgg gat ctc act caa tct 616
Ser Ser Cys Phe Gly Gly Glu Leu Leu Gln Trp Asp Leu Thr Gln Ser
39 44 49 54
tgg aga cgg aaa tac acc ctc ttc agt gcc tca tca gaa ggg caa aat 664
Trp Arg Arg Lys Tyr Thr Leu Phe Ser Ala Ser Ser Glu Gly Gln Asn
55 60 65 70
cat tca aga att gtg ttt aat tta tgt cct tta caa aca gag gat gac 712
His Ser Arg Ile Val Phe Asn Leu Cys Pro Leu Gln Thr Glu Asp Asp
71 76 81 86

aaa cag ctg tta ctt tct aca tca atg gat aga gat gta aaa tgt tgg	760
Lys Gln Leu Leu Leu Ser Thr Ser Met Asp Arg Asp Val Lys Cys Trp	
87 92 97 102	
gac ata gcc acc ttg gag tgc agc tgg acc ctt cct tcc ctt ggt ggg	808
Asp Ile Ala Thr Leu Glu Cys Ser Trp Thr Leu Pro Ser Leu Gly Gly	
103 108 113 118	
ttt gca tac agc ctg gct ttc tct tct gtg gac ata ggc tct ttg gcc	856
Phe Ala Tyr Ser Leu Ala Phe Ser Ser Val Asp Ile Gly Ser Leu Ala	
119 124 129 134	
ata ggt gtt ggg gat ggc atg atc cgt gta tgg aat aca ctc tcc ata	904
Ile Gly Val Gly Asp Gly Met Ile Arg Val Trp Asn Thr Leu Ser Ile	
135 140 145 150	
aag aac aac tat gat gtg aaa aat ttt tgg caa ggc gtg aag tcc aag	952
Lys Asn Asn Tyr Asp Val Lys Asn Phe Trp Gln Gly Val Lys Ser Lys	
151 156 161 166	
gtt aca gcg ctg tgc tgg cac cca acc aag gaa ggt tgc tta gct ttt	1000
Val Thr Ala Leu Cys Trp His Pro Thr Lys Glu Gly Cys Leu Ala Phe	
167 172 177 182	
gga act gat gat gga aaa gtg gga ttg tat gac acc tac tcc aac aag	1048
Gly Thr Asp Asp Gly Lys Val Gly Leu Tyr Asp Thr Tyr Ser Asn Lys	
183 188 193 198	
cct cca cag att tct agc aca tat cat aag aag act gta tat acg tta	1096
Pro Pro Gln Ile Ser Ser Thr Tyr His Lys Lys Thr Val Tyr Thr Leu	
199 204 209 214	
gcc tgg ggg cca cca gta ccc ccc atg tca ctt gga gga gaa gga gac	1144
Ala Trp Gly Pro Pro Val Pro Pro Met Ser Leu Gly Gly Glu Gly Asp	
215 220 225 230	
aga cct tcc ctt gct tta tac agc tgt gga gga gaa ggg att gtc tta	1192
Arg Pro Ser Leu Ala Leu Tyr Ser Cys Gly Gly Glu Gly Ile Val Leu	
231 236 241 246	
cag cat aat ccc tgg aag ctt agt gga gaa gcc ttt gac atc aac aaa	1240
Gln His Asn Pro Trp Lys Leu Ser Gly Glu Ala Phe Asp Ile Asn Lys	
247 252 257 262	
ctc atc agg gac acc aat tca atc aaa tac aaa ttg cct gta cac aca	1288
Leu Ile Arg Asp Thr Asn Ser Ile Lys Tyr Lys Leu Pro Val His Thr	
263 268 273 278	
gag ata agt tgg aaa gca gat ggc aaa atc atg gct ctt ggc aat gaa	1336
Glu Ile Ser Trp Lys Ala Asp Gly Lys Ile Met Ala Leu Gly Asn Glu	
279 284 289 294	
gat gga tca ata gaa ata ttt cag att ccc aac ctg aaa ctg atc tgt	1384
Asp Gly Ser Ile Glu Ile Phe Gln Ile Pro Asn Leu Lys Leu Ile Cys	
295 300 305 310	
act atc caa cag cat cac aag ctt gtg aat acc att agc tgg cat cat	1432

Thr Ile Gln Gln His His Lys Leu Val Asn Thr Ile Ser Trp His His	
311 316 321 326	
gag cat ggc agc cag cca gaa ttg agc tat ctg atg gcc tct ggc tcc	1480
Glu His Gly Ser Gln Pro Glu Leu Ser Tyr Leu Met Ala Ser Gly Ser	
327 332 337 342	
aac aat gca gtc att tac gtg cac aac ctg aag act gtc ata gag agc	1528
Asn Asn Ala Val Ile Tyr Val His Asn Leu Lys Thr Val Ile Glu Ser	
343 348 353 358	
agc cct gag tct cca gtg acc att aca gag ccc tac cgg acc ctc tca	1576
Ser Pro Glu Ser Pro Val Thr Ile Thr Glu Pro Tyr Arg Thr Leu Ser	
359 364 369 374	
ggg cat acg gcc aag att acc agt gtg gcg tgg agc cca cat cat gat	1624
Gly His Thr Ala Lys Ile Thr Ser Val Ala Trp Ser Pro His His Asp	
375 380 385 390	
gga agg ctg gta tct gct tcc tat gat ggt aca gcc cag gtg tgg gat	1672
Gly Arg Leu Val Ser Ala Ser Tyr Asp Gly Thr Ala Gln Val Trp Asp	
391 396 401 406	
gct ctc cgg gaa gag ccc ctg tgc aat ttc cga gga cat caa ggt cga	1720
Ala Leu Arg Glu Glu Pro Leu Cys Asn Phe Arg Gly His Gln Gly Arg	
407 412 417 422	
ctg ctt tgt gtg gca tgg tct cct ttg gat cca gac tgc atc tat tca	1768
Leu Leu Cys Val Ala Trp Ser Pro Leu Asp Pro Asp Cys Ile Tyr Ser	
423 428 433 438	
ggg gca gat gac ttt tgt gtg cac aag tgg ctc act tcc atg caa gat	1816
Gly Ala Asp Asp Phe Cys Val His Lys Trp Leu Thr Ser Met Gln Asp	
439 444 449 454	
cat tcc cgg cct cct caa ggc aaa aaa agt att gaa ttg gag aaa aaa	1864
His Ser Arg Pro Pro Gln Gly Lys Lys Ser Ile Glu Leu Glu Lys Lys	
455 460 465 470	
cgg ctc tct caa cct aag gca aag ccc aaa aag aag aaa aag ccc acc	1912
Arg Leu Ser Gln Pro Lys Ala Lys Pro Lys Lys Lys Lys Lys Pro Thr	
471 476 481 486	
ttg aga act cct gta aag ctg gaa tcg att gat gga aat gaa gaa gaa	1960
Leu Arg Thr Pro Val Lys Leu Glu Ser Ile Asp Gly Asn Glu Glu Glu	
487 492 497 502	
agc atg aag gag aac tca gga cct gtt gag aat ggt gtg tca gac caa	2008
Ser Met Lys Glu Asn Ser Gly Pro Val Glu Asn Gly Val Ser Asp Gln	
503 508 513 518	
gaa ggg gag gag caa gca cgg gag ccg gaa tta ccc tgt ggc ctt gct	2056
Glu Gly Glu Glu Gln Ala Arg Glu Pro Glu Leu Pro Cys Gly Leu Ala	
519 524 529 534	
cca gcg gtt tct aga gaa cca gtt atc tgc act cca gtt tcc tca ggc	2104
Pro Ala Val Ser Arg Glu Pro Val Ile Cys Thr Pro Val Ser Ser Gly	

535	540	545	550	
ttt gaa aag tca aaa gtc acc att aat aac aaa gtc att tta ctg aaa				2152
Phe Glu Lys Ser Lys Val Thr Ile Asn Asn Lys Val Ile Leu Leu Lys				
551	556	561	566	
aag gag cca cca aaa gag aag cca gaa acc tta atc aag aag aga aaa				2200
Lys Glu Pro Pro Lys Glu Lys Pro Glu Thr Leu Ile Lys Lys Arg Lys				
567	572	577	582	
gct cgt tcc ttg ctt ccc ctg agt aca agc ctg gac cac aga tcc aaa				2248
Ala Arg Ser Leu Leu Pro Leu Ser Thr Ser Leu Asp His Arg Ser Lys				
583	588	593	598	
gag gag ctt cat cag gac tgt ttg gta cta gca act gca aag cac tcc				2296
Glu Glu Leu His Gln Asp Cys Leu Val Leu Ala Thr Ala Lys His Ser				
599	604	609	614	
aga gag ctg aat gaa gat gtg tct gct gat gtt gag gaa aga ttt cat				2344
Arg Glu Leu Asn Glu Asp Val Ser Ala Asp Val Glu Glu Arg Phe His				
615	620	625	630	
ctg ggg ctt ttc aca gac agg gct acc ctg tat aga atg att gat att				2392
Leu Gly Leu Phe Thr Asp Arg Ala Thr Leu Tyr Arg Met Ile Asp Ile				
631	636	641	646	
gaa gga aaa ggt cac tta gaa aat ggc cac cct gag tta ttt cac cag				2440
Glu Gly Lys Gly His Leu Glu Asn Gly His Pro Glu Leu Phe His Gln				
647	652	657	662	
ctt atg ctt tgg aaa ggg gat ctc aaa ggt gtt ctc cag act gca gca				2488
Leu Met Leu Trp Lys Gly Asp Leu Lys Gly Val Leu Gln Thr Ala Ala				
663	668	673	678	
gaa aga ggg gag ctg aca gac aac ctt gtg gct atg gca cca gca gct				2536
Glu Arg Gly Glu Leu Thr Asp Asn Leu Val Ala Met Ala Pro Ala Ala				
679	684	689	694	
ggc tac cat gtg tgg cta tgg gct gtg gaa gct ttt gcc aaa cag ctg				2584
Gly Tyr His Val Trp Leu Trp Ala Val Glu Ala Phe Ala Lys Gln Leu				
695	700	705	710	
tgt ttt cag gat cag tat gtc aag gct gct tct cac cta ctt tcc atc				2632
Cys Phe Gln Asp Gln Tyr Val Lys Ala Ala Ser His Leu Leu Ser Ile				
711	716	721	726	
cac aaa gtg tat gaa gcg gtg gag ctg ctc aag tca aac cat ttt tac				2680
His Lys Val Tyr Glu Ala Val Glu Leu Leu Lys Ser Asn His Phe Tyr				
727	732	737	742	
agg gaa gct att gcg att gcc aag gcc cgg ctg cgc ccg gag gac cca				2728
Arg Glu Ala Ile Ala Ile Ala Lys Ala Arg Leu Arg Pro Glu Asp Pro				
743	748	753	758	
gtc ctg aag gac ttg tac ctc agc tgg gga acc gtc cta gaa aga gat				2776
Val Leu Lys Asp Leu Tyr Leu Ser Trp Gly Thr Val Leu Glu Arg Asp				
759	764	769	774	

ggc cac tat gct gta gct gcc aaa tgc tat tta ggg gcc act tgt gct	2824
Gly His Tyr Ala Val Ala Ala Lys Cys Tyr Leu Gly Ala Thr Cys Ala	
775 780 785 790	
tat gat gca gcc aaa gtt ttg gcc aaa aag ggg gat gcg gca tca ctt	2872
Tyr Asp Ala Ala Lys Val Leu Ala Lys Lys Gly Asp Ala Ala Ser Leu	
791 796 801 806	
aga acg gct gca gag ttg gct gcc atc gta gga gag gat gag ttg tct	2920
Arg Thr Ala Ala Glu Leu Ala Ala Ile Val Gly Glu Asp Glu Leu Ser	
807 812 817 822	
gct tcc ctg gct ctc aga tgt gcc caa gag ctg ctt ctg gcc aac aac	2968
Ala Ser Leu Ala Leu Arg Cys Ala Gln Glu Leu Leu Leu Ala Asn Asn	
823 828 833 838	
tgg gtg gga gcc cag gaa gcc ctg cag ctg cat gaa agt cta cag ggt	3016
Trp Val Gly Ala Gln Glu Ala Leu Gln Leu His Glu Ser Leu Gln Gly	
839 844 849 854	
cag aga ttg gtg ttt tgc ctt ctg gag cta ctg tcc agg cat ctg gag	3064
Gln Arg Leu Val Phe Cys Leu Leu Glu Leu Leu Ser Arg His Leu Glu	
855 860 865 870	
gaa aag cag ctt tca gag ggc aaa agc tcc tcc tct tac cac act tgg	3112
Glu Lys Gln Leu Ser Glu Gly Lys Ser Ser Ser Ser Tyr His Thr Trp	
871 876 881 886	
aac acg ggc acc gaa ggg cct ttc gtg gag agg gtg act gca gtg tgg	3160
Asn Thr Gly Thr Glu Gly Pro Phe Val Glu Arg Val Thr Ala Val Trp	
887 892 897 902	
aag agc atc ttc agc ctt gac acc cct gag cag tat cag gaa gcc ttt	3208
Lys Ser Ile Phe Ser Leu Asp Thr Pro Glu Gln Tyr Gln Glu Ala Phe	
903 908 913 918	
cag aag ctg cag aac atc aag tac cca tct gct aca aat aac aca cct	3256
Gln Lys Leu Gln Asn Ile Lys Tyr Pro Ser Ala Thr Asn Asn Thr Pro	
919 924 929 934	
gcc aaa cag ctc ctg ctt cac att tgc cat gac ttg acc ctg gca gtg	3304
Ala Lys Gln Leu Leu Leu His Ile Cys His Asp Leu Thr Leu Ala Val	
935 940 945 950	
ctg agc caa cag atg gcc tcc tgg gac gag gct gtg cag gcg ctc ctt	3352
Leu Ser Gln Gln Met Ala Ser Trp Asp Glu Ala Val Gln Ala Leu Leu	
951 956 961 966	
cgg gcg gtg gtc cgg agc tat gac tca ggg agc ttc acc atc atg cag	3400
Arg Ala Val Val Arg Ser Tyr Asp Ser Gly Ser Phe Thr Ile Met Gln	
967 972 977 982	
gaa gtg tac tca gcc ttt ctc cct gat ggc tgt gac cac cta aga gac	3448
Glu Val Tyr Ser Ala Phe Leu Pro Asp Gly Cys Asp His Leu Arg Asp	
983 988 993 998	

aag ttg ggg gac cat caa tcc cct gcc aca cca gct ttc aaa agt ttg	3496
Lys Leu Gly Asp His Gln Ser Pro Ala Thr Pro Ala Phe Lys Ser Leu	
999 1004 1009 1014	
gag gcc ttt ttt ctt tat ggg cgt ctg tat gaa ttc tgg tgg tct ctc	3544
Glu Ala Phe Phe Leu Tyr Gly Arg Leu Tyr Glu Phe Trp Trp Ser Leu	
1015 1020 1025 1030	
tcc aga cct tgc cca aat tcc agt gtc tgg gta agg gct ggt cac aga	3592
Ser Arg Pro Cys Pro Asn Ser Ser Val Trp Val Arg Ala Gly His Arg	
1031 1036 1041 1046	
aca ctc tct gtt gag cca agc cag cag tta gac act gcc agc act gaa	3640
Thr Leu Ser Val Glu Pro Ser Gln Gln Leu Asp Thr Ala Ser Thr Glu	
1047 1052 1057 1062	
gaa acg gac cct gaa act tct cag cca gag cca aac agg cct tca gaa	3688
Glu Thr Asp Pro Glu Thr Ser Gln Pro Glu Pro Asn Arg Pro Ser Glu	
1063 1068 1073 1078	
cta gac ttg aga ctc aca gaa gaa ggt gag cga atg ctg agt act ttt	3736
Leu Asp Leu Arg Leu Thr Glu Glu Gly Glu Arg Met Leu Ser Thr Phe	
1079 1084 1089 1094	
aag gag ctc ttt tca gaa aag cat gcc agt ctc caa aac tca cag aga	3784
Lys Glu Leu Phe Ser Glu Lys His Ala Ser Leu Gln Asn Ser Gln Arg	
1095 1100 1105 1110	
act gtt gct gaa gtc caa gag acc ttg gca gaa atg atc cga caa cac	3832
Thr Val Ala Glu Val Gln Glu Thr Leu Ala Glu Met Ile Arg Gln His	
1111 1116 1121 1126	
caa aag agt caa ctc tgt aaa tcc aca gca aat ggt cct gat aag aat	3880
Gln Lys Ser Gln Leu Cys Lys Ser Thr Ala Asn Gly Pro Asp Lys Asn	
1127 1132 1137 1142	
gaa ccg gaa gta gaa gca gag cag ccc ctc tgc agt tct cag agc cag	3928
Glu Pro Glu Val Glu Ala Glu Gln Pro Leu Cys Ser Ser Gln Ser Gln	
1143 1148 1153 1158	
tgt aaa gaa gaa aaa aat gag cca ctt tct ctg cct gag tta acc aaa	3976
Cys Lys Glu Glu Lys Asn Glu Pro Leu Ser Leu Pro Glu Leu Thr Lys	
1159 1164 1169 1174	
agg ctt acc gag gca aat cag aga atg gca aaa ttt cct gag agc att	4024
Arg Leu Thr Glu Ala Asn Gln Arg Met Ala Lys Phe Pro Glu Ser Ile	
1175 1180 1185 1190	
aag gcc tgg ccc ttc cca gat gtg ctg gag tgc tgc ctc gtc ctg ctt	4072
Lys Ala Trp Pro Phe Pro Asp Val Leu Glu Cys Cys Leu Val Leu Leu	
1191 1196 1201 1206	
ctc atc agg tcc cac ttt cct ggc tgt ctg gcc cag gaa atg cag cag	4120
Leu Ile Arg Ser His Phe Pro Gly Cys Leu Ala Gln Glu Met Gln Gln	
1207 1212 1217 1222	
cag gcc caa gag ctc ctt cag aaa tac ggc aac acg aaa act tac aga	4168

Gln	Ala	Gln	Glu	Leu	Leu	Gln	Lys	Tyr	Gly	Asn	Thr	Lys	Thr	Tyr	Arg	
1223						1228				1233					1238	
aga	cac	tgc	cag	acc	ttc	tgt	atg	tga	at	ttt	cacacac	ctt	gaagaa	actg		4220
Arg	His	Cys	Gln	Thr	Phe	Cys	Met	*								
1239						1244										
ccaaattgaa	aatgtttgac	atctttcacc	tctgcagtta	tgccacacca	gacattcact											4280
ctgggtcccta	gatgtttttg	cagtaatcca	aaagaataca	aacaaggatt	aagtttgaat											4340
caaccctgcc	tacccataga	caacgggtgga	tctgacttta	gactcaattg	tggtctccta											4400
ctggaggaggaa	gatcatgaaa	agcccacagt	agttattcag	aactaacacc	tcagagagtgt											4460
tggtcatctc	tacagcctta	ggcaggtttc	acccaaagag	gagaaacttc	tgctgtcacc											4520
caaagtgtta	catgcttaaa	acacaagcta	cctttgtaaa	tacttcatct	gatcagaagt											4580
gtgtcatgct	tgtttgagat	ggagttgctg	catttttagga	ctattgatac	cttttttttaa											4640
ttgtttttat	aatattttaat	ttgaaagagg	agacccttct	ctctctactc	tttcatagac											4700
tgaagtttga	atatgaaata	ggccttaacc	atcatgttga	ctctcctgtc	agaatttttag											4760
gttggaatt	tggttttatt	ctttcatgta	attgcttatt	tgaacagatc	acttactaaa											4820
gcttttagaag	aagtgattca	aatgtgtgtt	ttcccttcag	ttttataaca	aatggattga											4880
tggcagtcaa	atagctcagg	aataaattac	tgtttcaatg	gtttcttaaac	tttcttggat											4940
cataggatcc	ttttgagaat	cagattaaag	ccaaagatac	tctttggaga	aaaatgcata											5000
ttcctaattt	tgcatagatg	acctttggat	tattggactc	tgactattgg	gaccctaaat											5060
actattttaat	tataaatctt	tcttttctcc	tc													5092

<210> 154
 <211> 2274
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (116)..(460)

taattgggag	aatactccag	ccataagatc	tgcatgcata	gcatagcact	ggcttctctg		60
gactttgcac	acctccagga	gaagaaccca	gaaaattgat	cagttctaaa	aaacc atg		118
					Met		
					1		
ccc cac ttg ttg gtg act ttc agg gat gtg gcc att gac ttc tct cag							166

Pro	His	Leu	Leu	Val	Thr	Phe	Arg	Asp	Val	Ala	Ile	Asp	Phe	Ser	Gln	
2					7					12					17	
gag gaa tgg gaa tgc ctg gac cct gct cag agg gac ttg tac agg gat																214
Glu	Glu	Trp	Glu	Cys	Leu	Asp	Pro	Ala	Gln	Arg	Asp	Leu	Tyr	Arg	Asp	
18					23					28					33	
gtg atg ttg gag aac tac agc aac ctg atc tca ttg gac ttg gaa tcc																262
Val	Met	Leu	Glu	Asn	Tyr	Ser	Asn	Leu	Ile	Ser	Leu	Asp	Leu	Glu	Ser	
34					39					44					49	
agt tgt gtg acc aaa aag tta tct cca gaa aag gaa att tat gaa atg																310
Ser	Cys	Val	Thr	Lys	Lys	Leu	Ser	Pro	Glu	Lys	Glu	Ile	Tyr	Glu	Met	
50					55					60					65	
gaa tca ctc cag tgg gag aat atg ggg aaa cgt atc aac cat cac ctt																358
Glu	Ser	Leu	Gln	Trp	Glu	Asn	Met	Gly	Lys	Arg	Ile	Asn	His	His	Leu	
66					71					76					81	
tca ata caa tgg tct tgg aga caa tat gga gtg caa agg caa ctt aga																406
Ser	Ile	Gln	Trp	Ser	Trp	Arg	Gln	Tyr	Gly	Val	Gln	Arg	Gln	Leu	Arg	
82					87					92					97	
ggg tca agt aag caa gtc aga agg gct tta cat gtg tgt caa aat tac																454
Gly	Ser	Ser	Lys	Gln	Val	Arg	Arg	Ala	Leu	His	Val	Cys	Gln	Asn	Tyr	
98					103					108					113	
ctg tga agaaaaggcc actgaaagtc attcaacctc ttctactttt catcgataa																510
Leu	*															
114																
ttcctaccaa ggaaaaattg tcaaatgtaa ggaatgcaga caaggtttca gctacctgtc																570
atgccttatt caacatgagg aaaatcataa tatataaaaa tgctctgaag ttaataaaaca																630
caggaatacc tttagcaaaa agccaagcta tattttaacat cagagaattc agactgggtg																690
agaaacctta tgagtgtatg gaatgtggaa aggccttttg tcgtacttct gatctcattc																750
aacatcagaa aattcatact aatgaaaaac cttatcagtg taacgcatgt gggaaagctt																810
ttattcgtgg ttcacagctc actgaacatc agagagttca tacaggagag aaaccatatg																870
attgtaagaa atgtggaaaa gccttttagtt attgtcacia tatactcttc atcagagaat																930
tcatagtggg gaaaaaccct atgaatgtaa gattgtggga aggcctttat cttgggtctc																990
aacttactta ccatcagaga attcatagtg gtgagaaacc ttatgagtgt aaggaatgtg																1050
gaaaggcctt tattcttggt tcacacctta cataccatca gagagttcat actggtgaaa																1110
agccttacat atgtaaagaa tgtgggaaag cctttttatg tgcctcccaa ctgaatgaac																1170
atcagagaat tcatacagga gagaaaccct atgaatgtaa agaatgcggg aagacctttt																1230
ttcgtggctc acaacttact taccacctga gagttcattc aggtgagaga cttataaat																1290

gcaaagaatg tgggaaagcc tttattttcta attctaattct tattcaacat caaagaattc 1350
ataccggaga gaagccctac aaatgtaagg aatgtggaaa ggcctttatt tgtggcaaac 1410
aacttagtga acatcagaga attcatacag gtgagaaacc ctttgaatgt aaggaatgtg 1470
gaaaggcctt tattcgtgtt gcatatctta ctcaacatga gaaaattcat ggtgagaaac 1530
attatgaatg taaggaatgt gggaagacct ttgtacgtgc tacacaactt acattatcat 1590
caaagaattc atacagggtga aaagccctac aaatgtaagg aatgtgacaa ggcctttatt 1650
tatggctcac aatacttagt gaacatcaga gaattcacag aggtgaaaaa ccttatgaat 1710
gtaaacagtg tggaaggcct ttattcgtgg ctcacacctt acgaacatct gagaactcat 1770
actggagaga aaccctatga atgtaaggaa tgtgggaggg cctttagtcg tggctcagaa 1830
catactctgc atcaaaggat ccatactggg gagaaacctt atacatgtgt ccagtgtggg 1890
aaagacttta gatgtccttc acaacttact caacatacaa ggcttcataa ttgagaaagc 1950
cttgaatgtg attaaattta agaaaatctt catctatttc atatctataa tgaatgtaga 2010
acatcttgct tctgctcaga actgctcatt cttagaaggc ctacttaaca tggatgcaga 2070
ataatttcag aaaccctta aataattcct taacatctct ataaacgcta gaatataatg 2130
ctgaattata tcctttatta agcatcatct ccatttcacc atatacctaac tgaaacccta 2190
tatatttctt gtgtgttctt ttctatttgt aaatactgta attgtattac atgactaaat 2250
tatattaata ctataattcc ccgg 2274

<210> 155
<211> 6990
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (61)..(2397)

<400> 155
gggcggccgt tcccgcggcc ccctcggctt tgcagcgcc gcctgcgagg cggaggcagg 60
atg aag atg act ggg gat ttc gag gag tgt ctg aag gac tcg ccc cgc 108
Met Lys Met Thr Gly Asp Phe Glu Glu Cys Leu Lys Asp Ser Pro Arg
1 5 10 15
ttc agg gca gct ttg gaa gaa gta gaa ggt gat gtg gca gaa ttg gaa 156
Phe Arg Ala Ala Leu Glu Glu Val Glu Gly Asp Val Ala Glu Leu Glu
17 22 27 32

cta aaa ctt gat aag ctt gtg aaa ctt ggg att gca atg att gat act	204
Leu Lys Leu Asp Lys Leu Val Lys Leu Gly Ile Ala Met Ile Asp Thr	
33 38 43 48	
gga aaa gcc ttt tgt gtt gca aat aaa cag ttc atg aat ggg att cga	252
Gly Lys Ala Phe Cys Val Ala Asn Lys Gln Phe Met Asn Gly Ile Arg	
49 54 59 64	
gac ctg gcc cag tat tct agt aat gat gct gtc gtt gag aca agt ttg	300
Asp Leu Ala Gln Tyr Ser Ser Asn Asp Ala Val Val Glu Thr Ser Leu	
65 70 75 80	
acc aag ttt tct gac agt ctt caa gaa atg ata aat ttt cac aca atc	348
Thr Lys Phe Ser Asp Ser Leu Gln Glu Met Ile Asn Phe His Thr Ile	
81 86 91 96	
ctg ttg cca aac tca gag atc aat tta agg cac agc ttc agt aac ttt	396
Leu Leu Pro Asn Ser Glu Ile Asn Leu Arg His Ser Phe Ser Asn Phe	
97 102 107 112	
gtt aaa gaa gat ctt aga aaa ttc aaa gat gcc aag aag caa ttt gaa	444
Val Lys Glu Asp Leu Arg Lys Phe Lys Asp Ala Lys Lys Gln Phe Glu	
113 118 123 128	
aaa gtc agt gaa gaa aaa gaa aat gcg tta gta aaa aat gcc caa gta	492
Lys Val Ser Glu Glu Lys Glu Asn Ala Leu Val Lys Asn Ala Gln Val	
129 134 139 144	
caa aga aac aaa caa cat gaa gtt gaa gaa gcc acc aac att ctg aca	540
Gln Arg Asn Lys Gln His Glu Val Glu Glu Ala Thr Asn Ile Leu Thr	
145 150 155 160	
gca aca aga aaa tgt ttc cga cac ata gcc ctc gat tat gtg ctt cag	588
Ala Thr Arg Lys Cys Phe Arg His Ile Ala Leu Asp Tyr Val Leu Gln	
161 166 171 176	
att aat gtt ctt caa tca aaa agg aga tca gaa atc cta aaa tca atg	636
Ile Asn Val Leu Gln Ser Lys Arg Arg Ser Glu Ile Leu Lys Ser Met	
177 182 187 192	
ttg tca ttt atg tat gcc cat ttg gcc ttc ttt cat caa gga tat gat	684
Leu Ser Phe Met Tyr Ala His Leu Ala Phe Phe His Gln Gly Tyr Asp	
193 198 203 208	
ctg ttt agt gaa ctt gga ccc tac atg aag gat ctt ggt gca cag ttg	732
Leu Phe Ser Glu Leu Gly Pro Tyr Met Lys Asp Leu Gly Ala Gln Leu	
209 214 219 224	
gat cga ctg gtt gtg gat gca gca aag gag aaa aga gaa atg gag caa	780
Asp Arg Leu Val Val Asp Ala Ala Lys Glu Lys Arg Glu Met Glu Gln	
225 230 235 240	
aaa cat tcc acc att caa caa aag gat ttc tcc agt gat gat tct aag	828
Lys His Ser Thr Ile Gln Gln Lys Asp Phe Ser Ser Asp Asp Ser Lys	
241 246 251 256	
tta gaa tat aac gta gat gct gca aat ggc ata gtt atg gaa gga tat	876

Leu Glu Tyr Asn Val Asp Ala Ala Asn Gly Ile Val Met Glu Gly Tyr	
257 262 267 272	
ctg ttc aaa cga gcc agc aat gcc ttc aaa act tgg aac agg cgc tgg	924
Leu Phe Lys Arg Ala Ser Asn Ala Phe Lys Thr Trp Asn Arg Arg Trp	
273 278 283 288	
ttt tca ata cag aat aat cag ttg gtt tac cag aaa aaa ttt aag gat	972
Phe Ser Ile Gln Asn Asn Gln Leu Val Tyr Gln Lys Lys Phe Lys Asp	
289 294 299 304	
aat ccg act gtg gta gtt gaa gac ctc agg ctt tgc aca gtg aaa cat	1020
Asn Pro Thr Val Val Val Glu Asp Leu Arg Leu Cys Thr Val Lys His	
305 310 315 320	
tgt gaa gac ata gag cga cga ttc tgc ttt gag gtg gtc tcg cca aca	1068
Cys Glu Asp Ile Glu Arg Arg Phe Cys Phe Glu Val Val Ser Pro Thr	
321 326 331 336	
aaa agt tgc atg ctc cag gca gat tcc gaa aag ctg cgc cag gca tgg	1116
Lys Ser Cys Met Leu Gln Ala Asp Ser Glu Lys Leu Arg Gln Ala Trp	
337 342 347 352	
att aag gct gtt cag acc agt att gct act gct tat aga gag aag ggt	1164
Ile Lys Ala Val Gln Thr Ser Ile Ala Thr Ala Tyr Arg Glu Lys Gly	
353 358 363 368	
gat gaa tca gag aag ctg gat aag aaa tca tct cca tcc aca gga agc	1212
Asp Glu Ser Glu Lys Leu Asp Lys Lys Ser Ser Pro Ser Thr Gly Ser	
369 374 379 384	
cta gat tct gga aat gag tcc aaa gag aaa tta ttg aaa gga gaa agt	1260
Leu Asp Ser Gly Asn Glu Ser Lys Glu Lys Leu Leu Lys Gly Glu Ser	
385 390 395 400	
gcg ctt cag cgg gtc cag tgt atc cct ggc aat gcc agc tgt tgt gac	1308
Ala Leu Gln Arg Val Gln Cys Ile Pro Gly Asn Ala Ser Cys Cys Asp	
401 406 411 416	
tgt ggc ctg gca gat cca cgg tgg gcc agc atc aac ctg ggc atc acc	1356
Cys Gly Leu Ala Asp Pro Arg Trp Ala Ser Ile Asn Leu Gly Ile Thr	
417 422 427 432	
ttg tgt atc gag tgc tcc gga att cac cgg agc ctt ggg gtt cat ttt	1404
Leu Cys Ile Glu Cys Ser Gly Ile His Arg Ser Leu Gly Val His Phe	
433 438 443 448	
tca aaa gta cga tct tta act tta gac acc tgg gag cca gaa ctt tta	1452
Ser Lys Val Arg Ser Leu Thr Leu Asp Thr Trp Glu Pro Glu Leu Leu	
449 454 459 464	
aag ctt atg tgt gag ttg ggg aat gat gtt ata aat cga gtt tat gaa	1500
Lys Leu Met Cys Glu Leu Gly Asn Asp Val Ile Asn Arg Val Tyr Glu	
465 470 475 480	
gct aat gtg gaa aaa atg gga ata aag aaa ccc caa cca gga caa aga	1548
Ala Asn Val Glu Lys Met Gly Ile Lys Lys Pro Gln Pro Gly Gln Arg	

481	486	491	496	
cag gag aag gag gca tat atc aga gca aaa tat gtg gag agg aaa ttt				1596
Gln Glu Lys Glu Ala Tyr Ile Arg Ala Lys Tyr Val Glu Arg Lys Phe				
497	502	507	512	
gtg gat aaa tat tct ata tca tta tca cct cct gag cag caa aaa aag				1644
Val Asp Lys Tyr Ser Ile Ser Leu Ser Pro Pro Glu Gln Gln Lys Lys				
513	518	523	528	
ttt gtc tct aaa agt tct gaa gaa aag agg ctg agc att tct aaa ttt				1692
Phe Val Ser Lys Ser Ser Glu Glu Lys Arg Leu Ser Ile Ser Lys Phe				
529	534	539	544	
ggg cca ggg gac caa gtc aga gca tct gcc caa agt tca gtc aga agt				1740
Gly Pro Gly Asp Gln Val Arg Ala Ser Ala Gln Ser Ser Val Arg Ser				
545	550	555	560	
aat gac agt gga att cag cag agc tct gat gat gga aga gaa tct tta				1788
Asn Asp Ser Gly Ile Gln Gln Ser Ser Asp Asp Gly Arg Glu Ser Leu				
561	566	571	576	
ccc tcc acg gtg tca gcc aat agt tta tat gag cct gaa gga gaa agg				1836
Pro Ser Thr Val Ser Ala Asn Ser Leu Tyr Glu Pro Glu Gly Glu Arg				
577	582	587	592	
caa gat tct tct atg ttt ctt gac tcg aaa cat ctt aat cca gga ctt				1884
Gln Asp Ser Ser Met Phe Leu Asp Ser Lys His Leu Asn Pro Gly Leu				
593	598	603	608	
cag ctt tat agg gcg tca tat gaa aaa aac ctt cct aaa atg gct gag				1932
Gln Leu Tyr Arg Ala Ser Tyr Glu Lys Asn Leu Pro Lys Met Ala Glu				
609	614	619	624	
gct ttg gct cat ggt gca gac gtg aac tgg gcc aat tca gag gaa aac				1980
Ala Leu Ala His Gly Ala Asp Val Asn Trp Ala Asn Ser Glu Glu Asn				
625	630	635	640	
aaa gcg aca cca ctt att cag gct gta tta ggg ggc tct ttg gtg acg				2028
Lys Ala Thr Pro Leu Ile Gln Ala Val Leu Gly Gly Ser Leu Val Thr				
641	646	651	656	
tgt gag ttc ctc cta cag aat ggt gct aat gtc aac caa aga gat gtc				2076
Cys Glu Phe Leu Leu Gln Asn Gly Ala Asn Val Asn Gln Arg Asp Val				
657	662	667	672	
caa ggg cgg gga cca ttg cac cat gcc acc gtc tta ggg cac aca ggg				2124
Gln Gly Arg Gly Pro Leu His His Ala Thr Val Leu Gly His Thr Gly				
673	678	683	688	
cag gta tgt tta ttc cta aaa cga ggt gcc aat caa cat gcc act gat				2172
Gln Val Cys Leu Phe Leu Lys Arg Gly Ala Asn Gln His Ala Thr Asp				
689	694	699	704	
gaa gaa ggg aaa gac cct ttg agc ata gct gtg gaa gca gcc aat gct				2220
Glu Glu Gly Lys Asp Pro Leu Ser Ile Ala Val Glu Ala Ala Asn Ala				
705	710	715	720	

gat ata gtc acc ttg tta cgt tta gca aga atg aat gaa gag atg cgg	2268
Asp Ile Val Thr Leu Leu Arg Leu Ala Arg Met Asn Glu Glu Met Arg	
721 726 731 736	
gaa tca gaa gga ctt tat gga cag cca ggt gat gaa act tat cag gac	2316
Glu Ser Glu Gly Leu Tyr Gly Gln Pro Gly Asp Glu Thr Tyr Gln Asp	
737 742 747 752	
ata ttt cgt gat ttt tcc caa atg gca tcc aat aat cca gag aaa cta	2364
Ile Phe Arg Asp Phe Ser Gln Met Ala Ser Asn Asn Pro Glu Lys Leu	
753 758 763 768	
aat cgt ttc cag caa gat tca cag aaa ttc tga attttttt aaaaatggga	2415
Asn Arg Phe Gln Gln Asp Ser Gln Lys Phe *	
769 774 779	
aaatatgaaa tctggtgacc ccctaagtga tacagctaaa aattcacaat ttttttactg	2475
ctttaattct acttaatttt ggtagatatt gaatggcttg gaaaagaggt acccattcat	2535
atatttataa attaaaaacat agttatctag tagtaggaga ggaacctagt ttaggacctc	2595
ttttattaaa aaagcctatt taaagggcta tttctgtaga cagaagttca gtctagattt	2655
aggccatctc taggttacaa gatgatagga ggtagacaa aagtgattct tttgccaatg	2715
ggtggtggca ttgatttttt tcttccatgc atcttgccca ggatcactca gtcaagcatg	2775
tcttcatcaa gtggaagcca actgtctctgc ctgcctcaag aatatgtgtt ttcttttagct	2835
tccttgagga tttttggtgg ttcagaaata ggtgtgtgtg ttgatgtgtt tttggtaacc	2895
tagctttcat acacataata tatgatttat tagaactaga gaatgtgttt tccccgtttg	2955
ttcataaatg cggtcgggta tacttcttag gtgacagggt attgtccagt actttaatgt	3015
atgtatgtat aatggctgta caggtagacc ataattcagt ctttttagatt tatttttatgc	3075
agcaaaaaga agctcttttt ttttttaatc acaaaaaaaaa accccagttc aaaatgtgta	3135
gttcttcatt gttggggtga ttccccaaaa ccttgacaga tgtatcgatg gaataaaagt	3195
atgtttttaa ggttacttga atgtcacaaa attatggcct tcatccaaaa ctttaaaggg	3255
aaaatcaatt tataaaatca tgtaggccat ttttatattt gaaatttgtc cttttaaaga	3315
tagttttgct gttgctccta gtgaaagaaa aatctctgta caaaggagaa aaagaacccc	3375
acttattctt agttaatact aaaatatata gcaataaatt gctgtttatt ttttctacat	3435
ctattttgtg tacttgtaca cagtgtacat tcttttaaat tatatcgtgt atatagcttt	3495
agtattcggg tacatgattc acagaccctt gaattccaaa atattatgga taaacattac	3555
catttatatg ctacaaatta gtctgattcc atctttgaaa atgtcttaaa gtataaaata	3615

attaatttgc tttttttttt ttttttcccg agatggcgtc ttgctgtgtc acccaggctg	3675
gagtgcagtg gcacgatctc agctcactgc agcctcctcc tcttgggttc aagcaattct	3735
cctgcctcag cctcccgagt agctgggact acaggcaccg gccaccattc cgagctaatt	3795
tctatatatt tagtaaagac gggtttcacc attttggcca ggttgggtct gaactcctga	3855
cctcaggtga tcagcctgct ttagcctccc agagtgtctg gattacaggc gtgagccacc	3915
gcaccagacc taatttgcct tttgattcct tccattgtt gtcaaaaatt aagtctattc	3975
ttcttttaga aattatatgt aaatgatatt attgatactc tttctaaata agaggtttta	4035
aaatatataa aaactttatg atccaattat agataaattt tctaacattt cccagtcact	4095
agggttttat aagttgatta aacatcaaat cagaatctag ccaagcagga attatattga	4155
aataagttca cattacagaa aaggttccat aatttggcca aactgcatgc atgtaatgct	4215
tatttagtaa tggtcactgt atgttagata aggataaaaa tatatttgtg aattacttct	4275
gaggaaatgc taacttccac agcattgtat ttaattataa caataacagg aacattaaat	4335
ctttatcttt gctgtttcac ctcaaagtca tagatcatct ggcttttttag gcaccttcac	4395
taaaggcaaa aatctgattt gtagttttta ttagcatgta ccttgaaatt atttgaccaa	4455
gaagctcaaa gaaaagaagt acgttaaaga aaaagaaaaa acctcacttt tcttttatag	4515
tgtcccttcc tgttttaatt cctaaagatc ctgactttta tctgaggaag tctaggtagt	4575
tttcttttg gatctggcca ttggtgcgtg tttcattcag atcacctctg gaatctctgt	4635
ggttgtgaag gcaattcctt atgagactct tgccctctgt ggcttacgtg atgaattgtt	4695
aatatggcag taattaatta gtatctactt aaatttagtg gtcagaaatg tatttgaagt	4755
gccttaaaga tgatcatggt tcagaatatc ttcagagaaa gcaaaatctt taatattgca	4815
gggagcctag caatacaaat acacatttct gtggcttgat ttcttgaata tgctgagacc	4875
caatttggac tacatttggc agaaatcatg gagtaaacag caaggcttta aattaaatta	4935
atagttacaa ggtaggttgg ctcttaggtg aatttagcca tgtcaactaa tagcttttat	4995
atggtatgta acaaatctga attatgttat gctgtgaatt attcagtgca ttataagaaa	5055
tottagttaa tcatgctttt gggcttcatt agtcaatgtg attggccttt tattttcttt	5115
ccataactta totgctatta ttagtttctt attccttatt attaattctgt tagctcatta	5175
tcattagctt actaacttga aagttagatt aatatcaaaa taagaatagc agcactatga	5235
agagttaata aaatgcaatt tcatgttaga gctagaataa aagtaattga gcagtcattt	5295
gcaaatgctt cattataaca tttatgtgct taagatttct aaggttttta aaagttacct	5355

ttaataacaat ccttagaaac tcagaaat	5415
ttt cctgatattc attagattat ggtg	
ttt gcc	
taatttatac cggttttcac tgtatatt	5475
ttt aatgaacttt gattgggtta cttt	
ttt tocaga	
catacagatt taatttggga atatgga	5535
act ttggttcttc atgagtgc	
at tttgaaaaag	
aaaaaaaagta cacattcaga atctgg	5595
ccaa ttttaagttg tattttaaaa	
atattttatg	
catgttaagt atggctgcag taaatg	5655
aaat tgtgtttaag actaaattta	
ctaccgtttt	
gaacagacat tcccagatca ttcttat	5715
att gtcagataac acttgtgtat	
aatatcactt	
tggaccatgg acatgagctg gaaaaat	5775
gat gtatttttgt agattgtatg	
tccagaatga	
ctttagaacc gcatgatacg gtggaag	5835
gag cactggacta gtcgtcacta	
cccttttttg	
attcagggct cctcacaatt aaaatg	5895
agtg taatgaaaca aggtgaaaat	
atagaagcat	
ccctttgtat actgttttgc tactta	5955
cagt gtacttggca ttgctttatc	
tacttggatt	
ctcatggtag gatttctgag atctta	6015
atct aagctccaaa gttgtctact	
tttttgatcc	
tagggtgctc cttttgtttt acaga	6075
gcagg gtcacttgat ttgctagctg	
gtggcagaat	
tggcaccatt acccaggtct gactga	6135
ccac cagtcagagg cactttat	
ttt gtatcatgaa	
atgatttgaa atcattgtaa agcagc	6195
gaag tctgataatg aatgccagct	
ttccttgtgc	
tttgataaca aagactccaa atattc	6255
tctgga gaacctggat aaaagttga	
agggctagat	
tgggatttga agacaaaatt gtagga	6315
aatc ttacattttt gcaataacaa	
acattaatga	
aagcaaaaaca ttataaaagt aattt	6375
taatt caccacatac ttatcaatt	
ttt cttgatgctt	
ccaaatgaca tctacagata tggttt	6435
gtg gacatctttt tctgtttaca	
ttaaatttato	
cacttaaaat gtgataatgt ggaga	6495
caaa caagatttga ttacataaac	
ttttctctgc	
attggtcttt tcactatctt atttg	6555
ctaac ttttcttatt tttcttca	
ac cccccccc	
tccatttttt ggatattaaa caggga	6615
aagc ttgctacatt ataaagattg	
ttggcaccat	
ttattttaca caaaggctaa aggtta	6675
actt ttggaaatga tgagctactt	
ttatatatgt	
gtttactcat gctttgtgat atttct	6735
ggat cattccagtc ataaagactt	
attacatgta	
ctattttcttg ctacctgtga aaag	6795
gtatat tttaaagaat gtataacca	
acagtcattt	
actttttatt agtatgtaga ggattt	6855
gtat ctaattcatg aatgtagttt	
tacagtagtt	
tgtcattgta aatggagcaa agtac	6915
attat cttctaaaaat gtacattatg	
taagaattgt	
aaatatactt aagtaatttg tatgc	6975
aaaaa aattacaata agtcaataaa	
gatctcacct	
ctgaaaaaaaa aaaaa	6990

<210> 156
 <211> 4053
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (409) .. (3819)

<220>
 <221> misc_feature
 <222> (1) ... (4053)
 <223> n = a,t,c or g

<400> 156

```
cctaaggccc taattgaaga gctgttgcta tacaagcgct canaagatca gatagaactg      60
aaggaaaagc agttgtcaac tatgagggtg gatgtgtgca gcacagaaac tctcaaattgc      120
ttaaaagata aaacaggtgg gaagaagttc tccaaagnat ttgaagagggc aagctccaag      180
ctggaagaat ttgtgaatgg attagatann caggtgaaaa acggaccctc attaacagaa      240
gcactggaaa atgctggaat tttctatgaa gcacaataca aagaagtaaa agtgggtggct      300
aatgcatata aaacctttgc taaccgagta aacaatttaa agaagaagtt ggatcaattg      360
aagtcacccc ttccagatcc tgaagaatca ccagttcctt cccaagc atg gac gct      417
                                   Met Asp Ala
                                   1

ccc tcc ccg act ggt tct gag tct cct ttt cag gga atg gga ggt gag      465
Pro Ser Pro Thr Gly Ser Glu Ser Pro Phe Gln Gly Met Gly Gly Glu
  4              9              14              19

gaa tcc cag tca cca acc atg gag agt gag aaa tct gcc aca cct gaa      513
Glu Ser Gln Ser Pro Thr Met Glu Ser Glu Lys Ser Ala Thr Pro Glu
  20              25              30              35

cct gtg aca gat aat cgt gat gtg gaa gac atg gaa ctc tca gat gtg      561
Pro Val Thr Asp Asn Arg Asp Val Glu Asp Met Glu Leu Ser Asp Val
  36              41              46              51

gaa gat gat ggg tca aaa atc att gtc gag gac agg aag gaa aaa cct      609
Glu Asp Asp Gly Ser Lys Ile Ile Val Glu Asp Arg Lys Glu Lys Pro
  52              57              62              67

gca gag aag tca gct gta tcc act tct gta cct aca aag cca aca gaa      657
Ala Glu Lys Ser Ala Val Ser Thr Ser Val Pro Thr Lys Pro Thr Glu
  68              73              78              83

aat atc tca aag gcc tct tca tgt acc cca gtg cct gtg acc atg aca      705
Asn Ile Ser Lys Ala Ser Ser Cys Thr Pro Val Pro Val Thr Met Thr
  84              89              94              99
```

gca act cca cct ctt cca aag cct gtg aat act tct ctt tcc cct tcc	753
Ala Thr Pro Pro Leu Pro Lys Pro Val Asn Thr Ser Leu Ser Pro Ser	
100 105 110 115	
cca gca ttg gct ttg cca aac ctg gct aat gtg gat ctg gca aag atc	801
Pro Ala Leu Ala Leu Pro Asn Leu Ala Asn Val Asp Leu Ala Lys Ile	
116 121 126 131	
agt tcc atc ctt agc agt tta aca tca gtc atg aaa aat act ggg gtc	849
Ser Ser Ile Leu Ser Ser Leu Thr Ser Val Met Lys Asn Thr Gly Val	
132 137 142 147	
agt cct gca tca aga cct tct cca gga acg ccc acc agc ccc agc aac	897
Ser Pro Ala Ser Arg Pro Ser Pro Gly Thr Pro Thr Ser Pro Ser Asn	
148 153 158 163	
ctc acc agt ggc ctg aaa aca cct gca cct gcc acg aca aca tct cac	945
Leu Thr Ser Gly Leu Lys Thr Pro Ala Pro Ala Thr Thr Thr Ser His	
164 169 174 179	
aac cct ctg gca aat atc ctc tcc aag gtg gag atc acc cca gag agc	993
Asn Pro Leu Ala Asn Ile Leu Ser Lys Val Glu Ile Thr Pro Glu Ser	
180 185 190 195	
att ctg tct gca ctt tcc aaa acc cag aca cag tca gcc cct gca ctg	1041
Ile Leu Ser Ala Leu Ser Lys Thr Gln Thr Gln Ser Ala Pro Ala Leu	
196 201 206 211	
caa ggc ctg tca tct tta ctt cag agt gtt act ggg aac cca gtt cca	1089
Gln Gly Leu Ser Ser Leu Leu Gln Ser Val Thr Gly Asn Pro Val Pro	
212 217 222 227	
gcc agt gaa gct gcc tca cag agc act tca gcc tcc cct gcc aac acc	1137
Ala Ser Glu Ala Ala Ser Gln Ser Thr Ser Ala Ser Pro Ala Asn Thr	
228 233 238 243	
aca gtc tct acc ata aag gga aga aat ctg ccc tcc agt gcc caa cct	1185
Thr Val Ser Thr Ile Lys Gly Arg Asn Leu Pro Ser Ser Ala Gln Pro	
244 249 254 259	
ttt att ccc aaa agc ttc aac tat tct cct aac tca tca act tct gaa	1233
Phe Ile Pro Lys Ser Phe Asn Tyr Ser Pro Asn Ser Ser Thr Ser Glu	
260 265 270 275	
gtc tct tca act tca gcc agc aag gcc tca att ggg caa agc cca ggg	1281
Val Ser Ser Thr Ser Ala Ser Lys Ala Ser Ile Gly Gln Ser Pro Gly	
276 281 286 291	
ctc cca agc act act ttt aaa cta cct tcc aac tct ttg ggg ttt aca	1329
Leu Pro Ser Thr Thr Phe Lys Leu Pro Ser Asn Ser Leu Gly Phe Thr	
292 297 302 307	
gct acc cac aat act agc cct gct gcc cca cct act gaa gtt acc atc	1377
Ala Thr His Asn Thr Ser Pro Ala Ala Pro Pro Thr Glu Val Thr Ile	
308 313 318 323	

tgc caa tct tca gag gtc tcc aag cca aag ctg gag tca gag tcc acc	1425
Cys Gln Ser Ser Glu Val Ser Lys Pro Lys Leu Glu Ser Glu Ser Thr	
324 329 334 339	
tcc cca agc ctg gaa atg aag att cac aac ttc tta aaa ggt aat cct	1473
Ser Pro Ser Leu Glu Met Lys Ile His Asn Phe Leu Lys Gly Asn Pro	
340 345 350 355	
ggt ttc agt ggc tta aac tta aac atc cca atc ctg agc agt ttg ggg	1521
Gly Phe Ser Gly Leu Asn Leu Asn Ile Pro Ile Leu Ser Ser Leu Gly	
356 361 366 371	
tcc agc gcc cca tca gag agc cat ccc tca gac ttc cag cgt ggc cct	1569
Ser Ser Ala Pro Ser Glu Ser His Pro Ser Asp Phe Gln Arg Gly Pro	
372 377 382 387	
act agc acc tca atc gac aac att gat gga acc cct gta cgg gat gaa	1617
Thr Ser Thr Ser Ile Asp Asn Ile Asp Gly Thr Pro Val Arg Asp Glu	
388 393 398 403	
cgg agt ggg aca ccc acc cag gat gag atg atg gac aag ccc aca tcc	1665
Arg Ser Gly Thr Pro Thr Gln Asp Glu Met Met Asp Lys Pro Thr Ser	
404 409 414 419	
agc agt gta gat act atg tcc ctg ctt tct aag atc att agc cct ggt	1713
Ser Ser Val Asp Thr Met Ser Leu Leu Ser Lys Ile Ile Ser Pro Gly	
420 425 430 435	
tcc tca aca ccc agc agt aca aga tca cca ccc cct ggg aga gat gaa	1761
Ser Ser Thr Pro Ser Ser Thr Arg Ser Pro Pro Gly Arg Asp Glu	
436 441 446 451	
agc tac ccc cga gag ctc tcc aat tct gta tct aca tat cga ccc ttt	1809
Ser Tyr Pro Arg Glu Leu Ser Asn Ser Val Ser Thr Tyr Arg Pro Phe	
452 457 462 467	
ggt ctg ggc agt gaa tct ccc tat aag cag cct tct gat gga atg gag	1857
Gly Leu Gly Ser Glu Ser Pro Tyr Lys Gln Pro Ser Asp Gly Met Glu	
468 473 478 483	
aga cca tct tcc ctg atg gac tct tca cag gaa aag ttc tac cca gat	1905
Arg Pro Ser Ser Leu Met Asp Ser Ser Gln Glu Lys Phe Tyr Pro Asp	
484 489 494 499	
act tct ttc caa gaa gat gag gat tac cga gat ttt gag tat tca ggg	1953
Thr Ser Phe Gln Glu Asp Glu Asp Tyr Arg Asp Phe Glu Tyr Ser Gly	
500 505 510 515	
cct cca ccc tct gcc atg atg aac cta gag aag aaa cca gcc aaa tct	2001
Pro Pro Pro Ser Ala Met Met Asn Leu Glu Lys Lys Pro Ala Lys Ser	
516 521 526 531	
atc ctg aaa tca agc aag ctg tct gat acc acc gag tac cag cca att	2049
Ile Leu Lys Ser Ser Lys Leu Ser Asp Thr Thr Glu Tyr Gln Pro Ile	
532 537 542 547	
ctg tcc agt tat agc cac aga gcc caa gaa ttt ggg gta aag tct gcc	2097

Leu	Ser	Ser	Tyr	Ser	His	Arg	Ala	Gln	Glu	Phe	Gly	Val	Lys	Ser	Ala	
548					553					558					563	
ttc	oct	cca	tct	gta	agg	gcc	ctc	ctg	gac	tct	agt	gag	aac	tgt	gac	2145
Phe	Pro	Pro	Ser	Val	Arg	Ala	Leu	Leu	Asp	Ser	Ser	Glu	Asn	Cys	Asp	
564					569					574					579	
cgt	ctc	tca	tct	tcc	cct	ggg	cta	ttt	ggt	gcc	ttc	agc	gta	aga	ggg	2193
Arg	Leu	Ser	Ser	Ser	Pro	Gly	Leu	Phe	Gly	Ala	Phe	Ser	Val	Arg	Gly	
580					585					590					595	
aat	gaa	cct	ggg	tct	gac	cgg	tca	cca	tca	ccg	agt	aag	aat	gat	tca	2241
Asn	Glu	Pro	Gly	Ser	Asp	Arg	Ser	Pro	Ser	Pro	Ser	Lys	Asn	Asp	Ser	
596					601					606					611	
ttt	ttc	acc	cct	gac	tcc	aac	cac	aat	agc	ttg	tct	caa	tct	acc	act	2289
Phe	Phe	Thr	Pro	Asp	Ser	Asn	His	Asn	Ser	Leu	Ser	Gln	Ser	Thr	Thr	
612					617					622					627	
ggg	cat	ctc	agt	ttg	cca	cag	aag	cag	tac	cca	gac	tct	cct	cac	cca	2337
Gly	His	Leu	Ser	Leu	Pro	Gln	Lys	Gln	Tyr	Pro	Asp	Ser	Pro	His	Pro	
628					633					638					643	
gtc	cca	cat	cgt	tcc	ctt	ttc	tct	ccg	cag	aac	acc	ctt	gcc	gct	ccc	2385
Val	Pro	His	Arg	Ser	Leu	Phe	Ser	Pro	Gln	Asn	Thr	Leu	Ala	Ala	Pro	
644					649					654					659	
acg	ggt	cac	cca	ccc	acg	tca	ggc	gtg	gag	aaa	gtc	ctg	gcc	tcc	acc	2433
Thr	Gly	His	Pro	Pro	Thr	Ser	Gly	Val	Glu	Lys	Val	Leu	Ala	Ser	Thr	
660					665					670					675	
att	tcc	acc	acg	tcg	acg	att	gaa	ttt	aag	aat	atg	ctt	aaa	aac	gcc	2481
Ile	Ser	Thr	Thr	Ser	Thr	Ile	Glu	Phe	Lys	Asn	Met	Leu	Lys	Asn	Ala	
676					681					686					691	
tca	cgt	aag	ccc	tca	gat	gat	aag	cat	ttt	ggc	cag	gct	ccc	agc	aag	2529
Ser	Arg	Lys	Pro	Ser	Asp	Asp	Lys	His	Phe	Gly	Gln	Ala	Pro	Ser	Lys	
692					697					702					707	
ggc	act	cca	agt	gat	ggt	gtc	agt	ctc	tca	aac	ctc	acc	caa	ccc	agc	2577
Gly	Thr	Pro	Ser	Asp	Gly	Val	Ser	Leu	Ser	Asn	Leu	Thr	Gln	Pro	Ser	
708					713					718					723	
ttg	acc	gcc	act	gat	cag	cag	caa	caa	gaa	gag	cac	tac	cgc	ata	gaa	2625
Leu	Thr	Ala	Thr	Asp	Gln	Gln	Gln	Gln	Glu	Glu	His	Tyr	Arg	Ile	Glu	
724					729					734					739	
acc	cgc	gtc	tcc	tcc	tcc	tgc	tta	gac	ttg	cct	gat	agc	aca	gaa	gaa	2673
Thr	Arg	Val	Ser	Ser	Ser	Cys	Leu	Asp	Leu	Pro	Asp	Ser	Thr	Glu	Glu	
740					745					750					755	
aag	ggg	gcc	cct	ata	gaa	acc	ttg	ggt	tat	cac	agt	gca	tcc	aat	agg	2721
Lys	Gly	Ala	Pro	Ile	Glu	Thr	Leu	Gly	Tyr	His	Ser	Ala	Ser	Asn	Arg	
756					761					766					771	
agg	atg	tca	ggg	gag	ccg	atc	cag	acc	gta	gag	tcc	atc	cga	gtt	cct	2769
Arg	Met	Ser	Gly	Glu	Pro	Ile	Gln	Thr	Val	Glu	Ser	Ile	Arg	Val	Pro	

772	777	782	787	
ggg aag gga aat aga gga cat ggg cgt gag gct tca agg gtg ggt tgg				2817
Gly Lys Gly Asn Arg Gly His Gly Arg Glu Ala Ser Arg Val Gly Trp				
788	793	798	803	
ttt gat ctg agc aca tca ggt agc tct ttt gac aat ggc cct tca agt				2865
Phe Asp Leu Ser Thr Ser Gly Ser Ser Phe Asp Asn Gly Pro Ser Ser				
804	809	814	819	
gcc tct gag ttg gca tcc ctt ggg ggt ggg ggc agc gga ggc ctc act				2913
Ala Ser Glu Leu Ala Ser Leu Gly Gly Gly Gly Ser Gly Gly Leu Thr				
820	825	830	835	
ggc ttt aaa aca gca cca tac aag gaa cgg gca cct caa ttt cag gag				2961
Gly Phe Lys Thr Ala Pro Tyr Lys Glu Arg Ala Pro Gln Phe Gln Glu				
836	841	846	851	
agt gtc ggc cgc ttt cgt tcc aac agt ttc aac tca aca ttt gag cat				3009
Ser Val Gly Arg Phe Arg Ser Asn Ser Phe Asn Ser Thr Phe Glu His				
852	857	862	867	
cat ctt ccc cca tcc ccc ttg gaa cat ggg aca ccc ttc cag aga gag				3057
His Leu Pro Pro Ser Pro Leu Glu His Gly Thr Pro Phe Gln Arg Glu				
868	873	878	883	
cca gtg ggg cca tca tct gcc cca cct gtc cct cct aag gat cat ggt				3105
Pro Val Gly Pro Ser Ser Ala Pro Pro Val Pro Pro Lys Asp His Gly				
884	889	894	899	
ggt atc ttc tct cga gat gca ccc act cat cta ccc tct gtg gat ctt				3153
Gly Ile Phe Ser Arg Asp Ala Pro Thr His Leu Pro Ser Val Asp Leu				
900	905	910	915	
tcg aac ccc ttc aca aag gag gca gcc ctg gcc cat gct gcc cca ccc				3201
Ser Asn Pro Phe Thr Lys Glu Ala Ala Leu Ala His Ala Ala Pro Pro				
916	921	926	931	
cct cct cct gga gag cac agt gga att cct ttc cct acc cca cct cct				3249
Pro Pro Pro Gly Glu His Ser Gly Ile Pro Phe Pro Thr Pro Pro Pro				
932	937	942	947	
cct ccc cct cct ggg gaa cat agc agc agt ggt ggg agt ggt gtc ccc				3297
Pro Pro Pro Pro Gly Glu His Ser Ser Ser Gly Gly Ser Gly Val Pro				
948	953	958	963	
ttt tct act cca ccc cct cct cca ccc cct gtt gac cac tct gga gtt				3345
Phe Ser Thr Pro Pro Pro Pro Pro Pro Pro Val Asp His Ser Gly Val				
964	969	974	979	
gta ccc ttc cca gcc cca cca ctg gca gag cac gga gtg gca ggg gct				3393
Val Pro Phe Pro Ala Pro Pro Leu Ala Glu His Gly Val Ala Gly Ala				
980	985	990	995	
gtg gca gta ttt ccc aag gac cat agt tcc ctc ctt caa ggg acc ctg				3441
Val Ala Val Phe Pro Lys Asp His Ser Ser Leu Leu Gln Gly Thr Leu				
996	1001	1006	1011	

gct gag cat ttt ggg gta ctc cca gga ccc agg gac cac ggg ggc ccc	3489
Ala Glu His Phe Gly Val Leu Pro Gly Pro Arg Asp His Gly Gly Pro	
1012 1017 1022 1027	
acc caa cgg gac ctc aac ggc cct ggc ctt agc cgt gta cga gag agc	3537
Thr Gln Arg Asp Leu Asn Gly Pro Gly Leu Ser Arg Val Arg Glu Ser	
1028 1033 1038 1043	
ctc acc cta ccc tcc cat tct ctg gaa cac ctg ggc cca ccc cat gga	3585
Leu Thr Leu Pro Ser His Ser Leu Glu His Leu Gly Pro Pro His Gly	
1044 1049 1054 1059	
gga gga ggt ggg gga ggc agc aac agc agc agt ggc ccc ccc ttg ggt	3633
Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser Ser Gly Pro Pro Leu Gly	
1060 1065 1070 1075	
ccc tca cac aga gac acc atc agc cgg agt ggt ata atc tta cgg agt	3681
Pro Ser His Arg Asp Thr Ile Ser Arg Ser Gly Ile Ile Leu Arg Ser	
1076 1081 1086 1091	
ccc cgg cca gac ttt cgg cct agg gaa cct ttt ctc agc aga gac cca	3729
Pro Arg Pro Asp Phe Arg Pro Arg Glu Pro Phe Leu Ser Arg Asp Pro	
1092 1097 1102 1107	
ttt cac agt tta aag aga ccc agg cca cct ttt gct agg ggc cct ccg	3777
Phe His Ser Leu Lys Arg Pro Arg Pro Pro Phe Ala Arg Gly Pro Pro	
1108 1113 1118 1123	
ttc ttt gca cca aaa cgc cca ttc ttc cct ccc agg tac tga tggaaac	3826
Phe Phe Ala Pro Lys Arg Pro Phe Phe Pro Pro Arg Tyr *	
1124 1129 1134	
caagggaaag gcattttgaa cagtctagag aacattggaa gtaggagttt gggtttattgt	3886
tggttggtttt atttggttttc tctttctcga tttttttttt attataacaa agggcctctc	3946
ttccaaagta agaaatcaca tacgcttacg ttttactatt caattcaatc ctccctccca	4006
ttgcacttat ctaccttccc caagttgttt gtattaaaaa aaaaaaa	4053

<210> 157
 <211> 1091
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (112)..(927)

<400> 157	
gctataggag acccaagctg gctagcggtt aaacttaagc ttggtaccga gctcggatcc	60
actagtccag tgtggtggaa ttgcggtcgc gtagtgcggc gctgtttaaa g atg gcg	117

Met Ala
1

gcg gag gaa cct cag cag cag aag cag gag ccg ctg ggc agc gac tcc Ala Glu Glu Pro Gln Gln Gln Lys Gln Glu Pro Leu Gly Ser Asp Ser 3 8 13 18	165
gaa ggt gtt aac tgt ctg gcc tat gat gaa gcc atc atg gct cag cag Glu Gly Val Asn Cys Leu Ala Tyr Asp Glu Ala Ile Met Ala Gln Gln 19 24 29 34	213
gac cga att cag caa gag att gct gtg cag aac cct ctg gtg tca gag Asp Arg Ile Gln Gln Glu Ile Ala Val Gln Asn Pro Leu Val Ser Glu 35 40 45 50	261
cgg ctg gag ctc tcg gtc cta tac aag gag tat gct gaa gat gac aac Arg Leu Glu Leu Ser Val Leu Tyr Lys Glu Tyr Ala Glu Asp Asp Asn 51 56 61 66	309
atc tat caa cag aag atc aag gac ctc cac aaa aag tac tcg tac atc Ile Tyr Gln Gln Lys Ile Lys Asp Leu His Lys Lys Tyr Ser Tyr Ile 67 72 77 82	357
cgc aag acc agg cct gac gcc aac tgt ttc tat cgg gct ttc gga ttc Arg Lys Thr Arg Pro Asp Gly Asn Cys Phe Tyr Arg Ala Phe Gly Phe 83 88 93 98	405
tcc cac ttg gag gca ctg ctg gat gac agc aag gag ttg cag cgg ttc Ser His Leu Glu Ala Leu Leu Asp Asp Ser Lys Glu Leu Gln Arg Phe 99 104 109 114	453
aag gct gtg tct gcc aag agc aag gaa gac ctg gtg tcc cag gcc ttc Lys Ala Val Ser Ala Lys Ser Lys Glu Asp Leu Val Ser Gln Gly Phe 115 120 125 130	501
act gaa ttc aca att gag gat ttc cac aac acg ttc atg gac ctg att Thr Glu Phe Thr Ile Glu Asp Phe His Asn Thr Phe Met Asp Leu Ile 131 136 141 146	549
gag cag gtg gag aag cag acc tct gtc gcc gac ctg ctg gcc tcc ttc Glu Gln Val Glu Lys Gln Thr Ser Val Ala Asp Leu Leu Ala Ser Phe 147 152 157 162	597
aat gac cag agc acc tcc gac tac ctt gtg gtc tac ctg cgg ctg ctc Asn Asp Gln Ser Thr Ser Asp Tyr Leu Val Val Tyr Leu Arg Leu Leu 163 168 173 178	645
acc tcg ggc tac ctg cag cgc gag agc aag ttc ttc gag cac ttc atc Thr Ser Gly Tyr Leu Gln Arg Glu Ser Lys Phe Phe Glu His Phe Ile 179 184 189 194	693
gag ggt gga cgg act gtc aag gag ttc tgc cag cag gag gtg gag ccc Glu Gly Gly Arg Thr Val Lys Glu Phe Cys Gln Gln Glu Val Glu Pro 195 200 205 210	741
atg tgc aag gag agc gac cac atc cac atc att gcg ctg gcc cag gcc Met Cys Lys Glu Ser Asp His Ile His Ile Ile Ala Leu Ala Gln Ala	789

211	216	221	226	
ctc agc gtg tcc atc	cag gtg gag tac atg	gac cgc ggc gag ggc ggc		837
Leu Ser Val Ser Ile	Gln Val Glu Tyr Met	Asp Arg Gly Glu Gly Gly		
227	232	237	242	
acc acc aat ccg cac	atc ttc cct gag ggc	tcc gag ccc aag gtc tac		885
Thr Thr Asn Pro His	Ile Phe Pro Glu Gly	Ser Glu Pro Lys Val Tyr		
243	248	253	258	
ctt ctc tac cgg cct	gga cac tac gat atc	ctc tac aaa tag ggctggc		934
Leu Leu Tyr Arg Pro	Gly His Tyr Asp Ile	Leu Tyr Lys *		
259	264	269		
tocagccgc tgctgccctg ctgccccct ctgccaggcg ctagacatgt acagaggttt				994
ttctgtggtt gtaaattggtc ctatttcacc cccttcttcc tgtcacatga cccccccccc				1054
atgtttttatt aaagggggtg ctggtggtga aaaaaaa				1091
<p><210> 158</p> <p><211> 2418</p> <p><212> DNA</p> <p><213> Homo sapiens</p> <p><220></p> <p><221> CDS</p> <p><222> (467)..(2026)</p> <p><400> 158</p>				
gcgcacgtaa gcttggatcc tctagagcgg ccgcaatata tttgtggctt gttttcacta				60
cttttaagtt actatcaaat ctatacatct atctcgtttg catgctttta aattttattt				120
ttaaaaacat ttagtggtga tatttatgaa aggaaatgat tacttttttt cttgactctt				180
gtagaggaac ttaaattggtt tgaaattgtg actcagttta ctctgtatcc attcattccc				240
agaaacaagc cgcattttctc cttggggaga ctgataattt aaaagggttg ttgtgtcaga				300
aacattccca gcttcatcac caaccctttc cttccacctc tgcccaactgg agaccactta				360
catccogaag cggacgcggc agctgaagtc aggaaaccat gcatcacatt agcaggagcc				420
aactgcagac tttaaactcc gttcaacatg tggatgcggc agagaa atg acc tgt				475
				Met Thr Cys
				1
cca gac aag ccg ggg cag ctc ata aac tgg ttc atc tgc tcc ctg tgc				523
Pro Asp Lys Pro Gly Gln Leu Ile Asn Trp Phe Ile Cys Ser Leu Cys				
4	9	14	19	
gtc ccg ccg gtg cgt aag ctc tgg agc agc cgg cgt cca agg acc ccg				571
Val Pro Arg Val Arg Lys Leu Trp Ser Ser Arg Arg Pro Arg Thr Arg				

20	25	30	35	
aga aac ctt ctg ctg ggc act gcg tgt gcc atc tac ttg ggc ttc ctg				619
Arg Asn Leu Leu Leu Gly Thr Ala Cys Ala Ile Tyr Leu Gly Phe Leu				
36	41	46	51	
gtg agc cag gtg ggg agg gcc tct ctc cag cat gga cag gcg gct gag				667
Val Ser Gln Val Gly Arg Ala Ser Leu Gln His Gly Gln Ala Ala Glu				
52	57	62	67	
aag ggg cca cat cgc agc cgc gac acc gcc gag cca tcc ttc cct gag				715
Lys Gly Pro His Arg Ser Arg Asp Thr Ala Glu Pro Ser Phe Pro Glu				
68	73	78	83	
ata ccc ctg gat ggt acc ctg gcc cct cca gag tcc cag ggc aat ggg				763
Ile Pro Leu Asp Gly Thr Leu Ala Pro Pro Glu Ser Gln Gly Asn Gly				
84	89	94	99	
tcc act ctg cag ccc aat gtg gtg tac att acc cta cgc tcc aag cgc				811
Ser Thr Leu Gln Pro Asn Val Val Tyr Ile Thr Leu Arg Ser Lys Arg				
100	105	110	115	
agc aag ccg gcc aat atc cgt ggc acc gtg aag ccc aag cgc agg aaa				859
Ser Lys Pro Ala Asn Ile Arg Gly Thr Val Lys Pro Lys Arg Arg Lys				
116	121	126	131	
aag cat gca gtg gca tgc gct gcc cca ggg cag gag gct ttg gtc gga				907
Lys His Ala Val Ala Ser Ala Ala Pro Gly Gln Glu Ala Leu Val Gly				
132	137	142	147	
cca tcc ctt cag ccg cag gaa gcg gca agg gaa gct gat gct gta gca				955
Pro Ser Leu Gln Pro Gln Glu Ala Ala Arg Glu Ala Asp Ala Val Ala				
148	153	158	163	
cct ggg tac gct cag gga gca aac ctg gtt aag att gga gag cga ccc				1003
Pro Gly Tyr Ala Gln Gly Ala Asn Leu Val Lys Ile Gly Glu Arg Pro				
164	169	174	179	
tgg agg ttg gtg cgg ggt ccg gga gtg cga gcc ggg ggc cca gac ttc				1051
Trp Arg Leu Val Arg Gly Pro Gly Val Arg Ala Gly Gly Pro Asp Phe				
180	185	190	195	
ctg cag ccc agc tcc agg gag agc aac att agg atc tac agc gag agc				1099
Leu Gln Pro Ser Ser Arg Glu Ser Asn Ile Arg Ile Tyr Ser Glu Ser				
196	201	206	211	
gcc ccc tcc tgg ctg agc aaa gat gac atc cga aga atg cga ctc ttg				1147
Ala Pro Ser Trp Leu Ser Lys Asp Asp Ile Arg Arg Met Arg Leu Leu				
212	217	222	227	
gcg gac agc gca gtg gca ggg ctc cgg cct gtg tcc tct agg agc gga				1195
Ala Asp Ser Ala Val Ala Gly Leu Arg Pro Val Ser Ser Arg Ser Gly				
228	233	238	243	
gcc cgt ttg ctg gtg ctg gag ggg ggc gca cct ggc gct gtg ctc cgc				1243
Ala Arg Leu Leu Val Leu Glu Gly Gly Ala Pro Gly Ala Val Leu Arg				
244	249	254	259	

tgt ggc cct agc ccc tgt ggg ctt ctc aag cag ccc ttg gac atg agt	1291
Cys Gly Pro Ser Pro Cys Gly Leu Leu Lys Gln Pro Leu Asp Met Ser	
260 265 270 275	
gag gtg ttt gcc ttc cac cta gac agg atc ctg ggg ctc aac agg acc	1339
Glu Val Phe Ala Phe His Leu Asp Arg Ile Leu Gly Leu Asn Arg Thr	
276 281 286 291	
ctg ccg tct gtg agc agg aaa gca gag ttc atc caa gat ggc cgc cca	1387
Leu Pro Ser Val Ser Arg Lys Ala Glu Phe Ile Gln Asp Gly Arg Pro	
292 297 302 307	
tgc ccc atc att ctt tgg gat gca tct tta tct tca gca agt aat gac	1435
Cys Pro Ile Ile Leu Trp Asp Ala Ser Leu Ser Ser Ala Ser Asn Asp	
308 313 318 323	
acc cat tct tct gtt aag ctc acc tgg gga act tat cag cag ttg ctg	1483
Thr His Ser Ser Val Lys Leu Thr Trp Gly Thr Tyr Gln Gln Leu Leu	
324 329 334 339	
aaa cag aaa tgc tgg cag aat ggc cga gta ccc aag cct gaa tca ggt	1531
Lys Gln Lys Cys Trp Gln Asn Gly Arg Val Pro Lys Pro Glu Ser Gly	
340 345 350 355	
tgt act gaa ata cat cat cat gag tgg tcc aag atg gca ctc ttt gat	1579
Cys Thr Glu Ile His His His Glu Trp Ser Lys Met Ala Leu Phe Asp	
356 361 366 371	
ttt ttg tta cag att tat aat cgc tta gat aca aat tgc tgt gga ttc	1627
Phe Leu Leu Gln Ile Tyr Asn Arg Leu Asp Thr Asn Cys Cys Gly Phe	
372 377 382 387	
aga cct cgc aag gaa gat gcc tgt gta cag aat gga ttg agg cca aaa	1675
Arg Pro Arg Lys Glu Asp Ala Cys Val Gln Asn Gly Leu Arg Pro Lys	
388 393 398 403	
tgt gat gac caa ggt tct gcg gct cta gca cac att atc cag cga aag	1723
Cys Asp Asp Gln Gly Ser Ala Ala Leu Ala His Ile Ile Gln Arg Lys	
404 409 414 419	
cat gac cca agg cat ttg gtt ttt ata gac aac aag ggt ttc ttt gac	1771
His Asp Pro Arg His Leu Val Phe Ile Asp Asn Lys Gly Phe Phe Asp	
420 425 430 435	
agg agt gaa gat aac tta aac ttc aaa ttg tta gaa ggc atc aaa gag	1819
Arg Ser Glu Asp Asn Leu Asn Phe Lys Leu Leu Glu Gly Ile Lys Glu	
436 441 446 451	
ttt oca gct tct gca gtt tct gtt ttg aag agc cag cac tta cgg cag	1867
Phe Pro Ala Ser Ala Val Ser Val Leu Lys Ser Gln His Leu Arg Gln	
452 457 462 467	
aaa ctt ctt cag tct ctg ttt ctt gat aaa gtg tat tgg gaa agt caa	1915
Lys Leu Leu Gln Ser Leu Phe Leu Asp Lys Val Tyr Trp Glu Ser Gln	
468 473 478 483	

gga ggt aga caa gga att gaa aag ctt atc gat gta ata gaa cac aga	1963
Gly Gly Arg Gln Gly Ile Glu Lys Leu Ile Asp Val Ile Glu His Arg	
484 489 494 499	
gcc aaa att ctt atc acc tat atc aat gca cac ggg gtc aaa gta tta	2011
Ala Lys Ile Leu Ile Thr Tyr Ile Asn Ala His Gly Val Lys Val Leu	
500 505 510 515	
cct atg aat gaa tga caaaagaatc ttctggctag ggtgtagat atatttatgc	2066
Pro Met Asn Glu *	
516	
atTTTTggtt ttgtTTTTaa atcaagcaca tcaacctcaa gccggttttag caatgaggca	2126
gtgtagatga atacgtaaaa taaatgactt taaccaagta gctataatgg gacttagcac	2186
tgtatgcata cttaaaaagg ttttgaaaaa caaactactt gagaaatatt tgtttatatt	2246
tttctctaac atcatgctat gtgtcagtct gaacatctga caacagaaat ttcagttatt	2306
attctagcta agttttgaaa acatttgtca tgctgtttta tagaaaactg caaaccagag	2366
atactgactc cattaataaa ccatattttg tgccgttttg aaaaaaaaaa aa	2418

<210> 159
 <211> 1711
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (664)..(1551)

<400> 159	
ctccggaatt cccgggtcga cccacgcgtc cggcgagggc ctcggccatc caagggctctc	60
ccaggtgacc ttccctccac cccaggaagc tatgacagag gccgggaagc tgccctacc	120
gctaccccca cggttgact ggtttgtgca caccagatg ggccagctgg cccaagacgg	180
ggtccccgag tggttccatg gtgcaatctc aagagaggat gctgagaact tgctggagtc	240
acagccactg ggatcctttc tcatcagggt cagtcacagc catgtgggct acacactctc	300
ctacaagtaa ggccctgggc gggatccagg gcaggggcag gtgggctctt gggtttccct	360
ggagggggca aggggtgctt catgtcatag cttctcagaa agcagcagta actgaggctg	420
tggatctgag aacgggagct gctagccaag caatgagtga agcttttgtc cgtagtggca	480
tgttttatct gaggccagcc tttgtactcc tgtgttataa atgggggaaa ctgaggcaca	540
gcgaggttag taacctgctg ggtgttgcat ggccagttag tgaagaagcc tgcattggaa	600

cctggggtag tctggctgta gcagtgacgc tgccggccca agggctgggg acttggggca	660
ggg atg agg ggg agt agg atg tcc cag ccc ccg cag tgt ctc cgc aga	708
Met Arg Gly Ser Arg Met Ser Gln Pro Pro Gln Cys Leu Arg Arg	
1 5 10	
gcc caa agc agc tgc tgc cat ttc atg gtg aag ctc ttg gat gat ggg	756
Ala Gln Ser Ser Cys Cys His Phe Met Val Lys Leu Leu Asp Asp Gly	
16 21 26 31	
act ttc atg atc ccc ggg gag aag gtg gcc cac acc tcg ctg gac gcc	804
Thr Phe Met Ile Pro Gly Glu Lys Val Ala His Thr Ser Leu Asp Ala	
32 37 42 47	
ctg gtc acc ttc cac cag cag aag cca att gag ccg cgc agg gag ctg	852
Leu Val Thr Phe His Gln Gln Lys Pro Ile Glu Pro Arg Arg Glu Leu	
48 53 58 63	
ctg aca cag ccc tgc agg cag aag gat ccc gca aac gtg gat tac gag	900
Leu Thr Gln Pro Cys Arg Gln Lys Asp Pro Ala Asn Val Asp Tyr Glu	
64 69 74 79	
gat ctc ttc ctc tac tcc aac gca gtg gcc gag gaa gct gcc tgc ccg	948
Asp Leu Phe Leu Tyr Ser Asn Ala Val Ala Glu Glu Ala Ala Cys Pro	
80 85 90 95	
gtg tct gcc cct gag gag gcc tcc cca aag cca gtc ctg tgt cac caa	996
Val Ser Ala Pro Glu Glu Ala Ser Pro Lys Pro Val Leu Cys His Gln	
96 101 106 111	
tca aag gaa agg aag ccg tca gca gag atg aac aga ata acc acc aag	1044
Ser Lys Glu Arg Lys Pro Ser Ala Glu Met Asn Arg Ile Thr Thr Lys	
112 117 122 127	
gaa gcc act tcc tcc tgc ccc cca aaa tcc cct ctt gga gag acc cgc	1092
Glu Ala Thr Ser Ser Cys Pro Pro Lys Ser Pro Leu Gly Glu Thr Arg	
128 133 138 143	
cag aaa ctc tgg agg agc ctc aaa atg ctc ccc gag aga ggc cag agg	1140
Gln Lys Leu Trp Arg Ser Leu Lys Met Leu Pro Glu Arg Gly Gln Arg	
144 149 154 159	
gtc cgg cag cag cta aaa agc cac ctc gcc act gtg aac ttg tcg tca	1188
Val Arg Gln Gln Leu Lys Ser His Leu Ala Thr Val Asn Leu Ser Ser	
160 165 170 175	
ctc ttg gat gtc cgg aga tcc acg gtg atc tca ggc cct ggg acc gga	1236
Leu Leu Asp Val Arg Arg Ser Thr Val Ile Ser Gly Pro Gly Thr Gly	
176 181 186 191	
aaa ggc agc caa gat cac tca ggg gat ccc acc tcg ggg gac aga ggc	1284
Lys Gly Ser Gln Asp His Ser Gly Asp Pro Thr Ser Gly Asp Arg Gly	
192 197 202 207	
tac acg gat ccc tgt gtg gcc aca tct ctc aaa agc ccc tca cag ccc	1332
Tyr Thr Asp Pro Cys Val Ala Thr Ser Leu Lys Ser Pro Ser Gln Pro	
208 213 218 223	

cag gca cca aaa gac aga aag gtc ccc acc agg aag gcc gag agg tcg	1380
Gln Ala Pro Lys Asp Arg Lys Val Pro Thr Arg Lys Ala Glu Arg Ser	
224 229 234 239	
gtc agc tgc att gag gtg acc cca ggg gac agg agt tgg cac caa atg	1428
Val Ser Cys Ile Glu Val Thr Pro Gly Asp Arg Ser Trp His Gln Met	
240 245 250 255	
gta gtg aga gcc cta tcc tcc cag gag tcc aag cca gag cac cag ggc	1476
Val Val Arg Ala Leu Ser Ser Gln Glu Ser Lys Pro Glu His Gln Gly	
256 261 266 271	
ttg gca gag cct gag aac gac cag ctc ccg gag gag tac caa caa ccg	1524
Leu Ala Glu Pro Glu Asn Asp Gln Leu Pro Glu Glu Tyr Gln Gln Pro	
272 277 282 287	
cca ccc ttt gcc cct ggg tac tgc tag agaac aggtccaccc tggctctggg	1576
Pro Pro Phe Ala Pro Gly Tyr Cys *	
288 293	
actcgctgcc aggggctgcc acactcctga atgccttaac atttcttcca tggccccaca	1636
ccatggcatc cgggggtctt cggaacccg ggaaatggaa taaagatgtt tttggggctct	1696
gaaaaaaaaa aaaaa	1711

<210> 160
 <211> 2487
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (235)..(2469)

<400> 160	
gcacgagtaa ggacagaaaa gtgaaatgca gtatggtgaa gaggataccc tgaatatgta	60
tgaagacatg ctgttgtgag acggagttgt gaaacagagg ccacagaagc tgttgtgaag	120
gcagagcagc atctgctgaa gagacagaaa ccagccccag aggtgtcaca ggaaggcacc	180
agcaaggaca ttggtctttg atttgattca gcagtcctgt caagtataaa tgtg atg	237
	Met
	1
gct gtg ctg cct ggc cct ctg cag ctg ctg gga gtg ctg ctt acc att	285
Ala Val Leu Pro Gly Pro Leu Gln Leu Leu Gly Val Leu Leu Thr Ile	
2 7 12 17	
toc ctg agt tcc atc agg ctc att cag gct ggt gcc tac tat ggg atc	333
Ser Leu Ser Ser Ile Arg Leu Ile Gln Ala Gly Ala Tyr Tyr Gly Ile	
18 23 28 33	

aag ccg ctg cca cct caa att cct cct cag atg cca cca caa att cca	381
Lys Pro Leu Pro Pro Gln Ile Pro Pro Gln Met Pro Pro Gln Ile Pro	
34 39 44 49	
caa tac cag ccc ctg ggt cag caa gta cct cac atg cct ttg gcc aaa	429
Gln Tyr Gln Pro Leu Gly Gln Gln Val Pro His Met Pro Leu Ala Lys	
50 55 60 65	
gat ggc ctc gcc atg ggc aag gag atg ccc cac ttg cag tat ggc aaa	477
Asp Gly Leu Ala Met Gly Lys Glu Met Pro His Leu Gln Tyr Gly Lys	
66 71 76 81	
gag tat cca cac cta ccc caa tat atg aag gaa att caa ccg gcg cca	525
Glu Tyr Pro His Leu Pro Gln Tyr Met Lys Glu Ile Gln Pro Ala Pro	
82 87 92 97	
aga atg ggc aag gaa gcc gtt ccc aag aaa ggc aaa gaa ata cca tta	573
Arg Met Gly Lys Glu Ala Val Pro Lys Lys Gly Lys Glu Ile Pro Leu	
98 103 108 113	
gcc agt tta cga ggg gaa caa ggt ccc cgt gga gag cct ggc cca aga	621
Ala Ser Leu Arg Gly Glu Gln Gly Pro Arg Gly Glu Pro Gly Pro Arg	
114 119 124 129	
gga cca cct ggg ccc cct ggt tta cca ggt cat ggg ata cct gga att	669
Gly Pro Pro Gly Pro Pro Gly Leu Pro Gly His Gly Ile Pro Gly Ile	
130 135 140 145	
aaa gga aaa cca ggg cca cag gga tat cca gga gtt gga aag cca ggt	717
Lys Gly Lys Pro Gly Pro Gln Gly Tyr Pro Gly Val Gly Lys Pro Gly	
146 151 156 161	
atg cct gga atg cca ggg aag cca gga gcc atg ggc atg cct ggg gca	765
Met Pro Gly Met Pro Gly Lys Pro Gly Ala Met Gly Met Pro Gly Ala	
162 167 172 177	
aaa gga gaa att gga cag aaa ggg gaa att ggg cct atg ggg atc cca	813
Lys Gly Glu Ile Gly Gln Lys Gly Glu Ile Gly Pro Met Gly Ile Pro	
178 183 188 193	
gga cca caa gga cct cca ggg cct cat gga ctt cct ggc att ggg aag	861
Gly Pro Gln Gly Pro Pro Gly Pro His Gly Leu Pro Gly Ile Gly Lys	
194 199 204 209	
cca ggt ggg cca ggg tta cca ggg caa cca gga cca aag ggt gat cga	909
Pro Gly Gly Pro Gly Leu Pro Gly Gln Pro Gly Pro Lys Gly Asp Arg	
210 215 220 225	
gga ccc aaa gga cta cca gga cct caa ggc ctt cgg ggt cct aaa gga	957
Gly Pro Lys Gly Leu Pro Gly Pro Gln Gly Leu Arg Gly Pro Lys Gly	
226 231 236 241	
gac aag ggc ttc ggg atg cca ggt ggc cca ggt gta aag ggg cct cca	1005
Asp Lys Gly Phe Gly Met Pro Gly Ala Pro Gly Val Lys Gly Pro Pro	
242 247 252 257	

ggg atg cac ggc cct ccc ggc cct gtt gga ctg cca gga gtg ggc aaa Gly Met His Gly Pro Pro Gly Pro Val Gly Leu Pro Gly Val Gly Lys 258 263 268 273	1053
cca gga gtg aca ggc ttc cct ggg ccc cag ggc ccc ctg gga aag cca Pro Gly Val Thr Gly Phe Pro Gly Pro Gln Gly Pro Leu Gly Lys Pro 274 279 284 289	1101
ggg gct cca gga gaa cct ggg cca caa ggc cct att ggg gta ccg ggg Gly Ala Pro Gly Glu Pro Gly Pro Gln Gly Pro Ile Gly Val Pro Gly 290 295 300 305	1149
gtt caa gga cct cct ggg ata ccc gga att gga aag cca ggc cag gat Val Gln Gly Pro Pro Gly Ile Pro Gly Ile Gly Lys Pro Gly Gln Asp 306 311 316 321	1197
ggg atc cca ggc cag cca gga ttt cca ggt ggc aaa ggg gag caa gga Gly Ile Pro Gly Gln Pro Gly Phe Pro Gly Gly Lys Gly Glu Gln Gly 322 327 332 337	1245
ctg cca ggg cta cca gga ccc cca ggc ctt cca ggg att ggg aaa cca Leu Pro Gly Leu Pro Gly Pro Pro Gly Leu Pro Gly Ile Gly Lys Pro 338 343 348 353	1293
ggc ttc cca gga ccc aaa ggt gac cgg ggc atg gga ggt gtt cct ggg Gly Phe Pro Gly Pro Lys Gly Asp Arg Gly Met Gly Gly Val Pro Gly 354 359 364 369	1341
gct ctt gga cca aga ggg gag aaa gga cca ata ggt gcc cca gga ata Ala Leu Gly Pro Arg Gly Glu Lys Gly Pro Ile Gly Ala Pro Gly Ile 370 375 380 385	1389
ggg ggt cct cca gga gag cca ggc ctg cct gga atc cca ggt cct atg Gly Gly Pro Pro Gly Glu Pro Gly Leu Pro Gly Ile Pro Gly Pro Met 386 391 396 401	1437
ggc cct cca ggt gct att ggt ttt cct gga ccc aaa gga gaa ggt ggg Gly Pro Pro Gly Ala Ile Gly Phe Pro Gly Pro Lys Gly Glu Gly Gly 402 407 412 417	1485
att gta ggg cca cag ggg cca cca ggt ccc aag ggt gag cca ggg ctt Ile Val Gly Pro Gln Gly Pro Pro Gly Pro Lys Gly Glu Pro Gly Leu 418 423 428 433	1533
caa ggc ttc cca gga aag cca ggt ttc ctt ggt gaa gta ggg cct cct Gln Gly Phe Pro Gly Lys Pro Gly Phe Leu Gly Glu Val Gly Pro Pro 434 439 444 449	1581
ggc atg agg ggt ttc cca ggt ccc ata ggc ccc aag ggg gaa cat ggg Gly Met Arg Gly Phe Pro Gly Pro Ile Gly Pro Lys Gly Glu His Gly 450 455 460 465	1629
caa aaa ggt gta cca gga ctc cct ggt gtt cca ggg ctt ctc gga cct Gln Lys Gly Val Pro Gly Leu Pro Gly Val Pro Gly Leu Leu Gly Pro 466 471 476 481	1677
aag gga gaa cca gga atc cca ggg gat cag ggt tta cag ggc ccc cca	1725

Lys Gly Glu Pro Gly Ile Pro Gly Asp Gln Gly Leu Gln Gly Pro Pro	
482 487 492 497	
ggt atc cca ggg att ggg ggc cct agt ggc ccc att gga cca cct ggg	1773
Gly Ile Pro Gly Ile Gly Gly Pro Ser Gly Pro Ile Gly Pro Pro Gly	
498 503 508 513	
att cca ggc ccc aaa ggg gag cct ggc ctc cca ggg ccc cct ggg ttc	1821
Ile Pro Gly Pro Lys Gly Glu Pro Gly Leu Pro Gly Pro Pro Gly Phe	
514 519 524 529	
cct ggt ata ggg aaa ccc gga gtg gca gga ctt cat ggc ccc cca ggg	1869
Pro Gly Ile Gly Lys Pro Gly Val Ala Gly Leu His Gly Pro Pro Gly	
530 535 540 545	
aag cct ggt gcc ctt ggt cct caa ggc cag cct ggc ctt cca gga ccc	1917
Lys Pro Gly Ala Leu Gly Pro Gln Gly Gln Pro Gly Leu Pro Gly Pro	
546 551 556 561	
cca ggc cct cca gga cct cca gga ccc cca gct gtg atg ccc cct aca	1965
Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Ala Val Met Pro Pro Thr	
562 567 572 577	
cca cca ccc cag gga gag tat ctg cca gat atg ggg ctg gga att gat	2013
Pro Pro Pro Gln Gly Glu Tyr Leu Pro Asp Met Gly Leu Gly Ile Asp	
578 583 588 593	
ggc gtg aaa ccc ccc cat gcc tac ggg gct aag aaa ggc aag aat gga	2061
Gly Val Lys Pro Pro His Ala Tyr Gly Ala Lys Lys Gly Lys Asn Gly	
594 599 604 609	
ggg cca gcc tat gag atg cct gca ttt acc gcc gag cta acc gca cct	2109
Gly Pro Ala Tyr Glu Met Pro Ala Phe Thr Ala Glu Leu Thr Ala Pro	
610 615 620 625	
ttc cca ccg gtg ggg gcc cca gtg aag ttt aac aaa ctg ctg tat aac	2157
Phe Pro Pro Val Gly Ala Pro Val Lys Phe Asn Lys Leu Leu Tyr Asn	
626 631 636 641	
ggc aga cag aac tac aac ccg cag aca ggc atc ttc acc tgt gag gtc	2205
Gly Arg Gln Asn Tyr Asn Pro Gln Thr Gly Ile Phe Thr Cys Glu Val	
642 647 652 657	
cct ggt gtc tac tac ttt gca tac cac gtt cac tgc aag ggg ggc aac	2253
Pro Gly Val Tyr Tyr Phe Ala Tyr His Val His Cys Lys Gly Gly Asn	
658 663 668 673	
gtg tgg gtt gct cta ttc aag aac aac gag ccc gtg atg tac acg tac	2301
Val Trp Val Ala Leu Phe Lys Asn Asn Glu Pro Val Met Tyr Thr Tyr	
674 679 684 689	
gac gag tac aaa aag ggc ttc ctg gac cag gca tct ggg agt gca gtg	2349
Asp Glu Tyr Lys Lys Gly Phe Leu Asp Gln Ala Ser Gly Ser Ala Val	
690 695 700 705	
ctg ctg ctc agg ccc gga gac cgg gtg ttc ctc cag atg ccc tca gaa	2397
Leu Leu Leu Arg Pro Gly Asp Arg Val Phe Leu Gln Met Pro Ser Glu	

[illegible]

```
<220>
<221> CDS
<222> (258) .. (1697)
```

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

Tyr	Arg	Ala	Asn	Tyr	Asn	Phe	Arg	Gly	Met	Tyr	Asn	Gln	Arg	Tyr	His	
92					97					102					107	
tgc	cca	gtg	cct	aag	atc	ttt	tat	gtt	cag	ctc	act	gta	gga	aat	aat	626
Cys	Pro	Val	Pro	Lys	Ile	Phe	Tyr	Val	Gln	Leu	Thr	Val	Gly	Asn	Asn	
108					113					118					123	
gaa	ttt	ttt	ggg	gaa	gga	aag	act	cga	caa	gct	gct	aga	cac	aat	gct	674
Glu	Phe	Phe	Gly	Glu	Gly	Lys	Thr	Arg	Gln	Ala	Ala	Arg	His	Asn	Ala	
124					129					134					139	
gca	atg	aaa	gcc	ctc	caa	gca	ctg	cag	aat	gaa	cct	att	cca	gaa	aga	722
Ala	Met	Lys	Ala	Leu	Gln	Ala	Leu	Gln	Asn	Glu	Pro	Ile	Pro	Glu	Arg	
140					145					150					155	
tct	cct	cag	aat	ggg	gaa	tca	gga	aag	gat	atg	gat	gat	gac	aaa	gat	770
Ser	Pro	Gln	Asn	Gly	Glu	Ser	Gly	Lys	Asp	Met	Asp	Asp	Asp	Lys	Asp	
156					161					166					171	
gca	aat	aag	tct	gag	atc	agc	tta	gtg	ttt	gaa	att	gct	ctg	aag	cga	818
Ala	Asn	Lys	Ser	Glu	Ile	Ser	Leu	Val	Phe	Glu	Ile	Ala	Leu	Lys	Arg	
172					177					182					187	
aat	atg	cct	gtc	agt	ttt	gag	gtt	att	aaa	gaa	agt	gga	cca	cca	cat	866
Asn	Met	Pro	Val	Ser	Phe	Glu	Val	Ile	Lys	Glu	Ser	Gly	Pro	Pro	His	
188					193					198					203	
atg	aaa	agc	ttt	gtt	act	cga	gtg	tca	gta	gga	gag	ttc	tct	gca	gaa	914
Met	Lys	Ser	Phe	Val	Thr	Arg	Val	Ser	Val	Gly	Glu	Phe	Ser	Ala	Glu	
204					209					214					219	
gga	gaa	gga	aat	agc	aaa	aaa	ctc	tcc	aag	aag	cgc	gct	gcg	acc	acc	962
Gly	Glu	Gly	Asn	Ser	Lys	Lys	Leu	Ser	Lys	Lys	Arg	Ala	Ala	Thr	Thr	
220					225					230					235	
gtc	tta	cag	gag	ctt	aaa	aaa	ctt	cca	cct	ctt	cct	gtg	gtg	gaa	aag	1010
Val	Leu	Gln	Glu	Leu	Lys	Lys	Leu	Pro	Pro	Leu	Pro	Val	Val	Glu	Lys	
236					241					246					251	
cca	aaa	cta	ttt	ttt	aaa	aaa	cgc	cct	aaa	aca	ata	gta	aag	gcc	gga	1058
Pro	Lys	Leu	Phe	Phe	Lys	Lys	Arg	Pro	Lys	Thr	Ile	Val	Lys	Ala	Gly	
252					257					262					267	
cca	gaa	tat	ggc	caa	ggg	atg	aac	cct	att	agc	cgc	ctg	gcg	caa	att	1106
Pro	Glu	Tyr	Gly	Gln	Gly	Met	Asn	Pro	Ile	Ser	Arg	Leu	Ala	Gln	Ile	
268					273					278					283	
caa	cag	gcc	aaa	aag	gaa	aag	gag	ccg	gat	tat	gtt	ttg	ctt	tca	gaa	1154
Gln	Gln	Ala	Lys	Lys	Glu	Lys	Glu	Pro	Asp	Tyr	Val	Leu	Leu	Ser	Glu	
284					289					294					299	
aga	gga	atg	cct	cga	cgt	cga	gaa	ttt	gtg	atg	cag	gtg	aag	gta	ggc	1202
Arg	Gly	Met	Pro	Arg	Arg	Arg	Glu	Phe	Val	Met	Gln	Val	Lys	Val	Gly	
300					305					310					315	
aat	gaa	gtt	gct	aca	gga	aca	gga	cct	aat	aaa	aag	ata	gcc	aaa	aaa	1250
Asn	Glu	Val	Ala	Thr	Gly	Thr	Gly	Pro	Asn	Lys	Lys	Ile	Ala	Lys	Lys	

316	321	326	331	
aat gct gca gaa gca atg ctg tta caa ctt ggt tat aaa gca tcc act				1298
Asn Ala Ala Glu Ala Met Leu Leu Gln Leu Gly Tyr Lys Ala Ser Thr				
332	337	342	347	
aat ctt cag gat caa ctt gag aag aca ggg gaa aac aaa gga tgg agt				1346
Asn Leu Gln Asp Gln Leu Glu Lys Thr Gly Glu Asn Lys Gly Trp Ser				
348	353	358	363	
ggg cca aag cct ggg ttt cct gaa cca aca aat aat act cca aaa gga				1394
Gly Pro Lys Pro Gly Phe Pro Glu Pro Thr Asn Asn Thr Pro Lys Gly				
364	369	374	379	
att ctt cat ttg tct cct gat gtt tat caa gag atg gaa gcc agc cgc				1442
Ile Leu His Leu Ser Pro Asp Val Tyr Gln Glu Met Glu Ala Ser Arg				
380	385	390	395	
cac aaa gta atc tct ggc act act cta ggc tat ttg tca ccc aaa gat				1490
His Lys Val Ile Ser Gly Thr Thr Leu Gly Tyr Leu Ser Pro Lys Asp				
396	401	406	411	
atg aac caa cct tca agc tct ttc ttc agt ata tct ccc aca tcg aat				1538
Met Asn Gln Pro Ser Ser Ser Phe Phe Ser Ile Ser Pro Thr Ser Asn				
412	417	422	427	
agt tca gct aca att gcc agg gaa ctc ctt atg aat gga aca tct tct				1586
Ser Ser Ala Thr Ile Ala Arg Glu Leu Leu Met Asn Gly Thr Ser Ser				
428	433	438	443	
aca gct gaa gcc ata ggt tta aaa gga agt tct cct act ccc cct tgt				1634
Thr Ala Glu Ala Ile Gly Leu Lys Gly Ser Ser Pro Thr Pro Pro Cys				
444	449	454	459	
tct cca gta caa cct tca aaa caa ctg gaa tat tta gca agg att caa				1682
Ser Pro Val Gln Pro Ser Lys Gln Leu Glu Tyr Leu Ala Arg Ile Gln				
460	465	470	475	
ggc ttt cag gta tga attaaaagca aaaaaaaaaa a				1718
Gly Phe Gln Val *				
476				

<210> 162
 <211> 1221
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (263)..(862)

<400> 162

ccgcgcgcga attcccggt cgaccacgc gtccgggcgc cgagagtaga gaaaaggggc 60

ctctggtgac cgcccctacc tggcatccct ctaacccagg aggagcgtgg ggaaaggggc	120
tgtgggcctc tcggggagcg agctgcggtt agcggcgcac tgggtacagg cgcgcgcttg	180
gctgtgcct ctgccgtgt gtttgggagg actcgaactg gcgccaggaa atattaggaa	240
gctgtgattt tcaaagctaa tt atg aaa aca ttt atc att gga atc agt ggt	292
Met Lys Thr Phe Ile Ile Gly Ile Ser Gly	
1 5	
gtg aca aac agt ggc aaa aca aca ctg gct aag aat ttg cag aaa cac	340
Val Thr Asn Ser Gly Lys Thr Thr Leu Ala Lys Asn Leu Gln Lys His	
11 16 21 26	
ctc cca aat tgc agt gtc ata tct cag gat gat ttc ttc aag cca gag	388
Leu Pro Asn Cys Ser Val Ile Ser Gln Asp Asp Phe Phe Lys Pro Glu	
27 32 37 42	
tct gag ata gag aca gat aaa aat gga ttt ttg cag tac gat gtg ctt	436
Ser Glu Ile Glu Thr Asp Lys Asn Gly Phe Leu Gln Tyr Asp Val Leu	
43 48 53 58	
gaa gca ctt aac atg gaa aaa atg atg tca gcc att tcc tgc tgg atg	484
Glu Ala Leu Asn Met Glu Lys Met Met Ser Ala Ile Ser Cys Trp Met	
59 64 69 74	
gaa agc gca aga cac tct gtg gta tca aca gac cag gaa agt gct gag	532
Glu Ser Ala Arg His Ser Val Val Ser Thr Asp Gln Glu Ser Ala Glu	
75 80 85 90	
gaa att ccc att tta atc atc gaa ggt ttt ctt ctt ttt aat tat aag	580
Glu Ile Pro Ile Leu Ile Ile Glu Gly Phe Leu Leu Phe Asn Tyr Lys	
91 96 101 106	
ccc ctt gac act ata tgg aat aga agc tat ttc ctg act att cca tat	628
Pro Leu Asp Thr Ile Trp Asn Arg Ser Tyr Phe Leu Thr Ile Pro Tyr	
107 112 117 122	
gaa gaa tgt aaa agg agg agg agt aca agg gtc tat cag cct cca gac	676
Glu Glu Cys Lys Arg Arg Arg Ser Thr Arg Val Tyr Gln Pro Pro Asp	
123 128 133 138	
tct ccg gga tac ttt gat ggc cat gtg tgg ccc atg tat cta aag tac	724
Ser Pro Gly Tyr Phe Asp Gly His Val Trp Pro Met Tyr Leu Lys Tyr	
139 144 149 154	
aga caa gaa atg cag gac atc aca tgg gaa gtt gtg tac ctg gat gga	772
Arg Gln Glu Met Gln Asp Ile Thr Trp Glu Val Val Tyr Leu Asp Gly	
155 160 165 170	
aca aaa tct gaa gag gac ctc ttt ttg caa gta tat gaa gat cta ata	820
Thr Lys Ser Glu Glu Asp Leu Phe Leu Gln Val Tyr Glu Asp Leu Ile	
171 176 181 186	
caa gaa cta gca aag caa aag tgt ttg caa gtg aca gca taa agacgga	869
Gln Glu Leu Ala Lys Gln Lys Cys Leu Gln Val Thr Ala *	

187

192

197

acacaacaaa tcttctctga agtgaattag gaaactccaa ggagtaattt aagaaccttc 929
 accaagatac aatgtatact gtggtacaat gacagccatt gtttcatatg tttgattttt 989
 attgcacatg gttttcccaa catgtggaac aataaatatc catgccaatg gacaggactg 1049
 taccttagca agttgctccc tctccaggga gcgcatagat acagcagagc tcacagttag 1109
 tcagaaagtc tccactttct gaacatagct ctataacaat gattgtcaaa cttttctaac 1169
 tggagctcag agtaagaaat aaagattaca tcacaatcca aaaaaaaaaa aa 1221

<210> 163

<211> 2925

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (178)..(2433)

<400> 163

ttgcttgtcc accttccagc tttaacgctc tgcaacaggg tagacaacct cagcgtgttg 60
 cagattccct gcaaggggag ttagacatct gagtcctaga ccgagatacc agctgaagga 120
 acgctgcttg gcgaaccttg gtgttcaagt tccagaggaa cgggatgagc tcttgag 177
 atg gaa gat ctg tcc tct cca gac tcc acc ctt ctc caa ggg gga cat 225
 Met Glu Asp Leu Ser Ser Pro Asp Ser Thr Leu Leu Gln Gly Gly His
 1 5 10 15
 aat cta ctc tca tca gcc agt ttt cag gaa gcg gtg act ttc aag gat 273
 Asn Leu Leu Ser Ser Ala Ser Phe Gln Glu Ala Val Thr Phe Lys Asp
 17 22 27 32
 gtg ata gtg gac ttt acc cag gaa gaa tgg aaa cag ctg gac oct ggc 321
 Val Ile Val Asp Phe Thr Gln Glu Glu Trp Lys Gln Leu Asp Pro Gly
 33 38 43 48
 cag aga gat ttg ttc agg gat gtg aca ttg gaa aat tat aca cac ctg 369
 Gln Arg Asp Leu Phe Arg Asp Val Thr Leu Glu Asn Tyr Thr His Leu
 49 54 59 64
 gtc tct ata gga ctc caa gtt tct aaa cct gat gtg att tcc cag tta 417
 Val Ser Ile Gly Leu Gln Val Ser Lys Pro Asp Val Ile Ser Gln Leu
 65 70 75 80
 gag caa ggg aca gag cca tgg atc atg gag cca agc att cca gta ggt 465
 Glu Gln Gly Thr Glu Pro Trp Ile Met Glu Pro Ser Ile Pro Val Gly
 81 86 91 96
 acc tgt gca gac tgg gag aca aga ctt gaa aat agt gtg tca gcc cca 513

Thr Cys Ala Asp Trp Glu Thr Arg Leu Glu Asn Ser Val Ser Ala Pro	
97 102 107 112	
gag cct gac att tct gaa gaa gag cta tct cca gag gta ata gtg gaa	561
Glu Pro Asp Ile Ser Glu Glu Glu Leu Ser Pro Glu Val Ile Val Glu	
113 118 123 128	
aaa cac aaa aga gat gat tct tgg agt tcc aac ttg cta gaa agt tgg	609
Lys His Lys Arg Asp Asp Ser Trp Ser Ser Asn Leu Leu Glu Ser Trp	
129 134 139 144	
gaa tat gaa ggc agt tta gag aga cag cag gca aac caa cag aca ctg	657
Glu Tyr Glu Gly Ser Leu Glu Arg Gln Gln Ala Asn Gln Gln Thr Leu	
145 150 155 160	
cca aag gaa ata aag gta acc gaa aag aca ata ccc agt tgg gaa aaa	705
Pro Lys Glu Ile Lys Val Thr Glu Lys Thr Ile Pro Ser Trp Glu Lys	
161 166 171 176	
ggc cct gta aat aat gaa ttt ggg aaa agt gtc aat gtg agt tca aac	753
Gly Pro Val Asn Asn Glu Phe Gly Lys Ser Val Asn Val Ser Ser Asn	
177 182 187 192	
ctt gta aca caa gaa cca tct cca gaa gag acc tct act aaa aga agc	801
Leu Val Thr Gln Glu Pro Ser Pro Glu Glu Thr Ser Thr Lys Arg Ser	
193 198 203 208	
atc aaa cag aat tca aac cca gtt aaa aaa gag aaa tct tgt aag tgc	849
Ile Lys Gln Asn Ser Asn Pro Val Lys Lys Glu Lys Ser Cys Lys Cys	
209 214 219 224	
aat gaa tgt ggg aaa gcc ttt agt tat tgt tca gct ctt att cgc cat	897
Asn Glu Cys Gly Lys Ala Phe Ser Tyr Cys Ser Ala Leu Ile Arg His	
225 230 235 240	
cag aga aca cat act gga gaa aaa ccc tac aaa tgt aat gaa tgt gaa	945
Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Asn Glu Cys Glu	
241 246 251 256	
aaa gcc ttc agc cgg agt gaa aac ctt ata aac cat caa aga att cat	993
Lys Ala Phe Ser Arg Ser Glu Asn Leu Ile Asn His Gln Arg Ile His	
257 262 267 272	
act gga gat aaa cca tat aaa tgt gat cag tgt gga aaa ggc ttc att	1041
Thr Gly Asp Lys Pro Tyr Lys Cys Asp Gln Cys Gly Lys Gly Phe Ile	
273 278 283 288	
gag ggt cca tct ctt act caa cat caa aga att cat act gga gaa aaa	1089
Glu Gly Pro Ser Leu Thr Gln His Gln Arg Ile His Thr Gly Glu Lys	
289 294 299 304	
cca tat aaa tgt gat gaa tgt ggg aaa gcc ttt agt cag agg acc cat	1137
Pro Tyr Lys Cys Asp Glu Cys Gly Lys Ala Phe Ser Gln Arg Thr His	
305 310 315 320	
ctt gtt cag cat cag aga att cat act ggc gag aag cca tac act tgt	1185
Leu Val Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Thr Cys	

321	326	331	336	
aat gag tgt gga aaa gcc ttt agc cag aga ggc cac ttt atg gaa cat				1233
Asn Glu Cys Gly Lys Ala Phe Ser Gln Arg Gly His Phe Met Glu His				
337	342	347	352	
cag aaa att cat acg gga gaa aaa cct ttt aaa tgt gat gaa tgt gat				1281
Gln Lys Ile His Thr Gly Glu Lys Pro Phe Lys Cys Asp Glu Cys Asp				
353	358	363	368	
aaa acc ttc acc agg agc aca cac ctt act caa cat caa aaa att cat				1329
Lys Thr Phe Thr Arg Ser Thr His Leu Thr Gln His Gln Lys Ile His				
369	374	379	384	
act gga gaa aaa acc tat aaa tgt aat gaa tgt gga aag gcc ttc aac				1377
Thr Gly Glu Lys Thr Tyr Lys Cys Asn Glu Cys Gly Lys Ala Phe Asn				
385	390	395	400	
ggg ccc tca act ttt atc cgt cat cat atg att cat act ggt gaa aaa				1425
Gly Pro Ser Thr Phe Ile Arg His His Met Ile His Thr Gly Glu Lys				
401	406	411	416	
ccg tac gaa tgc aat gaa tgt ggg aaa gcc ttc agc cag cac tca aac				1473
Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ala Phe Ser Gln His Ser Asn				
417	422	427	432	
ctc act cag cat caa aaa act cat act ggg gag aaa ccc tat gat tgt				1521
Leu Thr Gln His Gln Lys Thr His Thr Gly Glu Lys Pro Tyr Asp Cys				
433	438	443	448	
gca gaa tgt gga aaa tct ttt agt tac tgg tca tcc ctt gct caa cac				1569
Ala Glu Cys Gly Lys Ser Phe Ser Tyr Trp Ser Ser Leu Ala Gln His				
449	454	459	464	
ctg aaa att cat act gga gaa aaa cct tac aaa tgc aat gaa tgt gga				1617
Leu Lys Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Asn Glu Cys Gly				
465	470	475	480	
aag gcc ttc agt tac tgc tca tcc ctt act caa cat cgg aga att cac				1665
Lys Ala Phe Ser Tyr Cys Ser Ser Leu Thr Gln His Arg Arg Ile His				
481	486	491	496	
acg aga gaa aag ccc ttt gaa tgc agt gaa tgt gga aag gct ttc agt				1713
Thr Arg Glu Lys Pro Phe Glu Cys Ser Glu Cys Gly Lys Ala Phe Ser				
497	502	507	512	
tat ctc tca aac ctt aat cag cat cag aaa act cat act caa gag aaa				1761
Tyr Leu Ser Asn Leu Asn Gln His Gln Lys Thr His Thr Gln Glu Lys				
513	518	523	528	
gct tat gaa tgt aaa gaa tgt ggg aaa gct ttt att cgg agt tca tct				1809
Ala Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Ile Arg Ser Ser Ser				
529	534	539	544	
ctt gct aag cat gaa aga att cat act gga gag aaa ccc tat cag tgt				1857
Leu Ala Lys His Glu Arg Ile His Thr Gly Glu Lys Pro Tyr Gln Cys				
545	550	555	560	

cat gaa tgt ggg aaa acc ttc agt tat ggt tca tcc ctt att cag cat	1905
His Glu Cys Gly Lys Thr Phe Ser Tyr Gly Ser Ser Leu Ile Gln His	
561 566 571 576	
agg aag atc cat act gga gaa cga cct tac aag tgt aat gag tgt ggg	1953
Arg Lys Ile His Thr Gly Glu Arg Pro Tyr Lys Cys Asn Glu Cys Gly	
577 582 587 592	
aga gca ttc aac cag aac ata cac ctt aca cag cat aag aga att cat	2001
Arg Ala Phe Asn Gln Asn Ile His Leu Thr Gln His Lys Arg Ile His	
593 598 603 608	
aca gga gcc aag cct tat gag tgt gct gag tgt ggt aaa gcc ttt cga	2049
Thr Gly Ala Lys Pro Tyr Glu Cys Ala Glu Cys Gly Lys Ala Phe Arg	
609 614 619 624	
cat tgt tca tct ctt gct caa cat caa aaa act cac aca gaa gaa aaa	2097
His Cys Ser Ser Leu Ala Gln His Gln Lys Thr His Thr Glu Glu Lys	
625 630 635 640	
ccc tac cag tgt aat aaa tgt gaa aag acc ttt agc cag agc tcc cat	2145
Pro Tyr Gln Cys Asn Lys Cys Glu Lys Thr Phe Ser Gln Ser Ser His	
641 646 651 656	
cta act cag cat caa cga att cac act ggg gag aag ccc tat aag tgc	2193
Leu Thr Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys	
657 662 667 672	
aat gaa tgt gac aaa gcc ttt agc cgg agc act cat ctg act gaa cat	2241
Asn Glu Cys Asp Lys Ala Phe Ser Arg Ser Thr His Leu Thr Glu His	
673 678 683 688	
cag aat act cat act gga gag aaa cct tat aac tgt aat gaa tgc aga	2289
Gln Asn Thr His Thr Gly Glu Lys Pro Tyr Asn Cys Asn Glu Cys Arg	
689 694 699 704	
aag act ttt agc cag agc aca tat ctc att cag cac cag aga att cat	2337
Lys Thr Phe Ser Gln Ser Thr Tyr Leu Ile Gln His Gln Arg Ile His	
705 710 715 720	
tca gga gag aag cct ttt gga tgt aat gat tgt gga aaa tcc ttc aga	2385
Ser Gly Glu Lys Pro Phe Gly Cys Asn Asp Cys Gly Lys Ser Phe Arg	
721 726 731 736	
tat cgc tct gct ctc aac aaa cat cag aga ctg cat cct ggc ata tga	2433
Tyr Arg Ser Ala Leu Asn Lys His Gln Arg Leu His Pro Gly Ile *	
737 742 747 752	
caattctagg aacatcataa atttagggga gatatttact ttagtttgtc cttttgttaa	2493
gtactgaaga atcagagtgg atttagaaac tgccttgaaa tcttttaaatt tttcactatc	2553
atgttatgga atggaaagta cattgggctg aactaatcca attgttatta agccactctg	2613
tgacattaga aaactctact gttttaagct ttagtttcoct ttatggaatg aaggctttgg	2673

agtagattat ttcaaaggta gtttgaggtt ttataatcag ttttgtatat ttacaatatt 2733
 ttcttgaatg ggtttactat acatcagcat tttgctgtgt tgcattctaga atgtgtatgt 2793
 ttatgcatgt tttgccaata gaatttgtgc ttcagtaact agatcgggga tctagtatgc 2853
 tctgtgtcta atgcatttac attgtttagg taactgggtc ctaataaaaa gaattataaa 2913
 ataaaaaaaa aa 2925

<210> 164
 <211> 4631
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (184)..(3003)

<400> 164
 aaggatcctt aattgacttt atccccgccc tcgtatgctg cgctgggacc ctgaggcggc 60
 cgtgggttagg cggctccccg gcggtcctc cgcggcggtg acggcgaccg cactccccgc 120
 ttcccgctcc ccgcgtcct ccgcccgggt ccgccagccg aggcgcgtcc cgagcgtcgg 180
 aag atg ccg gcc gtg tcc aag ggg gac ggg atg cgg ggc ctg gcg gtc 228
 Met Pro Ala Val Ser Lys Gly Asp Gly Met Arg Gly Leu Ala Val
 1 5 10
 ttc atc tcg gat atc cgc aac tgt aaa agt aaa gaa gca gaa ata aaa 276
 Phe Ile Ser Asp Ile Arg Asn Cys Lys Ser Lys Glu Ala Glu Ile Lys
 16 21 26 31
 agg ata aac aag gaa ctg gca aat atc aga tca aaa ttt aaa ggt gac 324
 Arg Ile Asn Lys Glu Leu Ala Asn Ile Arg Ser Lys Phe Lys Gly Asp
 32 37 42 47
 aag gct ctt gat ggc tat agt aaa aaa aag tac gtc tgc aag ttg ctc 372
 Lys Ala Leu Asp Gly Tyr Ser Lys Lys Lys Tyr Val Cys Lys Leu Leu
 48 53 58 63
 ttc atc ttt ctc ctt ggt cat gac att gac ttt gga cac atg gag gct 420
 Phe Ile Phe Leu Leu Gly His Asp Ile Asp Phe Gly His Met Glu Ala
 64 69 74 79
 gtg aac ctg ctg agt tca aac aga tac acg gaa aag cag atc ggc tac 468
 Val Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln Ile Gly Tyr
 80 85 90 95
 ctt ttc atc tct gtg ttg gtg aac tca aac agt gag ctg atc cgc ctg 516
 Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu Ile Arg Leu
 96 101 106 111

atc aac aac gcc atc aag aat gac ctg gcc agc cgc aac ccc acc ttc	564
Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn Pro Thr Phe	
112 117 122 127	
atg ggc ctg gcc ctg cac tgc atc gcc agc gtg ggc agc cgg gag atg	612
Met Gly Leu Ala Leu His Cys Ile Ala Ser Val Gly Ser Arg Glu Met	
128 133 138 143	
gcc gag gcc ttc gcc ggg gag atc cct aag gtc ctc gta gcc gga gac	660
Ala Glu Ala Phe Ala Gly Glu Ile Pro Lys Val Leu Val Ala Gly Asp	
144 149 154 159	
act atg gac agc gtg aag cag agc gcg gcc ctg tgc ttg ctg cgc ctg	708
Thr Met Asp Ser Val Lys Gln Ser Ala Ala Leu Cys Leu Leu Arg Leu	
160 165 170 175	
tac agg acg tcc ccc gat ctt gtc ccc atg ggc gac tgg aca tcc cga	756
Tyr Arg Thr Ser Pro Asp Leu Val Pro Met Gly Asp Trp Thr Ser Arg	
176 181 186 191	
gtg gtg cac ctg ctc aat gac cag cac ttg ggt gtg gta act gca gcc	804
Val Val His Leu Leu Asn Asp Gln His Leu Gly Val Val Thr Ala Ala	
192 197 202 207	
aca agt ctg atc acc act tta gca cag aag aac cca gaa gag ttt aaa	852
Thr Ser Leu Ile Thr Thr Leu Ala Gln Lys Asn Pro Glu Glu Phe Lys	
208 213 218 223	
acc tcc gtg tct ctg gct gtc tct agg cta agc aga atc gtg acg tct	900
Thr Ser Val Ser Leu Ala Val Ser Arg Leu Ser Arg Ile Val Thr Ser	
224 229 234 239	
gca tcc aca gat ctc cag gat tac act tac tat ttt gtc ccg gct ccc	948
Ala Ser Thr Asp Leu Gln Asp Tyr Thr Tyr Tyr Phe Val Pro Ala Pro	
240 245 250 255	
tgg ctg tct gtc aaa ctg ctg aga ctg ctg cag tgc tac cca ccc cca	996
Trp Leu Ser Val Lys Leu Leu Arg Leu Leu Gln Cys Tyr Pro Pro Pro	
256 261 266 271	
gac cct gca gtg cga ggc cgc ctg act gag tgc ctg gag acc atc ctg	1044
Asp Pro Ala Val Arg Gly Arg Leu Thr Glu Cys Leu Glu Thr Ile Leu	
272 277 282 287	
aac aaa gcc caa gaa ccg ccc aag tcg aag aag gtc cag cac tcc aac	1092
Asn Lys Ala Gln Glu Pro Pro Lys Ser Lys Lys Val Gln His Ser Asn	
288 293 298 303	
gcg aag aat gcc gtg ctc ttc gag gcc atc agc tta atc att cac cat	1140
Ala Lys Asn Ala Val Leu Phe Glu Ala Ile Ser Leu Ile Ile His His	
304 309 314 319	
gac agt gag ccg aac ctg ctc gtc cgt gcc tgc aac cag ttg ggc cag	1188
Asp Ser Glu Pro Asn Leu Leu Val Arg Ala Cys Asn Gln Leu Gly Gln	
320 325 330 335	
ttt ctg cag cac cgc gag acc aac ctg cgc tac ctg gcc ctg gag agc	1236

Phe	Leu	Gln	His	Arg	Glu	Thr	Asn	Leu	Arg	Tyr	Leu	Ala	Leu	Glu	Ser		
336					341					346					351		
atg	tgc	acg	ctg	gcc	agc	tct	gag	ttc	tcc	cat	gag	gct	gtc	aag	acg	1284	
Met	Cys	Thr	Leu	Ala	Ser	Ser	Glu	Phe	Ser	His	Glu	Ala	Val	Lys	Thr		
352					357					362					367		
cac	atc	gag	acg	gtc	atc	aac	gcc	ctg	aag	act	gag	cgg	gac	gtg	agc	1332	
His	Ile	Glu	Thr	Val	Ile	Asn	Ala	Leu	Lys	Thr	Glu	Arg	Asp	Val	Ser		
368					373					378					383		
gtg	cgg	cag	cgg	gcc	gtg	gac	ctc	ctc	tac	gcc	atg	tgc	gac	cgc	agc	1380	
Val	Arg	Gln	Arg	Ala	Val	Asp	Leu	Leu	Tyr	Ala	Met	Cys	Asp	Arg	Ser		
384					389					394					399		
aac	gcc	cca	cag	atc	gtg	gcc	gag	atg	ctg	agc	tat	ctg	gag	aca	gct	1428	
Asn	Ala	Pro	Gln	Ile	Val	Ala	Glu	Met	Leu	Ser	Tyr	Leu	Glu	Thr	Ala		
400					405					410					415		
gac	tac	tcc	atc	cga	gaa	gag	att	gtg	ctg	aag	gtc	gcc	atc	ctg	gct	1476	
Asp	Tyr	Ser	Ile	Arg	Glu	Glu	Ile	Val	Leu	Lys	Val	Ala	Ile	Leu	Ala		
416					421					426					431		
gag	aag	tac	gcg	gtg	gac	tac	acc	tgg	tat	gtg	gat	acc	atc	ttg	aac	1524	
Glu	Lys	Tyr	Ala	Val	Asp	Tyr	Thr	Trp	Tyr	Val	Asp	Thr	Ile	Leu	Asn		
432					437					442					447		
ttg	atc	cga	att	gct	ggg	gat	tac	gtg	agt	gaa	gag	gtg	tgg	tac	cga	1572	
Leu	Ile	Arg	Ile	Ala	Gly	Asp	Tyr	Val	Ser	Glu	Glu	Val	Trp	Tyr	Arg		
448					453					458					463		
gtc	att	cag	atc	gtc	atc	aac	cgg	gac	gac	gtg	cag	ggc	tac	gcg	gcc	1620	
Val	Ile	Gln	Ile	Val	Ile	Asn	Arg	Asp	Asp	Val	Gln	Gly	Tyr	Ala	Ala		
464					469					474					479		
aag	act	gtg	ttc	gag	gct	ctt	cag	gct	ccc	gcg	tgc	cac	gag	aac	ctg	1668	
Lys	Thr	Val	Phe	Glu	Ala	Leu	Gln	Ala	Pro	Ala	Cys	His	Glu	Asn	Leu		
480					485					490					495		
gtc	aaa	gtg	ggc	ggc	tac	atc	ctg	ggg	gag	ttt	gga	aac	ttg	ata	gct	1716	
Val	Lys	Val	Gly	Gly	Tyr	Ile	Leu	Gly	Glu	Phe	Gly	Asn	Leu	Ile	Ala		
496					501					506					511		
gga	gac	ccg	aga	tcc	agc	ccg	ctg	atc	cag	ttc	cac	ctg	ctg	cac	tcc	1764	
Gly	Asp	Pro	Arg	Ser	Ser	Pro	Leu	Ile	Gln	Phe	His	Leu	Leu	His	Ser		
512					517					522					527		
aag	ttc	cac	ctg	tgc	agc	gtc	ccc	acc	cgc	gcg	ctg	ctc	ctg	tcc	acc	1812	
Lys	Phe	His	Leu	Cys	Ser	Val	Pro	Thr	Arg	Ala	Leu	Leu	Leu	Ser	Thr		
528					533					538					543		
tac	atc	aag	ttc	gtg	aac	ctc	ttc	ccg	gag	gtg	aag	ccc	acc	atc	cag	1860	
Tyr	Ile	Lys	Phe	Val	Asn	Leu	Phe	Pro	Glu	Val	Lys	Pro	Thr	Ile	Gln		
544					549					554					559		
gac	gtg	ctg	cgc	agc	gac	agc	cag	ctc	agg	aac	gca	gac	gtg	gag	ctg	1908	
Asp	Val	Leu	Arg	Ser	Asp	Ser	Gln	Leu	Arg	Asn	Ala	Asp	Val	Glu	Leu		

560	565	570	575	
cag cag cgt gct gtg gag tac ctg cgg ctc agc acc gtg gcc agc acc				1956
Gln Gln Arg Ala Val Glu Tyr Leu Arg Leu Ser Thr Val Ala Ser Thr				
576	581	586	591	
gac att ctg gcg acc gtg ctg gag gag atg ccc cca ttc ccg gag cgg				2004
Asp Ile Leu Ala Thr Val Leu Glu Glu Met Pro Pro Phe Pro Glu Arg				
592	597	602	607	
gag tcc tcc atc ttg gca aag ctc aag aag aag aag ggc ccc agc acg				2052
Glu Ser Ser Ile Leu Ala Lys Leu Lys Lys Lys Lys Gly Pro Ser Thr				
608	613	618	623	
gtg aca gac ctg gag gac acc aag cgg gac agg agt gtg gac gtg aac				2100
Val Thr Asp Leu Glu Asp Thr Lys Arg Asp Arg Ser Val Asp Val Asn				
624	629	634	639	
ggg ggt cct gag cct gcc cca gcc agt acc agc gcc gtg tct acg cct				2148
Gly Gly Pro Glu Pro Ala Pro Ala Ser Thr Ser Ala Val Ser Thr Pro				
640	645	650	655	
tct ccg tcg gca gac ctg ctg ggt ctc ggg gct gcc ccc cct gcc ccc				2196
Ser Pro Ser Ala Asp Leu Leu Gly Leu Gly Ala Ala Pro Pro Ala Pro				
656	661	666	671	
gcg ggc ccc cca ccc tcc tcc ggc ggc agc ggg ctg ctc gtg gac gtg				2244
Ala Gly Pro Pro Pro Ser Ser Gly Gly Ser Gly Leu Leu Val Asp Val				
672	677	682	687	
ttc tca gac tcg gcc tct gtg gtc gcg cct ctc gct cct ggc tcc gaa				2292
Phe Ser Asp Ser Ala Ser Val Val Ala Pro Leu Ala Pro Gly Ser Glu				
688	693	698	703	
gac aac ttt gcc agg ttt gtt tgt aaa aac aat ggt gtg ttg ttt gaa				2340
Asp Asn Phe Ala Arg Phe Val Cys Lys Asn Asn Gly Val Leu Phe Glu				
704	709	714	719	
aac cag ctg ctt caa att gga ctt aag tct gaa ttt cgg cag aat tta				2388
Asn Gln Leu Leu Gln Ile Gly Leu Lys Ser Glu Phe Arg Gln Asn Leu				
720	725	730	735	
ggg cgg atg ttt atc ttt tat ggt aat aag acc tcc acg cag ttc cta				2436
Gly Arg Met Phe Ile Phe Tyr Gly Asn Lys Thr Ser Thr Gln Phe Leu				
736	741	746	751	
aac ttt acc cca aca cta atc tgt tca gac gac ctt cag cct aac ctg				2484
Asn Phe Thr Pro Thr Leu Ile Cys Ser Asp Asp Leu Gln Pro Asn Leu				
752	757	762	767	
aac ctg cag acc aag ccc gtg gac ccg acc gtg gag ggg ggc gcg cag				2532
Asn Leu Gln Thr Lys Pro Val Asp Pro Thr Val Glu Gly Gly Ala Gln				
768	773	778	783	
gtg cag cag gtg gtc aac ata gag tgc gtg tcc gac ttc acg gag gcg				2580
Val Gln Gln Val Val Asn Ile Glu Cys Val Ser Asp Phe Thr Glu Ala				
784	789	794	799	

cca gtc ctc aac att cag ttc agg tat ggg ggc acc ttc cag aac gtg	2628
Pro Val Leu Asn Ile Gln Phe Arg Tyr Gly Gly Thr Phe Gln Asn Val	
800 805 810 815	
tct gtg cag ctg ccc atc act ctc aac aaa ttc ttc cag ccg aca gaa	2676
Ser Val Gln Leu Pro Ile Thr Leu Asn Lys Phe Phe Gln Pro Thr Glu	
816 821 826 831	
atg gct tct cag gat ttc ttt caa cgt tgg aag cag ttg agc aat cca	2724
Met Ala Ser Gln Asp Phe Phe Gln Arg Trp Lys Gln Leu Ser Asn Pro	
832 837 842 847	
cag cag gaa gtg cag aac atc ttc aaa gca aag cac cca atg gac aca	2772
Gln Gln Glu Val Gln Asn Ile Phe Lys Ala Lys His Pro Met Asp Thr	
848 853 858 863	
gaa gtc acc aaa gcc aag atc att gga ttt ggt tct gca ctt ctt gaa	2820
Glu Val Thr Lys Ala Lys Ile Ile Gly Phe Gly Ser Ala Leu Leu Glu	
864 869 874 879	
gaa gtt gat cct aat cct gcg aat ttc gtg gga gct gga atc atc cac	2868
Glu Val Asp Pro Asn Pro Ala Asn Phe Val Gly Ala Gly Ile Ile His	
880 885 890 895	
acg aaa acc acc cag att gga tgc ctg ctg cgc ttg gag ccg aac ctg	2916
Thr Lys Thr Thr Gln Ile Gly Cys Leu Leu Arg Leu Glu Pro Asn Leu	
896 901 906 911	
caa gcc cag atg tac cgg ctc acg ctg cgc aca agt aag gaa gcc gtt	2964
Gln Ala Gln Met Tyr Arg Leu Thr Leu Arg Thr Ser Lys Glu Ala Val	
912 917 922 927	
tct cag aga tta tgt gaa ttg ctc tca gcg cag ttt tag tctgaggat	3013
Ser Gln Arg Leu Cys Glu Leu Leu Ser Ala Gln Phe *	
928 933 938	
ggaagaccag gctcgtgtgt cttgtgttgt cttcgtctgt gccgtttgtc ttcgtggcta	3073
tcttcagat gagcaccgtg tccagtgcc aagcacaagg cgcctccccg cccaccgcc	3133
ccacacctot cccctttggg ctggacggga acacacgtgt gtggctcagg aggaaaagct	3193
cagcctggac tgtggcagcc acggcagaag gtggatcttg ggatcaattt ttataaaaat	3253
cgagacagtt ctgtggttaa atctacaaat taaagggaaa ttagaagttg gcgtgaacgt	3313
ggcgtttgtg ggagtgtcac tgagatggcc cgtgctgccg cccaccccg ctcggagcct	3373
ctgggagcag cagtgccact gtgcatggcg tgggctgagc cttggtgtgt ggccgtcctg	3433
gtggctgcac acctggcgtc gtccctgggc cttgggagga gcacagctga ccctggtttt	3493
gtgcagtc cagctggact gtttccag gcaggatttt aatctagaat ttagaaacat	3553
ttgtatttgt aatgacttct ggcaaaagca cgtgtcctgg ccgcatgtaa ctgttctcct	3613

ttcccagctc ctgtttgtga agggcgctctg ttatgctcct gcagtcgcog aggccttgga	3673
tgtgcagcca ggggaggagc gtcctgccgg ccccgaggg cccccaggac tccagggtaa	3733
agtgtggggc ggtggcgcaa gactcagagg tgtgctcgtc tctttcctgt cagagtgggc	3793
gtccccaggc cacggtgcag gcctgagtcc ttccaccggc cccgtccagt cgtccctgga	3853
ggggctgtgg aggaaggacg cctctgtgtg gtcaggaagt gaaggggcca ttggccgcat	3913
gccatgtgcc acctgcggct tgtgtctcac ctgtcatctg gactcagcac ccaggctgca	3973
cgtctgacac ctgagaggcg agagagtggg gccggcctag gagccaaggc tggggccttg	4033
cgctctgtcc ccaggatggt ggccttgttt gtccaaaca caccagcac aggttctggc	4093
ttcctgacat gctgtggagg cagggagggg ggggtggccac atgtgcttga gggttttcac	4153
cctggccctc agttgcctgc tgtgcgggtc cctggggcag ctgcaggggc tcatggaccc	4213
atcagggtct ccacagctcc cctgcagtgt gtgcaccca caatgtctgc ggctcttctt	4273
ccggcgctgc gggctttgat cacagcatag ccacgtcagt ggcgtgcgcc tctcgcacag	4333
gccattctgg gtctggtggt gccagggtgcc gtgacacgcc gtgctgggct tgtgctgcag	4393
ctgggtggtg tggccctcat tctcatgttc cagctgctgg gcagtgctct gcctgtgtgc	4453
tgcgcctgca ggctgcgtgt gctgccgtgg atctcctgca tcccttgacc cctcccgcca	4513
tcagaggaaa ggctgctccc cgaggcaccg cttccctgtg cggcgctgca gaggggccct	4573
cagtgtggca ctctcgtca aagaaaaata aaggctagaa ctgccaaaaa aaaaaaaa	4631

<210> 165
 <211> 3292
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (118)..(2313)

<220>
 <221> misc_feature
 <222> (1)...(3292)
 <223> n = a,t,c or g

<400> 165	
tgaacaann nnntttgatn gcctttgatg ggcgatccag ctggctagcg tttaaactta	60
agctcgggac cgagctcgga tccactagtc cagtgtggtg gaattccaga tccctgc	117
atg tca ctg agt cca cca tgc ttt aca gaa gaa gac aga ttt agt ctg	165
Met Ser Leu Ser Pro Pro Cys Phe Thr Glu Glu Asp Arg Phe Ser Leu	

1	5	10	15	
gaa gct ctt caa aca ata cat aaa caa atg gat gat gac aaa gat ggt				213
Glu Ala Leu Gln Thr Ile His Lys Gln Met Asp Asp Asp Lys Asp Gly				
17	22	27	32	
gga att gaa gta gag gaa agt gat gaa ttc atc aga gaa gat atg aaa				261
Gly Ile Glu Val Glu Glu Ser Asp Glu Phe Ile Arg Glu Asp Met Lys				
33	38	43	48	
tat aaa gat gct act aat aaa cac agc cat ctg cac aga gaa gat aaa				309
Tyr Lys Asp Ala Thr Asn Lys His Ser His Leu His Arg Glu Asp Lys				
49	54	59	64	
cat ata acg att gag gat tta tgg aaa cga tgg aaa aca tca gaa gtt				357
His Ile Thr Ile Glu Asp Leu Trp Lys Arg Trp Lys Thr Ser Glu Val				
65	70	75	80	
cat aat tgg acc ctt gaa gac act ctt cag tgg ttg ata gag ttt gtt				405
His Asn Trp Thr Leu Glu Asp Thr Leu Gln Trp Leu Ile Glu Phe Val				
81	86	91	96	
gaa cta ccc caa tat gag aag aat ttt aga gac aac aat gtc aaa gga				453
Glu Leu Pro Gln Tyr Glu Lys Asn Phe Arg Asp Asn Asn Val Lys Gly				
97	102	107	112	
acg aca ctt ccc agg ata gca gtg cac gaa cct tca ttt atg atc tcc				501
Thr Thr Leu Pro Arg Ile Ala Val His Glu Pro Ser Phe Met Ile Ser				
113	118	123	128	
cag ttg aaa atc agt gac cgg agt cac aga caa aaa ctt cag ctc aag				549
Gln Leu Lys Ile Ser Asp Arg Ser His Arg Gln Lys Leu Gln Leu Lys				
129	134	139	144	
gca ttg gat gtg gtt ttg ttt gga cct cta aca cgc cca cct cat aac				597
Ala Leu Asp Val Val Leu Phe Gly Pro Leu Thr Arg Pro Pro His Asn				
145	150	155	160	
tgg atg aaa gat ttt atc ctc aca gtt tct ata gta att ggt gtt gga				645
Trp Met Lys Asp Phe Ile Leu Thr Val Ser Ile Val Ile Gly Val Gly				
161	166	171	176	
ggc tgc tgg ttt gct tat acg cag aat aag aca tca aaa gaa cat gtt				693
Gly Cys Trp Phe Ala Tyr Thr Gln Asn Lys Thr Ser Lys Glu His Val				
177	182	187	192	
gca aaa atg atg aaa gat tta gag agc tta caa act gca gag caa agt				741
Ala Lys Met Met Lys Asp Leu Glu Ser Leu Gln Thr Ala Glu Gln Ser				
193	198	203	208	
cta atg gac tta caa gag agg ctt gaa aag gca cag gaa gaa aac aga				789
Leu Met Asp Leu Gln Glu Arg Leu Glu Lys Ala Gln Glu Glu Asn Arg				
209	214	219	224	
aat gtt gct gta gaa aag caa aat tta gag cgc aaa atg atg gat gaa				837
Asn Val Ala Val Glu Lys Gln Asn Leu Glu Arg Lys Met Met Asp Glu				
225	230	235	240	

atc aat tat gca aag gag gag gct tgt cgg ctg aga gag cta agg gag	885
Ile Asn Tyr Ala Lys Glu Glu Ala Cys Arg Leu Arg Glu Leu Arg Glu	
241 246 251 256	
gga gct gaa tgt gaa ttg agt aga cgt cag tat gca gaa cag gaa ttg	933
Gly Ala Glu Cys Glu Leu Ser Arg Arg Gln Tyr Ala Glu Gln Glu Leu	
257 262 267 272	
gaa cag gtt cgc atg gct ctg aaa aag gcc gaa aaa gaa ttt gaa ctg	981
Glu Gln Val Arg Met Ala Leu Lys Lys Ala Glu Lys Glu Phe Glu Leu	
273 278 283 288	
aga agc agt tgg tct gtt cca gat gca ctt cag aaa tgg ctt cag tta	1029
Arg Ser Ser Trp Ser Val Pro Asp Ala Leu Gln Lys Trp Leu Gln Leu	
289 294 299 304	
aca cat gaa gta gaa gtg caa tac tac aat att aaa aga caa aac gct	1077
Thr His Glu Val Glu Val Gln Tyr Tyr Asn Ile Lys Arg Gln Asn Ala	
305 310 315 320	
gaa atg cag cta gct att gct aaa gat gag gca gaa aaa att aaa aag	1125
Glu Met Gln Leu Ala Ile Ala Lys Asp Glu Ala Glu Lys Ile Lys Lys	
321 326 331 336	
aag aga agc aca gtc ttt ggg act ctg cac gtt gca cac agc tcc tcc	1173
Lys Arg Ser Thr Val Phe Gly Thr Leu His Val Ala His Ser Ser Ser	
337 342 347 352	
cta gat gag gta gac cac aaa att ctg gaa gca aag aaa gct ctc tct	1221
Leu Asp Glu Val Asp His Lys Ile Leu Glu Ala Lys Lys Ala Leu Ser	
353 358 363 368	
gag ttg aca act tgt tta cga gaa cga ctt ttt cgc tgg caa caa att	1269
Glu Leu Thr Thr Cys Leu Arg Glu Arg Leu Phe Arg Trp Gln Gln Ile	
369 374 379 384	
gag aag atc tgt ggc ttt cag ata gcc cat aac tca gga ctc ccc agc	1317
Glu Lys Ile Cys Gly Phe Gln Ile Ala His Asn Ser Gly Leu Pro Ser	
385 390 395 400	
ctg acc tct tcc ctt tat tct gat cac agc tgg gtg gtg atg ccc aga	1365
Leu Thr Ser Ser Leu Tyr Ser Asp His Ser Trp Val Val Met Pro Arg	
401 406 411 416	
gtc tcc att cca ccc tat cca att gct gga gga gtt gat gac tta gat	1413
Val Ser Ile Pro Pro Tyr Pro Ile Ala Gly Gly Val Asp Asp Leu Asp	
417 422 427 432	
gaa gac aca ccc cca ata gtg tca caa ttt ccc ggg acc atg gct aaa	1461
Glu Asp Thr Pro Pro Ile Val Ser Gln Phe Pro Gly Thr Met Ala Lys	
433 438 443 448	
cct cct gga tca tta gcc aga agc agc agc ctg tgc cgt tca cgc cgc	1509
Pro Pro Gly Ser Leu Ala Arg Ser Ser Ser Leu Cys Arg Ser Arg Arg	
449 454 459 464	

agc att gtg ccg tcc tcg cct cag cct cag cga gct cag ctt gct cca	1557
Ser Ile Val Pro Ser Ser Pro Gln Pro Gln Arg Ala Gln Leu Ala Pro	
465 470 475 480	
cac gcc ccc cac ccg tca cac cct cgg cac cct cac cac ccg caa cac	1605
His Ala Pro His Pro Ser His Pro Arg His Pro His His Pro Gln His	
481 486 491 496	
aca cca cac tcc ttg cct tcc cct gat cca gat atc ctc tca gtg tca	1653
Thr Pro His Ser Leu Pro Ser Pro Asp Pro Asp Ile Leu Ser Val Ser	
497 502 507 512	
agt tgc cct gcg ctt tat cga aat gaa gag gag gaa gag gcc att tac	1701
Ser Cys Pro Ala Leu Tyr Arg Asn Glu Glu Glu Glu Glu Ala Ile Tyr	
513 518 523 528	
ttc tct gct gaa aag caa tgg aac aca agg gag tgt gca gtt gga gac	1749
Phe Ser Ala Glu Lys Gln Trp Asn Thr Arg Glu Cys Ala Val Gly Asp	
529 534 539 544	
agc cag gga cca cat gta cac ggc ctg gta cgc ttt gac aag gac ttt	1797
Ser Gln Gly Pro His Val His Gly Leu Val Arg Phe Asp Lys Asp Phe	
545 550 555 560	
gga tct tac tct gag tat gag aga aag cac tgg gaa gtt tca atg cca	1845
Gly Ser Tyr Ser Glu Tyr Glu Arg Lys His Trp Glu Val Ser Met Pro	
561 566 571 576	
gac aca gct tca gaa tgt gac tcc tta aat tct tcc att gga agg aaa	1893
Asp Thr Ala Ser Glu Cys Asp Ser Leu Asn Ser Ser Ile Gly Arg Lys	
577 582 587 592	
cag tct cct cct tta agc ctc gag ata tac caa aca tta tct ccg cga	1941
Gln Ser Pro Pro Leu Ser Leu Glu Ile Tyr Gln Thr Leu Ser Pro Arg	
593 598 603 608	
aag ata tca aga gat gag gtg tcc cta gag gat tcc tcc cga ggg gat	1989
Lys Ile Ser Arg Asp Glu Val Ser Leu Glu Asp Ser Ser Arg Gly Asp	
609 614 619 624	
tcg cct gta act gtg gat gtg tct tgg ggt tct ccc gac tgt gta ggt	2037
Ser Pro Val Thr Val Asp Val Ser Trp Gly Ser Pro Asp Cys Val Gly	
625 630 635 640	
ctg aca gaa act aag agt atg atc ttc agt cct gca agc aaa gtg tac	2085
Leu Thr Glu Thr Lys Ser Met Ile Phe Ser Pro Ala Ser Lys Val Tyr	
641 646 651 656	
aat ggc att ttg gag aaa tcc tgt agc atg aac cag ctt tcc agt ggc	2133
Asn Gly Ile Leu Glu Lys Ser Cys Ser Met Asn Gln Leu Ser Ser Gly	
657 662 667 672	
atc ccg gtg cct aaa cct cgc cac aca tca tgt tcc tca gct ggc aac	2181
Ile Pro Val Pro Lys Pro Arg His Thr Ser Cys Ser Ser Ala Gly Asn	
673 678 683 688	
gac agt aaa cca gtt cag gaa gcc cca agt gtt gcc aga ata agc agc	2229

Asp	Ser	Lys	Pro	Val	Gln	Glu	Ala	Pro	Ser	Val	Ala	Arg	Ile	Ser	Ser	
689					694					699					704	
atc cca cat gac ctt tgt cat aat gga gag aaa agc aaa aag cca tca																2277
Ile	Pro	His	Asp	Leu	Cys	His	Asn	Gly	Glu	Lys	Ser	Lys	Lys	Pro	Ser	
705					710					715					720	
aaa atc aaa agc ctt ttt aag aag aaa tct aag tga actg gctgacttga																2327
Lys	Ile	Lys	Ser	Leu	Phe	Lys	Lys	Lys	Ser	Lys	*					
721					726					731						
tggaatcatg ttcaagtggc atctgtaaac tattatcccc caccctccac tccccacctt																2387
ttttttgggt taatttttagg aatgtaactc cattgggggt ttccaggccg gatgccatag																2447
tggaacatcc cagaagggca actgtctact gtctgcttat ttaagtgact atatataatc																2507
aattcatcaa gccagttatt actgaaaaat cattgaaatg agacagttta cagtcatttc																2567
tgcctattta tttctgcttt gttctcagt atgtatatgc aacattttgt tgaaagccac																2627
gatggactta caagctttaa tggactcgta agccagcatg ggcttgcaaa aatttcttgt																2687
ttaccagagc atcttcttat ctttocacag agctatttac atcctggact atataactta																2747
aaagaagtaa aacgtaattg cactactgtt ttccagactg gaaaaaaaa aaaaatctct																2807
gcaagtgaaa ctgtatagag tttataaaat gactatggat aggggactgt tttcactttt																2867
agatcaaaat gggtttttaa gtagaaccta gggtttctaa ttgacttgat ttctggaaat																2927
gaaaacccgc gcttttatta tgggaagctt cttgaactgc atttactatt gtgaagtttc																2987
aagtcccgct gtaaagatca tgttgttttg ttttcccag ggctttccct gtgatttact																3047
gcattgcagg ctgtatgata aaacccccat aatttaaaga gagaaggctc ttgattcctt																3107
atgcaagtgg aaaagttgaa acttgattga aggacttaaa acattcccac cottaagccg																3167
aggtgggggg atatggggat tcaggcagtt gtttaccgcc tttgaataac tgcaaaggat																3227
ttacggtttg tgaaaaatgt gtactgtgga aaagataata aattgaagcc cttaaaaaaa																3287
aaaaaa																3292

<210> 166
<211> 2306
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(2232)

<400> 166

atg ctc cac ttt aac cga tgt cat cat ctg aaa aag ata aca cag aaa	48
Met Leu His Phe Asn Arg Cys His His Leu Lys Lys Ile Thr Gln Lys	
1 5 10	
tgt ttt tct agt ata cat gtt aaa acg gat aaa cat gca cag cga ttt	96
Cys Phe Ser Ser Ile His Val Lys Thr Asp Lys His Ala Gln Arg Phe	
17 22 27 32	
ctt tca aga acc ttt gca ctt gcg gaa ttg agg aag tca tgg tat tca	144
Leu Ser Arg Thr Phe Ala Leu Ala Glu Leu Arg Lys Ser Trp Tyr Ser	
33 38 43 48	
acc cac tct ctt gtt gga gac aaa aat att atc ctg atg gga cct cct	192
Thr His Ser Leu Val Gly Asp Lys Asn Ile Ile Leu Met Gly Pro Pro	
49 54 59 64	
ggg gct ggg aaa aca aca gta ggc aga ata ata ggt cag aaa cta ggt	240
Gly Ala Gly Lys Thr Thr Val Gly Arg Ile Ile Gly Gln Lys Leu Gly	
65 70 75 80	
tgt tgt gtc ata gat gtg gat gat gat atc ctt gaa aaa acc tgg aat	288
Cys Cys Val Ile Asp Val Asp Asp Asp Ile Leu Glu Lys Thr Trp Asn	
81 86 91 96	
atg agt gtg tct gaa aaa tta cag gat gtt ggt aat gag caa ttt tta	336
Met Ser Val Ser Glu Lys Leu Gln Asp Val Gly Asn Glu Gln Phe Leu	
97 102 107 112	
gaa gag gaa gga aaa gct gtg tta aac ttc tct gca tct gga agt gtg	384
Glu Glu Glu Gly Lys Ala Val Leu Asn Phe Ser Ala Ser Gly Ser Val	
113 118 123 128	
att tcc ctt act ggg tcc aat cca atg cat gat gct agc atg tgg cat	432
Ile Ser Leu Thr Gly Ser Asn Pro Met His Asp Ala Ser Met Trp His	
129 134 139 144	
ctg aag aaa aat gga ata att gta tac ctg gat gta cct cta cta aat	480
Leu Lys Lys Asn Gly Ile Ile Val Tyr Leu Asp Val Pro Leu Leu Asn	
145 150 155 160	
cta att tgt cgt cta aaa tta atg aag aca gat agg att gta ggt cag	528
Leu Ile Cys Arg Leu Lys Leu Met Lys Thr Asp Arg Ile Val Gly Gln	
161 166 171 176	
aat tct gga aca tct atg aaa gac tta ctt aaa ttt aga aga cag tat	576
Asn Ser Gly Thr Ser Met Lys Asp Leu Leu Lys Phe Arg Arg Gln Tyr	
177 182 187 192	
tat aag aag tgg tat gat gct cgt gtt ttc tgt gaa agt ggg gct tcc	624
Tyr Lys Lys Trp Tyr Asp Ala Arg Val Phe Cys Glu Ser Gly Ala Ser	
193 198 203 208	
cca gag gag gta gct gac aaa gtg ctg aat gca att aaa aga tac caa	672
Pro Glu Glu Val Ala Asp Lys Val Leu Asn Ala Ile Lys Arg Tyr Gln	
209 214 219 224	

gat gtg gac tcg gaa aca ttc att tca aca aga cac gtt tgg cct gaa	720
Asp Val Asp Ser Glu Thr Phe Ile Ser Thr Arg His Val Trp Pro Glu	
225 230 235 240	
gac tgt gaa cag aag gtt tca gca aaa ttc ttt agt gaa gct gta att	768
Asp Cys Glu Gln Lys Val Ser Ala Lys Phe Phe Ser Glu Ala Val Ile	
241 246 251 256	
gag ggg ttg gct tct gat ggt ggc ctc ttt gtt cct gca aag gag ttt	816
Glu Gly Leu Ala Ser Asp Gly Gly Leu Phe Val Pro Ala Lys Glu Phe	
257 262 267 272	
cca aaa tta agc tgc ggg gag tgg aaa agc cta gta gga gca acc tac	864
Pro Lys Leu Ser Cys Gly Glu Trp Lys Ser Leu Val Gly Ala Thr Tyr	
273 278 283 288	
gta gaa aga gca cag ata ctg ttg gaa aga tgt atc cat cct gca gac	912
Val Glu Arg Ala Gln Ile Leu Leu Glu Arg Cys Ile His Pro Ala Asp	
289 294 299 304	
ata cct gct gcc agg ttg gga gaa atg att gaa act gct tat ggg gaa	960
Ile Pro Ala Ala Arg Leu Gly Glu Met Ile Glu Thr Ala Tyr Gly Glu	
305 310 315 320	
aac ttt gcc tgc tca aaa att gct cct gtc agg cac ctt tca ggc aac	1008
Asn Phe Ala Cys Ser Lys Ile Ala Pro Val Arg His Leu Ser Gly Asn	
321 326 331 336	
cag ttc atc ctg gag ttg ttt cat gga cca aca gga tca ttt aaa gat	1056
Gln Phe Ile Leu Glu Leu Phe His Gly Pro Thr Gly Ser Phe Lys Asp	
337 342 347 352	
ttg tct tta cag ctt atg cct cat att ttt gca cac tgt atc cca cca	1104
Leu Ser Leu Gln Leu Met Pro His Ile Phe Ala His Cys Ile Pro Pro	
353 358 363 368	
agt tgc aat tat atg ata ctt gta gct act tca gga gac aca ggg agt	1152
Ser Cys Asn Tyr Met Ile Leu Val Ala Thr Ser Gly Asp Thr Gly Ser	
369 374 379 384	
gca gtc tta aat ggt ttt agt cgt cta aat aag aat gat aag caa agg	1200
Ala Val Leu Asn Gly Phe Ser Arg Leu Asn Lys Asn Asp Lys Gln Arg	
385 390 395 400	
ata gct gtg gtt gca ttt ttt cct gag aat gga gta agt gat ttt caa	1248
Ile Ala Val Val Ala Phe Phe Pro Glu Asn Gly Val Ser Asp Phe Gln	
401 406 411 416	
aaa gca caa ata att ggc agt cag aga gaa aat gga tgg gca gtg ggt	1296
Lys Ala Gln Ile Ile Gly Ser Gln Arg Glu Asn Gly Trp Ala Val Gly	
417 422 427 432	
gtt gag tca gat ttt gat ttt tgc cag aca gct ata aaa aga att ttt	1344
Val Glu Ser Asp Phe Asp Phe Cys Gln Thr Ala Ile Lys Arg Ile Phe	
433 438 443 448	
aat gat tct gat ttt act ggc ttt ctt act gtg gaa tat gga aca atc	1392

673	678	683	688	
tca agt cag ctc tat ttg ctg ggt tca tac aat gca tta cct cca ctg				2112
Ser Ser Gln Leu Tyr Leu Leu Gly Ser Tyr Asn Ala Leu Pro Pro Leu				
689	694	699	704	
cat gag gct tta tta gag aga aca aaa cag caa gag aag atg gag tac				2160
His Glu Ala Leu Leu Glu Arg Thr Lys Gln Gln Glu Lys Met Glu Tyr				
705	710	715	720	
cag gtc tgt gca gct gat atg aat gtc ttg aag agt cat gtg gaa caa				2208
Gln Val Cys Ala Ala Asp Met Asn Val Leu Lys Ser His Val Glu Gln				
721	726	731	736	
ctt gtc caa aat caa ttc ata tga aagctttcag agtaaatttt tttttctagc				2262
Leu Val Gln Asn Gln Phe Ile *				
737	742			
tataagcatg caataataaa tctcaaacac tgaaaaaaaaaaaa				2306

<210> 167
 <211> 3454
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (340)..(2055)

<400> 167

atttggccct cgaggccaag aattcggcac gaggagctgg ctcagggcgt ccgctaggct	60
cggacgacct gctgagcctc ccaaaccgct tccataaggc tttgcctttc caacttcagc	120
tacagtgtta gctaagtttg gaaagaagga aaaaagaaaa tccctggggc ccttttcttt	180
tggtcctttgc caaagtcgtc gttgtagtct ttttgcccaa ggctgttggtg ttttttagagg	240
tgctatctcc agttccttgc actcctgtta acaagcacct cagcgagagc agcagcagcg	300
atagcagccg cagaagagcc agcgggggtcg cctagtgtc atg acc agg gcg gga	354
Met Thr Arg Ala Gly	
1	
gat cac aac cgc cag aga gga tgc tgt gga tcc ttg gcc gac tac ctg	402
Asp His Asn Arg Gln Arg Gly Cys Cys Gly Ser Leu Ala Asp Tyr Leu	
6 11 16 21	
acc tct gca aaa ttc ctt ctc tac ctt ggt cat tct ctc tct act tgg	450
Thr Ser Ala Lys Phe Leu Leu Tyr Leu Gly His Ser Leu Ser Thr Trp	
22 27 32 37	
gga gat cgg atg tgg cac ttt gcg gtg tct gtg ttt ctg gta gag ctc	498
Gly Asp Arg Met Trp His Phe Ala Val Ser Val Phe Leu Val Glu Leu	

38	43	48	53	
tat gga aac agc ctc ctt ttg aca gca gtc tac ggg ctg gtg gtg gca				546
Tyr Gly Asn Ser Leu Leu Leu Thr Ala Val Tyr Gly Leu Val Val Ala				
54	59	64	69	
ggg tct gtt ctg gtc ctg gga gcc atc atc ggt gac tgg gtg gac aag				594
Gly Ser Val Leu Val Leu Gly Ala Ile Ile Gly Asp Trp Val Asp Lys				
70	75	80	85	
aat gct aga ctt aaa gtg gcc cag acc tcg ctg gtg gta cag aat gtt				642
Asn Ala Arg Leu Lys Val Ala Gln Thr Ser Leu Val Val Gln Asn Val				
86	91	96	101	
tca gtc atc ctg tgt gga atc atc ctg atg atg gtt ttc tta cat aaa				690
Ser Val Ile Leu Cys Gly Ile Ile Leu Met Met Val Phe Leu His Lys				
102	107	112	117	
cat gag ctt ctg acc atg tac cat gga tgg gtt ctc act tcc tgc tat				738
His Glu Leu Leu Thr Met Tyr His Gly Trp Val Leu Thr Ser Cys Tyr				
118	123	128	133	
atc ctg atc atc act att gca aat att gca aat ttg gcc agt act gct				786
Ile Leu Ile Ile Thr Ile Ala Asn Ile Ala Asn Leu Ala Ser Thr Ala				
134	139	144	149	
act gca atc aca atc caa agg gat tgg att gtt gtt gtt gca gga gaa				834
Thr Ala Ile Thr Ile Gln Arg Asp Trp Ile Val Val Val Ala Gly Glu				
150	155	160	165	
gac aga agc aaa cta gca aat atg aat gcc aca ata cga agg att gac				882
Asp Arg Ser Lys Leu Ala Asn Met Asn Ala Thr Ile Arg Arg Ile Asp				
166	171	176	181	
cag tta acc aac atc tta gcc ccc atg gct gtt ggc cag att atg aca				930
Gln Leu Thr Asn Ile Leu Ala Pro Met Ala Val Gly Gln Ile Met Thr				
182	187	192	197	
ttt ggc tcc cca gtc atc ggc tgt ggc ttt att tcg gga tgg aac ttg				978
Phe Gly Ser Pro Val Ile Gly Cys Gly Phe Ile Ser Gly Trp Asn Leu				
198	203	208	213	
gta tcc atg tgc gtg gag tac gtt ctg ctc tgg aag gtt tac cag aaa				1026
Val Ser Met Cys Val Glu Tyr Val Leu Leu Trp Lys Val Tyr Gln Lys				
214	219	224	229	
acc cca gct cta gct gtg aaa gct ggt ctt aaa gaa gag gaa act gaa				1074
Thr Pro Ala Leu Ala Val Lys Ala Gly Leu Lys Glu Glu Glu Thr Glu				
230	235	240	245	
ttg aaa cag ctg aat tta cac aaa gat act gag cca aaa ccc ctg gag				1122
Leu Lys Gln Leu Asn Leu His Lys Asp Thr Glu Pro Lys Pro Leu Glu				
246	251	256	261	
gga act cat cta atg ggt gtg aaa gac tct aac atc cat gag ott gaa				1170
Gly Thr His Leu Met Gly Val Lys Asp Ser Asn Ile His Glu Leu Glu				
262	267	272	277	

cat gag caa gag cct act tgt gcc tcc cag atg gct gag ccc ttc cgt	1218
His Glu Gln Glu Pro Thr Cys Ala Ser Gln Met Ala Glu Pro Phe Arg	
278 283 288 293	
acc ttc cga gat gga tgg gtc tcc tac tac aac cag cct gtg ttt ctg	1266
Thr Phe Arg Asp Gly Trp Val Ser Tyr Tyr Asn Gln Pro Val Phe Leu	
294 299 304 309	
gct ggc atg ggt ctt gct ttc ctt tat atg act gtc ctg ggc ttt gac	1314
Ala Gly Met Gly Leu Ala Phe Leu Tyr Met Thr Val Leu Gly Phe Asp	
310 315 320 325	
tgc atc acc aca ggg tac gcc tac act cag gga ctg agt ggt tcc atc	1362
Cys Ile Thr Thr Gly Tyr Ala Tyr Thr Gln Gly Leu Ser Gly Ser Ile	
326 331 336 341	
ctc agt att ttg atg gga gca tca gct ata act gga ata atg gga act	1410
Leu Ser Ile Leu Met Gly Ala Ser Ala Ile Thr Gly Ile Met Gly Thr	
342 347 352 357	
gta gct ttt act tgg cta cgt cga aaa tgt ggt ttg gtt cgg aca ggt	1458
Val Ala Phe Thr Trp Leu Arg Arg Lys Cys Gly Leu Val Arg Thr Gly	
358 363 368 373	
ctg atc tca gga ttg gca cag ctt tcc tgt ttg atc ttg tgt gtg atc	1506
Leu Ile Ser Gly Leu Ala Gln Leu Ser Cys Leu Ile Leu Cys Val Ile	
374 379 384 389	
tct gta ttc atg cct gga agc ccc ctg gac ttg tcc gtt tct cct ttt	1554
Ser Val Phe Met Pro Gly Ser Pro Leu Asp Leu Ser Val Ser Pro Phe	
390 395 400 405	
gaa gat atc cga tca agg ttc att caa gga gag tca att aca cct acc	1602
Glu Asp Ile Arg Ser Arg Phe Ile Gln Gly Glu Ser Ile Thr Pro Thr	
406 411 416 421	
aag ata cct gaa att aca act gaa ata tac atg tct aat ggg tct aat	1650
Lys Ile Pro Glu Ile Thr Thr Glu Ile Tyr Met Ser Asn Gly Ser Asn	
422 427 432 437	
tct gct aat att gtc ccg gag aca agt cct gaa tct gtg ccc ata atc	1698
Ser Ala Asn Ile Val Pro Glu Thr Ser Pro Glu Ser Val Pro Ile Ile	
438 443 448 453	
tct gtc agt ctg ctg ttt gca ggc gtc att gct gct aga atc ggt ctt	1746
Ser Val Ser Leu Leu Phe Ala Gly Val Ile Ala Ala Arg Ile Gly Leu	
454 459 464 469	
tgg tcc ttt gat tta act gtg aca cag ttg ctg caa gaa aat gta att	1794
Trp Ser Phe Asp Leu Thr Val Thr Gln Leu Leu Gln Glu Asn Val Ile	
470 475 480 485	
gaa tct gaa aga ggc att ata aat ggt gta cag aac tcc atg aac tat	1842
Glu Ser Glu Arg Gly Ile Ile Asn Gly Val Gln Asn Ser Met Asn Tyr	
486 491 496 501	

ctt ctt gat ctt ctg cat ttc atc atg gtc atc ctg gct cca aat cct	1890
Leu Leu Asp Leu Leu His Phe Ile Met Val Ile Leu Ala Pro Asn Pro	
502 507 512 517	
gaa gct ttt ggc ttg ctc gta ttg att tca gtc tcc ttt gtg gca atg	1938
Glu Ala Phe Gly Leu Leu Val Leu Ile Ser Val Ser Phe Val Ala Met	
518 523 528 533	
ggc cac att atg tat ttc cga ttt gcc caa aat act ctg gga aac aag	1986
Gly His Ile Met Tyr Phe Arg Phe Ala Gln Asn Thr Leu Gly Asn Lys	
534 539 544 549	
ctc ttt gct tgc ggt cct gat gca aaa gaa gtt agg aag gaa aat caa	2034
Leu Phe Ala Cys Gly Pro Asp Ala Lys Glu Val Arg Lys Glu Asn Gln	
550 555 560 565	
gca aat aca tct gtt gtt tga ga cagtttaact gttgctatcc tgttactaga	2087
Ala Asn Thr Ser Val Val *	
566 571	
ttatatagag cacatgtgct tattttgtac tgcagaattc caataaatgg ctgggtgttt	2147
tgctctgttt ttaccacagc tgtgccttga gaactaaaag ctgttttagga aacctaagtc	2207
agcagaaatt aactgattaa tttcccttat gttgaggeat ggaaaaaaaaa ttggaaaaga	2267
aaaactcagt ttaaatacgg agactataat gataacactg aattccccta tttctcatga	2327
gtagatacaa tcttacgtaa aagagtgggt agtcacgtga attcagttat catttgacag	2387
attcttatct gtactagaat tcagatatgt cagttttctg caaaactcac tcttgttcaa	2447
gactagctaa tttatTTTTT tgcactcttag ttatttttaa aaacaaattc ttcaagtatg	2507
aagactaaat tttgataact aatattatcc ttattgatcc tattgatctt aagggtattta	2567
catgtatgtg gaaaaacaaa acacttaact agaattctct aataagggtt atgggttagc	2627
ttaaagagca cctttgtatt tttattatca gatggggcaa catattgtat gaagcatatg	2687
tagcacttca cagcatgggt atcatgtaag ctgcaggtag aagcaaagct gtaaagtaga	2747
tttatcacac aatgactgca tacagacttc aaatatgtca atagtttggt catagaacct	2807
agaagccaaa agccacacag aagggaaga atcccaattt aactcatgtt atcatcatta	2867
gtgatctgtg ttgtagaaca tgagggtgta agccttcagc ctggcaagtt acatgtagaa	2927
agccacact tgtgaagggt ttgttttaca aatcacttga tttaacacac tcaggtagaa	2987
tatttttatt tttactgttt tataccaga agttatttct acattgttct acagcaagaa	3047
tattcataaa agtatccctt tcaaatgcct ttgagaagaa tagaagaaaa aaagtttgta	3107
tatatttttaa aaaattgttt taaaagtcag tttgcaacat gtctgtacca agatggtact	3167
ttgccttaac cgttttatatg cactttcatg gagactgcaa tacgttgcta tgagcacttt	3227

ctttatcctt ggagtttaat cctttgcttc atctttctac agtatgacat aatgatttgc 3287
 tatgttgtaa aatctttgta aaaaatttct atataaaaaat attttgaaaa tctcaaaaaa 3347
 aagtcgacgc ggccgcgaat tcggatcctc gagagatctc tttttttggg tttggtgggg 3407
 tatcttcac atcgaataga tagttatata catcagcctg tctaatag 3454

<210> 168
 <211> 1197
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (96)..(548)

<400> 168

atggagatag ggcccggaat tgcgggcgtc actctgctcc tgcgacctag ccaggcgtga 60
 gggagtgaca gcagcgcatc cgcgggacga gagcgc atg agt gag aac gcc gca 113
 Met Ser Glu Asn Ala Ala
 1
 cca ggt ctg atc tca gag ctg aag ctg gct gtg ccc tgg ggc cac atc 161
 Pro Gly Leu Ile Ser Glu Leu Lys Leu Ala Val Pro Trp Gly His Ile
 7 12 17 22
 gca gcc aaa gcc tgg ggc tcc ctg cag ggc cct cca gtt ctc tgc ctg 209
 Ala Ala Lys Ala Trp Gly Ser Leu Gln Gly Pro Pro Val Leu Cys Leu
 23 28 33 38
 cac ggc tgg ctg gac aat gcc aac tcc ttc gac aga ctc atc cct ctt 257
 His Gly Trp Leu Asp Asn Ala Asn Ser Phe Asp Arg Leu Ile Pro Leu
 39 44 49 54
 ctc ccg caa gac ttt tat tac gtt gcc atg gat ttc gga ggt cat ggg 305
 Leu Pro Gln Asp Phe Tyr Tyr Val Ala Met Asp Phe Gly Gly His Gly
 55 60 65 70
 ctc tcg tcc cat tac agc cca ggt gtc cca tat tac ctc cag act ttt 353
 Leu Ser Ser His Tyr Ser Pro Gly Val Pro Tyr Tyr Leu Gln Thr Phe
 71 76 81 86
 gtg agt gag atc cga aga gtt gtg gca ggt aag aaa cag agt gtg tat 401
 Val Ser Glu Ile Arg Arg Val Val Ala Gly Lys Lys Gln Ser Val Tyr
 87 92 97 102
 ttt cgg cgg tgt ggg ggg tgc tct agg gca ccc cct ctt atc act gga 449
 Phe Arg Arg Cys Gly Gly Cys Ser Arg Ala Pro Pro Leu Ile Thr Gly
 103 108 113 118
 ggc ggg gta gga tcc agg aag cag cgc tgg cct gag agt ggg gcc tgg 497

cgg ccg gtg tca ctc aca ggc ctc act ctg gtt gta gta gcc gct cag	399
Arg Pro Val Ser Leu Thr Gly Leu Thr Leu Val Val Val Ala Ala Gln	
10 15 20 25	
ggt ccg cag gtt cac tcg gta aaa ctg tgc ttt ggc ctt ggc ggt ccc	447
Gly Pro Gln Val His Ser Val Lys Leu Cys Phe Gly Leu Gly Gly Pro	
26 31 36 41	
tgt ctc ctc ttc cca ata ttc cgg ccc ctc ctg ctc cat cca cgg cgc	495
Cys Leu Leu Phe Pro Ile Phe Arg Pro Leu Leu Leu His Pro Arg Arg	
42 47 52 57	
ccg cgg ctc cat cct ggg act cgt ggc gtc gct gtc gag ccg cac gca	543
Pro Arg Leu His Pro Gly Thr Arg Gly Val Ala Val Glu Pro His Ala	
58 63 68 73	
ctg cgt gtc gtc cac gtc gcc cac gga gag gaa gcg ggg atc cgc gcg	591
Leu Arg Val Val His Val Ala His Gly Glu Glu Ala Gly Ile Arg Ala	
74 79 84 89	
gcc ggg ccg gga cat ggt ggt gtg gaa ata cct caa gga gta agc ctg	639
Ala Gly Pro Gly His Gly Gly Val Glu Ile Pro Gln Gly Val Ser Leu	
90 95 100 105	
gga gca agg agg ggg ctg aga ccc tcc cga ccc tcc tcc cgg cac cgc	687
Gly Ala Arg Arg Gly Leu Arg Pro Ser Arg Pro Ser Ser Arg His Arg	
106 111 116 121	
aac cgg gtt cct gcg ccc ccg ccg ggc agg ccc cta gct act ccc cac	735
Asn Arg Val Pro Ala Pro Pro Pro Gly Arg Pro Leu Ala Thr Pro His	
122 127 132 137	
aga cgc cgt ttc cct ccc gac ccc gca ctc acc tgc cca ggt ctg ggt	783
Arg Arg Arg Phe Pro Pro Asp Pro Ala Leu Thr Cys Pro Gly Leu Gly	
138 143 148 153	
cag gac cag ggc ccc cga gag cag cag aag cag ggt tcg ggg cgc cat	831
Gln Asp Gln Gly Pro Arg Glu Gln Gln Lys Gln Gly Ser Gly Arg His	
154 159 164 169	
gac acc atc ctc ggc gac tgg gaa gaa tcg gag tcc cgg tgg gtg cgt	879
Asp Thr Ile Leu Gly Asp Trp Glu Glu Ser Glu Ser Arg Trp Val Arg	
170 175 180 185	
ggg aac ttt aga acc ggg acc gcg gct aca ttg att ggc ttc tct aga	927
Gly Asn Phe Arg Thr Gly Thr Ala Ala Thr Leu Ile Gly Phe Ser Arg	
186 191 196 201	
aac ccg aca ctc aat ggg agt gag aac tgg ggc agc ccg gtg agt acc	975
Asn Pro Thr Leu Asn Gly Ser Glu Asn Trp Gly Ser Pro Val Ser Thr	
202 207 212 217	
cag gaa gaa gga ccc gac aca ggt tgg gag agg gag aag aga aac cct	1023
Gln Glu Glu Gly Pro Asp Thr Gly Trp Glu Arg Glu Lys Arg Asn Pro	
218 223 228 233	

gca aag atg ggg aat gcc cag cgc tgg gcc tcc cca atc cat aca ccg	1071
Ala Lys Met Gly Asn Ala Gln Arg Trp Ala Ser Pro Ile His Thr Pro	
234 239 244 249	
cct ttg ggg cct gag atc ctg aga gcc acg cct gag gcc ctg gga ctt	1119
Pro Leu Gly Pro Glu Ile Leu Arg Ala Thr Pro Glu Ala Leu Gly Leu	
250 255 260 265	
cgc cct gac ccc gct act tct gtg cca agc gct ctg tct caa tgt ttc	1167
Arg Pro Asp Pro Ala Thr Ser Val Pro Ser Ala Leu Ser Gln Cys Phe	
266 271 276 281	
cct gag tct tgg ccc agg agc tgt ctg aga aac cag gga gaa acc ctc	1215
Pro Glu Ser Trp Pro Arg Ser Cys Leu Arg Asn Gln Gly Glu Thr Leu	
282 287 292 297	
gga atg ggc ccc gtc cct ctc tct tca ctt tgc atc acg gaa tcc ccg	1263
Gly Met Gly Pro Val Pro Leu Ser Ser Leu Cys Ile Thr Glu Ser Pro	
298 303 308 313	
tcc cag aac tgg act ccc tgc ctc cta ctc ctt acc tgt ccc cgt gga	1311
Ser Gln Asn Trp Thr Pro Cys Leu Leu Leu Leu Thr Cys Pro Arg Gly	
314 319 324 329	
ctc ttc tag aagaaaa atcacccag ggagcttggt gccagagagt gagcttgccc	1367
Leu Phe *	
330	
tggaatgga ggtgtagaga cagggttttt tgttgttggt gtttgtttgt tttttaaatc	1427
tggaaggtt gtgcctgagt gcatgagata gaatagagac cagtttgctt tttgtttatt	1487
aactacagtg ggtagcagaa tcttggtaac tcctaataat caggaatcta atcggccaaa	1547
aatgtgactt tgggtcccttg acatataaat gtgtctaaaa gcattacaac aggaatcaca	1607
aagctcctaa gtttcacttt ccagacaaat gtatctgtga ctcccgcttg tagtatttta	1667
aatttacctt cattccatag ccctgagttt ctgtgtgagt ccaggacatc tcctaataca	1727
aggtagccac tgtgttacta tatgttgtaa ccaggagcca gtacggactt tattcatctc	1787
acagtggcaa gcactcaatg cagtcacaat gcccctcacc agtgctcatg cactgcctgt	1847
tttttaggaag tatccacttc taagtgttgt gtatatattta tatgaacact tagtattttt	1907
taaacctgat taacataaaa aaattagttt ttaggcagac ccacataagg tattaagggc	1967
caactgcaaa gatcacccctg caaggctctg tagattgatg tattaataata tataaaacaa	2027
tgtgtttaaa aaaaaaaaaa	2046

<210> 170
<211> 2062

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (785)..(994)

<400> 170

```
tgcacgaccg gtccggaatt cccgggtcga cccacgcgtc cgggcggaac ggggaatagtt      60
ttcaacgtct atttcattcc ctgcttcaga ggacctcttt aatctttgat tttggtccct      120
gtttctaaga aaagcaactg aaaaggctcg aataccgccc ctgagaaaaa aggagcagcg      180
ctaaataatc gagaaaatgc ctctcttga aacggatata gagatggaaa caagatataa      240
gaaggattga gaatcatata atacaggagc ttaaacaact atgcgcgatg ataaagaggg      300
tactattaga gcgcttgaa aataccagga agttgagaga gttaacagaa gggcgcacgc      360
tggattggcc acaaaatcga attactgaag taagtgcaaa acgacaaatt gtcacagaat      420
acagagaaaa ggggaaaaga aattaagagg agaaaaagag agatctagag ggccgggtcca      480
ggagatacaa tctatgcata ataggaatac ctgaaactga ggacagagca agtggagctg      540
aaacaataaa ggatctactt gaaaaaattt tccagaattg aagaacgaac tagatctaca      600
aatggaaaag gctcatagga taccttttaa gtttaatgaa aagaaagcag catctagaca      660
tatccgggtg acgtttttga atttcaaaga cgaaacattt tacaagcatc cagtcagaga      720
aagcagggtta cttacaaagg ggcaaaagtc aggctgacct cagatttttc tcttgcaatt      780
ctaa atg cca gaa gac agt gga aca ata tct aga gtg tta agg gaa aat      829
Met Pro Glu Asp Ser Gly Thr Ile Ser Arg Val Leu Arg Glu Asn
      1          5          10

aat ttt gag cca aga att ata tac tct gcc aag tta tca ttt ctt tac      877
Asn Phe Glu Pro Arg Ile Ile Tyr Ser Ala Lys Leu Ser Phe Leu Tyr
      16          21          26          31

aaa gga aac tgg aag aca ttc tta gat ata cag ggg tta gga aag tat      925
Lys Gly Asn Trp Lys Thr Phe Leu Asp Ile Gln Gly Leu Gly Lys Tyr
      32          37          42          47

atc aac caa gaa ctt tcc ctg aaa att ttg ctg aag gat tta ctg cag      973
Ile Asn Gln Glu Leu Ser Leu Lys Ile Leu Leu Lys Asp Leu Leu Gln
      48          53          58          63

cta aca gag aac ctg aat taa aa taagaatagg gaggcaattg tatgaaagaa      1026
Leu Thr Glu Asn Leu Asn *
      64          69

ctgatgggtat gcattaaaac tagttaagga gcattaagtt taaattgtta tgtatagggc      1086
attaaaaacta aatacaaaaa tagaaacata agctgggtgt aaaatttcag tttacgttta      1146
```


aactggaagg gcataccaca tgttcaatat attggacaaa tactgtttta tttttagcat	1206
gtagtattgt agatacaaat acgcatgttc ttaagctaaa cctaagtaaa agggccttgt	1266
cactgtagat ttgacaaata acattctaaa tgtcaaatct gacaattgga aaacagtaca	1326
gttttatttc ccttattttt aagtatagca ggaaaaaaat aacaagtttg tccatgttac	1386
tactgatact gtaaagaaac ttccaaatca ctggtttggg agggggtgga tacatcctca	1446
ttttctgtac atgatgcacg gggaaaaaca gtagttactg catcatatag ttccaagtaa	1506
atcatatagt tccaagtaaa ttgacatgg aaataagtgt taactacaaa aatagaatat	1566
atacattcca atgtttggaa aagaagtggg aaaaagaaaa atagcaaaaa gacactaaaa	1626
ttagcaaaaa gtagattgac agtacagatg acctataaac tggttaaata gccctattac	1686
aattgaaatt gggtaaaaa tcaatctcta acctgagata catttgtata aaacaaatga	1746
tcaaagagtt taaagataat ggaaactata aatcatagaa atagcaacat ttttcttaaa	1806
atctaaacat aagacatttt atgtaaaaca tacaatatag gatgtaacat ttaacaaact	1866
atatggtaaa taatatgaca ttaatatata aaatatatgt tccagatcct gatgtgggtg	1926
atagttttac ttatgtacat cgatatacat ctatttaaaa acatgtacat ttaaattgtt	1986
gcattttatg tatttaaaat ttattgagta atccttctgt atgtattatt aaagagaata	2046
tagcaaaaaa aaaaaa	2062

<210> 171

<211> 2809

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1936)..(2364)

<400> 171

tcccgggtcg acccacgogt ccgctgggga cgctagggtc cggaacctga cctgagctgg	60
ggcctgtgct tccagcgggt ggtggggggc ctggtgtgct ggcacaaagt aagccgacta	120
cctcggaaca ggcttaggga caagagacca gcagcctgaa ctggctgggg catccggaag	180
gcttagatct tgtggccaag agttcagacc gtggcgaagt ggagagtga atgcagttgg	240
atggcggtga ctgcgtggtc ctgcaaccct ggttcagtc tggcaagcat tgtagacctg	300
gctgctgaag actgacgggg cccaggggtc gctgccccca ccgccatcac cacctcgga	360

cccagggtaa	cgctgtcagt	ctttggacca	acctcgctgt	gcctaacaag	aattccagaa	420								
gtcaccatc	cgaaggcac	tggcccatga	cactctccac	ttccaatctt	aaatctttta	480								
cttcatacct	tgtctcagat	ctctcctggt	accccttccc	cacgccctta	gataatccat	540								
ctcaattcct	catgctaatt	gaggagctat	ggctgcaagg	caccttccag	gatttcacac	600								
ctacacaaat	ctcctttttc	tccttttgcc	ttctctgctt	atgggatatt	ctgagtcccc	660								
acccccaatc	actgacagct	gggccccctt	catcagcctc	acacaccacg	tattaagtca	720								
gtcacaaatc	ccctctcct	ctaactgctg	gatttgtctt	tctacacaca	cccaatgatt	780								
cacggctctt	cgggtgacc	tacttacatg	gacacagtcc	aacgtgagct	tacacatttc	840								
ttacttggct	ataccattct	tggctgattc	attcctgaaa	cgggttcata	acctggaaac	900								
tcagctaaac	acctttcctt	caaactcagc	tctctcagca	tggtttcagg	tagggctggt	960								
gccctccttc	acctaatagc	ttctggacta	acatccatac	aaaccaaacac	agcatcatct	1020								
aaaccaccaa	tatgggggta	ccatttctac	tcaaacttcc	ttcatatccc	cacccccctt	1080								
atgtctcagc	cgaacctacc	ctaattcagc	ccacgccaca	atggtgggac	aggttccccca	1140								
gtccctatgt	ggtcttattt	ttacccttgc	actccctgta	gaccatcaat	tctacaccct	1200								
aattacaaaa	tcatatccac	ctctgcctgg	cagaagggtg	tatgcttttc	tggctcgcct	1260								
accatccaca	catccctaca	cctcaccacc	ggatcctctt	ttctttcctt	ccatccaatt	1320								
cctggcttcc	cgcgtgccaa	ctctgctctc	tatgtctcca	gtttaaaggt	gccccctgga	1380								
aaaaatgtaa	caattccctc	acctgtgact	ggtacctgac	agccaccaca	ccggggcagc	1440								
aatgggtaac	ggttgacaaa	gacaatttct	ttctctctcc	aaaaccaaac	agccttcctc	1500								
aactccctag	ccaagactcc	ctatcaggcc	cttacagggtg	cgcctctggc	tggcagttac	1560								
ccaatttggg	aaaacgaaaa	taccctatca	tggctacctc	ccttcacctc	caacttctgc	1620								
ctgtccaccc	ccagtctctt	ctttttgtgt	gatacaaact	gatatctttg	cctaccagcc	1680								
aactggtcag	gaacttgac	cctgggtctt	cagggtccaa	ccatcaacat	cctacccccct	1740								
aaccaaacta	ttctaatttc	tgtagaagcc	tttatctcct	cttcacccat	aagaaataaa	1800								
tgggctctac	atctcatcac	cctgctaaca	ggattaggca	tcactgctgc	acttggcact	1860								
ggaatagcag	gcataaccac	ctcaatcacc	tcataccaaa	cactattcac	aaccttttct	1920								
aacaccgtag	aagat	atg	cac	act	tcc	att	acc	agt	ctc	caa	cga	caa	tta	1971
		Met	His	Thr	Ser	Ile	Thr	Ser	Leu	Gln	Arg	Gln	Leu	
		1					5						10	

gac ttc ctc gtg gga gtc atc ctt caa aac tgg aga gtc ctg gac ctc	2019
Asp Phe Leu Val Gly Val Ile Leu Gln Asn Trp Arg Val Leu Asp Leu	
13 18 23 28	
cta acc act gag aaa ggg ggt acc tgc ata tac ctc cag gaa gaa tgc	2067
Leu Thr Thr Glu Lys Gly Gly Thr Cys Ile Tyr Leu Gln Glu Glu Cys	
29 34 39 44	
tgt ttc tgt gtt aat gaa tct ggc att gtt cat atc gca gtt cgt agg	2115
Cys Phe Cys Val Asn Glu Ser Gly Ile Val His Ile Ala Val Arg Arg	
45 50 55 60	
ctt cat gac agg gct gca gag ctt aga cat caa gtc gct gac tcc tgg	2163
Leu His Asp Arg Ala Ala Glu Leu Arg His Gln Val Ala Asp Ser Trp	
61 66 71 76	
tgg caa gga tca tcc ctt cta aga tgg ata ccc tgg gtt gcc ccc ttc	2211
Trp Gln Gly Ser Ser Leu Leu Arg Trp Ile Pro Trp Val Ala Pro Phe	
77 82 87 92	
cta gga ccc ctg atc ttc ctc ttc ctg tta cta atg att ggg cca tgc	2259
Leu Gly Pro Leu Ile Phe Leu Phe Leu Leu Leu Met Ile Gly Pro Cys	
93 98 103 108	
ata ttt aac ctt gta tcc cgc ttc att tcc caa agg ctg aat tgt ttt	2307
Ile Phe Asn Leu Val Ser Arg Phe Ile Ser Gln Arg Leu Asn Cys Phe	
109 114 119 124	
atc cag gca agc atg caa aaa cac att gat aat ata ttt cac ctt tgc	2355
Ile Gln Ala Ser Met Gln Lys His Ile Asp Asn Ile Phe His Leu Cys	
125 130 135 140	
cac gtc taa taccaga gcctacgagg aaaccattcg gaagctccag aacccaggcc	2411
His Val *	
141	
ctaatacaca cgccttatc cagcaggaag cagccagatg atcaacgacg ccccttttcc	2471
tttttataact aaagtaagaa ataagaatgt tagcccaaac tgcactatgt tgcagacccc	2531
taccatttta caaactggtc agagtggaaa attccaccag ggctgagct gtgagaaaca	2591
tctgtcagg caggtcccag gcctaacccc tggctgcact aaattccttc attatcagca	2651
gccaacacaca ccgccccac cccattttca caacaatccc agacctctcc tgcccgggac	2711
tgtaactggt ccagcctgta agcgggaagg gggctctggc actagctggt accccctctc	2771
cgcagggtctt tctcccaata aatctgtgtt gccattga	2809

<210> 172
 <211> 1882
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (181)..(1194)

<400> 172

```

ctccggcagg cgtgatgtat ataactatct attcgatgat gaagataccc caccaaaccc      60

aaaaaaagag atctctcgag gatccgaatt cgcggccgcg tcgactttta aaagaataga      120

tagacgttga attattgata ttctccctct ctctctctag gataactaca gagagctaca      180

atg gaa aag tcc tgg atg ctg tgg aac ttt gtt gaa aga tgg cta ata      228
Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp Leu Ile
  1             5             10             15

gcc ttg gct tca tgg tct tgg gct ctc tgc cgt att tct ctt tta cct      276
Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu Leu Pro
 17             22             27             32

tta ata gtg act ttt cat ctg tat gga ggc att atc tta ctt ttg tta      324
Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu Leu Leu
 33             38             43             48

ata ttc ata tca ata gca ggt att ctg tat aaa ttc cag gat gta ttg      372
Ile Phe Ile Ser Ile Ala Gly Ile Leu Tyr Lys Phe Gln Asp Val Leu
 49             54             59             64

ctt tat ttt cca gaa cag cca tcc tct tca cgt ctt tat gtt ccc atg      420
Leu Tyr Phe Pro Glu Gln Pro Ser Ser Ser Arg Leu Tyr Val Pro Met
 65             70             75             80

ccc act ggc att cca cat gaa aac att ttc atc aga acc aaa gat gga      468
Pro Thr Gly Ile Pro His Glu Asn Ile Phe Ile Arg Thr Lys Asp Gly
 81             86             91             96

ata cgt ctg aat ctt att ttg ata cga tac act gga gac aat tca ccc      516
Ile Arg Leu Asn Leu Ile Leu Ile Arg Tyr Thr Gly Asp Asn Ser Pro
 97             102            107            112

tat tcc cca act ata att tat ttt cat ggg aat gca ggc aac ata ggt      564
Tyr Ser Pro Thr Ile Ile Tyr Phe His Gly Asn Ala Gly Asn Ile Gly
113             118            123            128

cac agg ttg cca aat gca tta ctt atg ttg gtt aac ctc aaa gtt aac      612
His Arg Leu Pro Asn Ala Leu Leu Met Leu Val Asn Leu Lys Val Asn
129             134            139            144

ctt ttg ctg gtt gat tat cga gga tat gga aaa agt gaa gga gaa gca      660
Leu Leu Leu Val Asp Tyr Arg Gly Tyr Gly Lys Ser Glu Gly Glu Ala
145             150            155            160

agt gaa gaa gga ctc tac tta gat tct gaa gct gtg tta gac tac gtg      708
Ser Glu Glu Gly Leu Tyr Leu Asp Ser Glu Ala Val Leu Asp Tyr Val
161             166            171            176

atg act agc cct gac ctt gat aaa aca aaa att ttt ctt ttt ggc cgt      756

```

Met Thr Ser Pro Asp Leu Asp Lys Thr Lys Ile Phe Leu Phe Gly Arg	
177 182 187 192	
tcc ttg ggt gga gca gtg gct att cat ttg gct tct gaa aat tca cat	804
Ser Leu Gly Gly Ala Val Ala Ile His Leu Ala Ser Glu Asn Ser His	
193 198 203 208	
agg att tca gcc att atg gtg gag aac aca ttt tta agc ata cca cat	852
Arg Ile Ser Ala Ile Met Val Glu Asn Thr Phe Leu Ser Ile Pro His	
209 214 219 224	
atg gcc agc act tta ttt tca ttc ttt ccg atg cgt tac ctt cct tta	900
Met Ala Ser Thr Leu Phe Ser Phe Phe Pro Met Arg Tyr Leu Pro Leu	
225 230 235 240	
tgg tgc tac aaa aat aaa ttt ttg tcc tac aga aaa atc tct cag tgt	948
Trp Cys Tyr Lys Asn Lys Phe Leu Ser Tyr Arg Lys Ile Ser Gln Cys	
241 246 251 256	
aga atg cct tca ctt ttc atc tct gga ctc tca gat caa tta att cca	996
Arg Met Pro Ser Leu Phe Ile Ser Gly Leu Ser Asp Gln Leu Ile Pro	
257 262 267 272	
cca gta atg atg aaa caa ctt tat gaa ctc tcc cca tct cgg act aag	1044
Pro Val Met Met Lys Gln Leu Tyr Glu Leu Ser Pro Ser Arg Thr Lys	
273 278 283 288	
aga tta gcc att ttt cca gat ggg act cac aat gac aca tgg cag tgc	1092
Arg Leu Ala Ile Phe Pro Asp Gly Thr His Asn Asp Thr Trp Gln Cys	
289 294 299 304	
caa ggc tat ttc act gca ctt gaa cag ttc atc aaa gaa gtc gta aag	1140
Gln Gly Tyr Phe Thr Ala Leu Glu Gln Phe Ile Lys Glu Val Val Lys	
305 310 315 320	
agc cat tct cct gaa gaa atg gca aaa act tca tct aat gta aca att	1188
Ser His Ser Pro Glu Glu Met Ala Lys Thr Ser Ser Asn Val Thr Ile	
321 326 331 336	
ata taa tgtttccctt tttgattatt gcattgtatt ttaatttgtg cagaatgata	1244
Ile *	
337	
aagaatgttc cttttagaag tgtgttatgt ctgtacctgt ctgaagagtg acattaaact	1304
ttgaaaggac ttactgctc ctttacgata ttccaaatag ttttttacat tggaaaaact	1364
aattottggg attotttcat acattttcat caaaactttc agtgtgatta tgtattcata	1424
tottcagttt aatatgtcag tataatagat attgttcaaa agtttcttgt tgctaaagt	1484
gtgtaatctg ttacacagat gaatagctag atgtggaaag agatatgtaa acaagaaacc	1544
tttgggtatt gttttottaag taaatattgg gacaatcatg gtaagcaaac ttagttctgt	1604
aactgcattt ttcaccttaa aagttaaatg aaatgcatga tggatatttta ttcottgaat	1664

aac att tca gta atg cag agt cct ctt gtt gga gtt aca tct act cct	559
Asn Ile Ser Val Met Gln Ser Pro Leu Val Gly Val Thr Ser Thr Pro	
115 120 125 130	
gga aca ggg caa agt atg ttt agt cca gca agt atc ggt cag cca cga	607
Gly Thr Gly Gln Ser Met Phe Ser Pro Ala Ser Ile Gly Gln Pro Arg	
131 136 141 146	
aag acg aca tta tct cct gcc cag ttg gat cct ttt tat act caa gga	655
Lys Thr Thr Leu Ser Pro Ala Gln Leu Asp Pro Phe Tyr Thr Gln Gly	
147 152 157 162	
gat tct ttg act tca gaa gat cac ctc gat gac tct tgg gtg act gta	703
Asp Ser Leu Thr Ser Glu Asp His Leu Asp Asp Ser Trp Val Thr Val	
163 168 173 178	
ttt ggg ttt cct caa gca tct gct tcc tac ata tta cta caa ttt gca	751
Phe Gly Phe Pro Gln Ala Ser Ala Ser Tyr Ile Leu Leu Gln Phe Ala	
179 184 189 194	
cag tat ggg gga ata tct tat aac atg tgg atg tct aat aca gga aat	799
Gln Tyr Gly Gly Ile Ser Tyr Asn Met Trp Met Ser Asn Thr Gly Asn	
195 200 205 210	
tgg atg cat att cgt tat caa tct aaa ctg cag gct cgg aaa gcc tta	847
Trp Met His Ile Arg Tyr Gln Ser Lys Leu Gln Ala Arg Lys Ala Leu	
211 216 221 226	
agc aaa gat ggg agg att ttt gga gaa tcc atc atg att ggt gta aaa	895
Ser Lys Asp Gly Arg Ile Phe Gly Glu Ser Ile Met Ile Gly Val Lys	
227 232 237 242	
cca tgt att gac aaa agt gtt atg gaa agc agt gac aga tgt gct tta	943
Pro Cys Ile Asp Lys Ser Val Met Glu Ser Ser Asp Arg Cys Ala Leu	
243 248 253 258	
tca tct cca tct tta gcc ttt aca cca cca atc aaa act cta ggt aca	991
Ser Ser Pro Ser Leu Ala Phe Thr Pro Pro Ile Lys Thr Leu Gly Thr	
259 264 269 274	
cca aca caa cct gga agt act cct agg att tct acc atg aga cct ctt	1039
Pro Thr Gln Pro Gly Ser Thr Pro Arg Ile Ser Thr Met Arg Pro Leu	
275 280 285 290	
gct aca gca tac aaa gcc tct act agt gat tat cag gtt att tct gac	1087
Ala Thr Ala Tyr Lys Ala Ser Thr Ser Asp Tyr Gln Val Ile Ser Asp	
291 296 301 306	
aga caa acg cca aaa aaa gat gaa agt ctt gta tcc aaa gca atg gag	1135
Arg Gln Thr Pro Lys Lys Asp Glu Ser Leu Val Ser Lys Ala Met Glu	
307 312 317 322	
tac atg ttt ggc tgg tag tagaac accaagaagg aggttgctac actaaaacag	1189
Tyr Met Phe Gly Trp *	
323 328	
agtttagcaga gtgctgctgg ttcttccggt tagttatata actgttctctg cagtattgga	1249

```

tagctatctc atacttcttt tagaaagaag cctttttcat taaggataca acctatttgt 1309
agctcgcaact ttaaaagatg cttgagatac attttaaaga aaactaaaaa tccctgtaaa 1369
taggatttttg tgctttctgt aacagtgcac gcttcagcac agaaaactca gcattgatta 1429
ttgtaaatta aataactgaa attgtggtga gacgtcatag tcttcatgag aacgtggggg 1489
tgaatttcat gaaggggaac tatagttatt tctaccgaca caaatattat aattagcaat 1549
ttgaattatg gtcttttaaat ttagatagta ttaatatatt taattatcct tgtttgata 1609
tgtcctgtca cagagtgtcc tcttggtgta ttctaaaacg agcattcttt taaaaaacct 1669
aaagtttctt gataataaac attgtcaatg ataaaaaaaa aaaa 1713

```

```

<210> 174
<211> 4069
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (771)..(2894)

<220>
<221> misc_feature
<222> (1)...(4069)
<223> n = a,t,c or g

```

```

<400> 174
tttttgggaa tttttggacg cggttaacca aattttctcca aaogggaaca cggttttgtc 60
cctgttttttc gcggttttta atcaggcacc cactatgagg ggaaattttg ccctcggagg 120
ccaagaatt ggggcaggag ggtttttttt aaaatagtgc ccagtccaag tgggaaatgg 180
agaatgaaac aaataaatct gtaaactggt tgtgatcaat tagttgtaaa caccgccgca 240
ctcagaccag ccatgggttt gccctttgat aaggggcaaag acacattttt cgtggtatca 300
gggaaaaaga tttaaaaaga caaggcaaat ttaagtaggc tcatggcttt tccagttggg 360
ttggaaagtt cctctccgat gactgttata ttctcaaaga aatatgagga gaggggcagg 420
gcatggtggc tcacatccgt aatcctagca aatcatatgt gcctacagcc aacgccttct 480
tcgctcactg gccaaactgga aacttcagtc ccccatgcc tccgcctct caccagggg 540
ccaataggaa tgatcagagg ttcgcaactt agtgtcatca agcatagtaa ttgcaattgg 600
ctattggagc tgtcgatcgt gaagtatgcg gggccgtcca gcttgctat ataagacgag 660

```


gacannacgc cgccgcctgt gtcacccgcc attttgtgag aagcaagggtg gcctccacgt	720
ttcctgagcg tcttcttcgc ttttgctcg accgcccctt gaccacagac atg tct	776
	Met Ser
	1
egg gat cgg ttc cgg agt cgt ggc ggt ggc ggt ggt ggc ttc cac agg	824
Arg Asp Arg Phe Arg Ser Arg Gly Gly Gly Gly Gly Gly Phe His Arg	
3 8 13 18	
cgt gga gga ggc ggc ggc cgc ggc ggc ctc cac gac ttc cgt tct ccg	872
Arg Gly Gly Gly Gly Gly Arg Gly Gly Leu His Asp Phe Arg Ser Pro	
19 24 29 34	
ccg ccc ggc atg ggc ctc aat cag aat cgc ggc ccc atg ggt cct ggc	920
Pro Pro Gly Met Gly Leu Asn Gln Asn Arg Gly Pro Met Gly Pro Gly	
35 40 45 50	
ccg ggc cag agc ggc cct aag cct cgc atc ccg cca ccg cct cca cac	968
Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro Pro His	
51 56 61 66	
caa cag cag caa cag cca cca ccg cag cag cca ccg ccg cag cag ccg	1016
Gln Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln Gln Pro	
67 72 77 82	
cca ccg cat cag ccg ccg ccg cat cca cag ccg cat cag cag cag cag	1064
Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln Gln Gln	
83 88 93 98	
ccg ccg cca ccg ccg cag gac tct tcc aag ccc gtc gtt gct cag gga	1112
Pro Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala Gln Gly	
99 104 109 114	
ccc ggc ccc gct ccc gga gta ggc agc gca cca cca gcc tcc agc tcg	1160
Pro Gly Pro Ala Pro Gly Val Gly Ser Ala Pro Pro Ala Ser Ser Ser	
115 120 125 130	
gcc ccg ccc gcc act cca cca acc tcg ggg gcc ccg cca ggg tcc ggg	1208
Ala Pro Pro Ala Thr Pro Pro Thr Ser Gly Ala Pro Pro Gly Ser Gly	
131 136 141 146	
cca ggc ccg act ccg acc ccg ccg cct gca gtc acc tcg gcc cct ccc	1256
Pro Gly Pro Thr Pro Thr Pro Pro Pro Ala Val Thr Ser Ala Pro Pro	
147 152 157 162	
ggg gcg ccg cca ccc acc ccg cca agc agc ggg gtc cct acc aca cct	1304
Gly Ala Pro Pro Pro Thr Pro Pro Ser Ser Gly Val Pro Thr Thr Pro	
163 168 173 178	
cct cag gcc gga ggc ccg ccg cct ccg ccc gcg gca gtc ccg ggc ccg	1352
Pro Gln Ala Gly Gly Pro Pro Pro Pro Pro Ala Ala Val Pro Gly Pro	
179 184 189 194	
ggg cca ggg cct aag cag ggc cca ggt ccg ggt ggt ccc aaa ggc ggc	1400
Gly Pro Gly Pro Lys Gln Gly Pro Gly Pro Gly Gly Pro Lys Gly Gly	
195 200 205 210	

aaa atg cct ggc ggg ccg aag cca ggt ggc ggc ccg ggc cta agt acg	1448
Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Gly Pro Gly Leu Ser Thr	
211 216 221 226	
cct ggc ggc cac ccc aag ccg ccg cat cga ggc ggc ggg gag ccc cgc	1496
Pro Gly Gly His Pro Lys Pro Pro His Arg Gly Gly Gly Glu Pro Arg	
227 232 237 242	
ggg ggc cgc cag cac cac ccg ccc tac cac cag cag cat cac cag ggg	1544
Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His Gln Gly	
243 248 253 258	
ccc ccg ccc ggc ggg ccc ggc ggc cgc agc gag gag aag atc tcg gac	1592
Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile Ser Asp	
259 264 269 274	
tcg gag ggg ttt aaa gcc aat ttg tct ctc ttg agg agg cct gga gag	1640
Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro Gly Glu	
275 280 285 290	
aaa act tac aca cag cga tgt cgg ttg ttt gtt ggg aat cta cct gct	1688
Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu Pro Ala	
291 296 301 306	
gat atc acg gag gat gaa ttc aaa aga cta ttt gct aaa tat gga gaa	1736
Asp Ile Thr Glu Asp Glu Phe Lys Arg Leu Phe Ala Lys Tyr Gly Glu	
307 312 317 322	
cca gga gaa gtt ttt atc aac aaa ggc aaa gga ttc gga ttt att aag	1784
Pro Gly Glu Val Phe Ile Asn Lys Gly Lys Gly Phe Gly Phe Ile Lys	
323 328 333 338	
ctt gaa tct aga gct ttg gct gaa att gcc aaa gcc gaa ctg gat gat	1832
Leu Glu Ser Arg Ala Leu Ala Glu Ile Ala Lys Ala Glu Leu Asp Asp	
339 344 349 354	
aca ccc atg aga ggt aga cag ctt cga gtt cgc ttt gcc aca cat gct	1880
Thr Pro Met Arg Gly Arg Gln Leu Arg Val Arg Phe Ala Thr His Ala	
355 360 365 370	
gct gcc ctt tct gtt cgt aat ctt tca cct tat gtt tcc aat gaa ctg	1928
Ala Ala Leu Ser Val Arg Asn Leu Ser Pro Tyr Val Ser Asn Glu Leu	
371 376 381 386	
ttg gaa gaa gcc ttt agc caa ttt ggt cct att gaa agg gct gtt gta	1976
Leu Glu Glu Ala Phe Ser Gln Phe Gly Pro Ile Glu Arg Ala Val Val	
387 392 397 402	
ata gtg gat gat cgt gga aga tct aca ggg aaa ggc att gtt gaa ttt	2024
Ile Val Asp Asp Arg Gly Arg Ser Thr Gly Lys Gly Ile Val Glu Phe	
403 408 413 418	
gct tct aag cca gca gca aga aag gca ttt gaa cga tgc agt gaa ggt	2072
Ala Ser Lys Pro Ala Ala Arg Lys Ala Phe Glu Arg Cys Ser Glu Gly	
419 424 429 434	

gtt ttc tta ctg acg aca act cct cgt cca gtc att gtg gaa cca ctt	2120
Val Phe Leu Leu Thr Thr Thr Pro Arg Pro Val Ile Val Glu Pro Leu	
435 440 445 450	
gaa caa cta gat gat gaa gat ggt ctt cct gaa aaa ctt gcc cag aag	2168
Glu Gln Leu Asp Asp Glu Asp Gly Leu Pro Glu Lys Leu Ala Gln Lys	
451 456 461 466	
aat cca atg tat caa aag gag aga gaa acc cct cct cgt ttt gcc cag	2216
Asn Pro Met Tyr Gln Lys Glu Arg Glu Thr Pro Pro Arg Phe Ala Gln	
467 472 477 482	
cat ggc acg ttt gag tac gaa tat tct cag cga tgg aag tct ttg gat	2264
His Gly Thr Phe Glu Tyr Glu Tyr Ser Gln Arg Trp Lys Ser Leu Asp	
483 488 493 498	
gaa atg gaa aaa cag caa agg gaa caa gtt gaa aaa aac atg aaa gat	2312
Glu Met Glu Lys Gln Gln Arg Glu Gln Val Glu Lys Asn Met Lys Asp	
499 504 509 514	
gca aaa gac aaa ttg gaa agt gaa atg gaa gat gcc tat cat gaa cat	2360
Ala Lys Asp Lys Leu Glu Ser Glu Met Glu Asp Ala Tyr His Glu His	
515 520 525 530	
cag gca aat ctt ttg cgc caa gat ctg atg aga cga cag gaa gaa tta	2408
Gln Ala Asn Leu Leu Arg Gln Asp Leu Met Arg Arg Gln Glu Glu Leu	
531 536 541 546	
aga cgc atg gaa gaa ctt cac aat caa gaa atg cag aaa cgt aaa gaa	2456
Arg Arg Met Glu Glu Leu His Asn Gln Glu Met Gln Lys Arg Lys Glu	
547 552 557 562	
atg caa ttg agg caa gag gag gaa cga cgt aga aga gag gaa gag atg	2504
Met Gln Leu Arg Gln Glu Glu Glu Arg Arg Arg Glu Glu Glu Met	
563 568 573 578	
atg att cgt caa cgt gag atg gaa gaa caa atg agg cgc caa aga gag	2552
Met Ile Arg Gln Arg Glu Met Glu Glu Gln Met Arg Arg Gln Arg Glu	
579 584 589 594	
gaa agt tac agc cga atg ggc tac atg gat cca cgg gaa aga gac atg	2600
Glu Ser Tyr Ser Arg Met Gly Tyr Met Asp Pro Arg Glu Arg Asp Met	
595 600 605 610	
cga atg ggt ggc gga gga gca atg aac atg gga gat ccc tat ggt tca	2648
Arg Met Gly Gly Gly Gly Ala Met Asn Met Gly Asp Pro Tyr Gly Ser	
611 616 621 626	
gga ggc cag aaa ttt cca cct cta gga ggt ggt ggt ggc ata ggt tat	2696
Gly Gly Gln Lys Phe Pro Pro Leu Gly Gly Gly Gly Gly Ile Gly Tyr	
627 632 637 642	
gaa gct aat cct ggc gtt cca cca gca acc atg agt ggt tcc atg atg	2744
Glu Ala Asn Pro Gly Val Pro Pro Ala Thr Met Ser Gly Ser Met Met	
643 648 653 658	
gga agt gac atg cgt act gag cgc ttt ggg cag gga ggt gcg ggg cct	2792

<211> 1830
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (104)..(1000)

<400> 175

```
attgataacg gagatcgagc tcgctagcgt ttaaacttaa gcttggtacc gagctcggat      60

ccactagtcc agtgtggtgg aattcagaac acctcatgaa ata  atg aga aga gaa      115
                                   Met Arg Arg Glu
                                   1

agc aac aga tta tct gca cct tct tat ctt gcc aga agt cta gca gat      163
Ser Asn Arg Leu Ser Ala Pro Ser Tyr Leu Ala Arg Ser Leu Ala Asp
  5                      10                      15                      20

gtc cct aga gag tat ggt tct tct cag tca ttt gta acg gaa gtt agt      211
Val Pro Arg Glu Tyr Gly Ser Ser Gln Ser Phe Val Thr Glu Val Ser
  21                      26                      31                      36

ttt gct gtt gaa aat gga gac tct ggt tcc cga tat tat tat tca gac      259
Phe Ala Val Glu Asn Gly Asp Ser Gly Ser Arg Tyr Tyr Tyr Ser Asp
  37                      42                      47                      52

aat ttt ttt gat ggt cag aga aag cgg cca ctt gga gat cgt gca cat      307
Asn Phe Phe Asp Gly Gln Arg Lys Arg Pro Leu Gly Asp Arg Ala His
  53                      58                      63                      68

gaa gac tac aga tat tat gaa tac aac cat gat ctc ttc caa aga atg      355
Glu Asp Tyr Arg Tyr Tyr Glu Tyr Asn His Asp Leu Phe Gln Arg Met
  69                      74                      79                      84

cca cag aat cag ggg agg cat gct tca ggt att ggg aga gtt gct gct      403
Pro Gln Asn Gln Gly Arg His Ala Ser Gly Ile Gly Arg Val Ala Ala
  85                      90                      95                      100

aca tct tta gga aat ttg act aac cat ggt tct gaa gat tta ccc ctt      451
Thr Ser Leu Gly Asn Leu Thr Asn His Gly Ser Glu Asp Leu Pro Leu
  101                      106                      111                      116

cct cct ggc tgg tct gtg gac tgg aca atg aga ggg aga aaa tat tat      499
Pro Pro Gly Trp Ser Val Asp Trp Thr Met Arg Gly Arg Lys Tyr Tyr
  117                      122                      127                      132

ata gat cat aac aca aat aca act cac tgg agc cat cct ctt gag cga      547
Ile Asp His Asn Thr Asn Thr Thr His Trp Ser His Pro Leu Glu Arg
  133                      138                      143                      148

gaa gga ctt cct cct gga tgg gaa cga gtt gag tca tcc gaa ttt gga      595
Glu Gly Leu Pro Pro Gly Trp Glu Arg Val Glu Ser Ser Glu Phe Gly
  149                      154                      159                      164

acc tat tat gta gat cac aca aat aag aag gcc caa tac agg cat ccc      643
Thr Tyr Tyr Val Asp His Thr Asn Lys Lys Ala Gln Tyr Arg His Pro
```

165	170	175	180	
tgt gct cct agt gta	cct cgg tat gat caa cca cct cct gtc aca tac			691
Cys Ala Pro Ser Val	Pro Arg Tyr Asp Gln Pro Pro Pro Val Thr Tyr			
181	186	191	196	
cag cca cag caa act	gaa aga aat cag tcc ctt ctg gta cct gca aat			739
Gln Pro Gln Gln Thr	Glu Arg Asn Gln Ser Leu Leu Val Pro Ala Asn			
197	202	207	212	
cca tat cat act gca	gaa att cct gac tgg ctt cag gtt tac gca cga			787
Pro Tyr His Thr Ala	Glu Ile Pro Asp Trp Leu Gln Val Tyr Ala Arg			
213	218	223	228	
gcc cct gtg aaa tat	gac cac att ctg aag tgg gaa ctc ttc cag ctg			835
Ala Pro Val Lys Tyr	Asp His Ile Leu Lys Trp Glu Leu Phe Gln Leu			
229	234	239	244	
gct gac ctg gat aca	tac cag gga atg cta aag ttg ctc ttc atg aaa			883
Ala Asp Leu Asp Thr	Tyr Gln Gly Met Leu Lys Leu Leu Phe Met Lys			
245	250	255	260	
gaa ttg gag cag att	gtt aaa atg tat gaa gca tac aga caa gcc ctt			931
Glu Leu Glu Gln Ile	Val Lys Met Tyr Glu Ala Tyr Arg Gln Ala Leu			
261	266	271	276	
ctt aca gag ttg gaa	aac cga aag cag aga cag cag tgg tat gcc caa			979
Leu Thr Glu Leu Glu	Asn Arg Lys Gln Arg Gln Gln Trp Tyr Ala Gln			
277	282	287	292	
caa cat gga aaa aat	ttt tga gc tgatttttta aaaatttaag ttttgtaaga			1032
Gln His Gly Lys Asn	Phe *			
293	298			
gctttaaaat attttcacag	ataaaaaaatt gcaaacaagt actctgggta ataaatgctg			1092
cttcctttgt ggaaattata	aaattctaac tttacatgta ttttggttatt agaaattttc			1152
ttttattgga tgagaaaaat	tagtctatca ttttaagagc caatatggca aacactttca			1212
aatactgtat attaggaaac	tgttttggtta ttcttgatgg aaaaaaatgc agcggaaatg			1272
tcattatgaa cagatgttaa	ataggaaatt attacttggt aacttcttac agcagtagta			1332
ccttcttttaa aaaaaaaaaa	gaatctgogg tattttttta aaaaaaaagt ttactgctgt			1392
agtggtgaaat attgtctgga	aagggatggg ttaaatatcc ccatgatgta gttgaaatat			1452
aaaataggat ttggaacctt	attgtgataa atatttata atgatgtatg tttgtctccc			1512
ctctccaaag taaggaaccc	agctgggctg ggtggctcac tcctgtaatc ccagcatttt			1572
gggaggccga ggtgggtgga	ccgcttgagt ccacgagttt aagaccagcc tgggcaacat			1632
ggtgaagccc tacaaaaaat	acaaaaaaat tagccgggta tgatggtgtg tgcctctagt			1692
cccagctact tgggaggctg	aggctcagagg atggcttgag cccaagaggc agagggttgca			1752

gggtcaagat cgcaccactt gcactgcagc ctgagagaga gagagccaga ccttgtctca 1812

aaaaataaaa aaaaaaaa 1830

<210> 176
<211> 2430
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1668)

<400> 176

atg ggc ccc ccc atc gag acc cta gtc cgt gtg gtg gaa ttc ccg ctg 48
Met Gly Pro Pro Ile Glu Thr Leu Val Arg Val Val Glu Phe Pro Leu
1 5 10

tgt cct gga ggc ggc aaa gca caa ctt tcc tcc gct tct ctc ctc gga 96
Cys Pro Gly Gly Gly Lys Ala Gln Leu Ser Ser Ala Ser Leu Leu Gly
17 22 27 32

gcc ggg ctc ctg ctg cag ccc ccg acg cca cct ccg ctg ctg ctg ctg 144
Ala Gly Leu Leu Leu Gln Pro Pro Thr Pro Pro Pro Leu Leu Leu Leu
33 38 43 48

ctc ttc ccg ctg ctg ctc ttc tcc agg ctc tgt ggt gcc tta gct gga 192
Leu Phe Pro Leu Leu Leu Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly
49 54 59 64

cca att att gtg gag cca cat gtc aca gca gta tgg gga aag aat gtt 240
Pro Ile Ile Val Glu Pro His Val Thr Ala Val Trp Gly Lys Asn Val
65 70 75 80

tca tta aag tgt tta att gaa gta aat gaa acc ata aca cag att tca 288
Ser Leu Lys Cys Leu Ile Glu Val Asn Glu Thr Ile Thr Gln Ile Ser
81 86 91 96

tgg gag aag ata cat ggc aaa agt tca cag act gtt gca gtt cac cat 336
Trp Glu Lys Ile His Gly Lys Ser Ser Gln Thr Val Ala Val His His
97 102 107 112

ccc caa tat gga ttc tct gtt caa gga gaa tat cag gga aga gtc ttg 384
Pro Gln Tyr Gly Phe Ser Val Gln Gly Glu Tyr Gln Gly Arg Val Leu
113 118 123 128

ttt aaa aat tac tca ctt aat gat gca aca att act ctg cat aac ata 432
Phe Lys Asn Tyr Ser Leu Asn Asp Ala Thr Ile Thr Leu His Asn Ile
129 134 139 144

gga ttc tct gat tct gga aaa tac atc tgc aaa gct gtt aca ttc ccg 480
Gly Phe Ser Asp Ser Gly Lys Tyr Ile Cys Lys Ala Val Thr Phe Pro
145 150 155 160

ctt gga aat gcc cag tcc tct aca act gta act gtg tta gtt gaa ccc	528
Leu Gly Asn Ala Gln Ser Ser Thr Thr Val Thr Val Leu Val Glu Pro	
161 166 171 176	
act gtg agc ctg ata aaa ggg cca gat tct tta att gat gga gga aat	576
Thr Val Ser Leu Ile Lys Gly Pro Asp Ser Leu Ile Asp Gly Gly Asn	
177 182 187 192	
gaa aca gta gca gcc att tgc atc gca gcc act gga aaa ccc gtt gca	624
Glu Thr Val Ala Ala Ile Cys Ile Ala Ala Thr Gly Lys Pro Val Ala	
193 198 203 208	
cat att gac tgg gaa ggt gat ctt ggt gaa atg gaa tcc act aca act	672
His Ile Asp Trp Glu Gly Asp Leu Gly Glu Met Glu Ser Thr Thr Thr	
209 214 219 224	
tct ttt cca aat gaa acg gca acg att atc agc cag tac aag cta ttt	720
Ser Phe Pro Asn Glu Thr Ala Thr Ile Ile Ser Gln Tyr Lys Leu Phe	
225 230 235 240	
cca acc aga ttt gct aga gga agg cga att act tgt gtt gta aaa cat	768
Pro Thr Arg Phe Ala Arg Gly Arg Arg Ile Thr Cys Val Val Lys His	
241 246 251 256	
cca gcc ttg gaa aag gac atc cga tac tct ttc ata tta gac ata cag	816
Pro Ala Leu Glu Lys Asp Ile Arg Tyr Ser Phe Ile Leu Asp Ile Gln	
257 262 267 272	
tat gct cct gaa gtt tgc gta aca gga tat gat gga aat tgg ttt gta	864
Tyr Ala Pro Glu Val Ser Val Thr Gly Tyr Asp Gly Asn Trp Phe Val	
273 278 283 288	
gga aga aaa ggt gtt aat ctc aaa tgt aat gct gat gca aat cca cca	912
Gly Arg Lys Gly Val Asn Leu Lys Cys Asn Ala Asp Ala Asn Pro Pro	
289 294 299 304	
ccc ttc aaa tct gtg tgg agc agg ttg gat gga caa tgg cct gat ggt	960
Pro Phe Lys Ser Val Trp Ser Arg Leu Asp Gly Gln Trp Pro Asp Gly	
305 310 315 320	
tta ttg gct tca gac aat act ctt cat ttt gtc cat cca ttg act ttc	1008
Leu Leu Ala Ser Asp Asn Thr Leu His Phe Val His Pro Leu Thr Phe	
321 326 331 336	
aat tat tct ggt gtt tat atc tgt aaa gtg acc aat tcc ctt ggt caa	1056
Asn Tyr Ser Gly Val Tyr Ile Cys Lys Val Thr Asn Ser Leu Gly Gln	
337 342 347 352	
aga agt gac caa aaa gtc atc tac att tca gat cct cct act act acc	1104
Arg Ser Asp Gln Lys Val Ile Tyr Ile Ser Asp Pro Pro Thr Thr Thr	
353 358 363 368	
acc ctt cag cct aca att cag tgg cat ccc tca act gct gac atc gag	1152
Thr Leu Gln Pro Thr Ile Gln Trp His Pro Ser Thr Ala Asp Ile Glu	
369 374 379 384	

gat cta gca aca gaa cct aaa aaa ttg ccc ttc cca ttg tca act ttg	1200
Asp Leu Ala Thr Glu Pro Lys Lys Leu Pro Phe Pro Leu Ser Thr Leu	
385 390 395 400	
gca aca att aag gat gac aca att gcc acg atc att gct agt gta gtg	1248
Ala Thr Ile Lys Asp Asp Thr Ile Ala Thr Ile Ile Ala Ser Val Val	
401 406 411 416	
ggg ggt gct ctc ttc ata gta ctt gta agt gtt ttg gct gga ata ttc	1296
Gly Gly Ala Leu Phe Ile Val Leu Val Ser Val Leu Ala Gly Ile Phe	
417 422 427 432	
tgc tat agg aga aga cgg acg ttt cgt gga gac tac ttt gcc aag aac	1344
Cys Tyr Arg Arg Arg Arg Thr Phe Arg Gly Asp Tyr Phe Ala Lys Asn	
433 438 443 448	
tac att cca cca tca gat atg caa aaa gaa tca caa ata gat gtt ctt	1392
Tyr Ile Pro Pro Ser Asp Met Gln Lys Glu Ser Gln Ile Asp Val Leu	
449 454 459 464	
caa caa gat gag ctt gat tct tac cca gac agt gta aaa aaa gaa aaa	1440
Gln Gln Asp Glu Leu Asp Ser Tyr Pro Asp Ser Val Lys Lys Glu Lys	
465 470 475 480	
aaa aat cca gtg aac aat cta ata cgt aaa gac tat tta gaa gag cct	1488
Lys Asn Pro Val Asn Asn Leu Ile Arg Lys Asp Tyr Leu Glu Glu Pro	
481 486 491 496	
gaa aaa act cag tgg aac aat gta gaa aat ctc aat agg ttt gaa aga	1536
Glu Lys Thr Gln Trp Asn Asn Val Glu Asn Leu Asn Arg Phe Glu Arg	
497 502 507 512	
cca atg gat tat tat gaa gat cta aaa atg gga atg aag ttt gtc agt	1584
Pro Met Asp Tyr Tyr Glu Asp Leu Lys Met Gly Met Lys Phe Val Ser	
513 518 523 528	
gat gaa cat tat gat gaa aac gaa gat gac tta gtt tca cat gta gat	1632
Asp Glu His Tyr Asp Glu Asn Glu Asp Asp Leu Val Ser His Val Asp	
529 534 539 544	
ggg tcc gta att tcc agg agg gag tgg tat gtt tag caac cactgaatgt	1682
Gly Ser Val Ile Ser Arg Arg Glu Trp Tyr Val *	
545 550 555	
gacttaacta tgtacaatgt tcattcacac tagttgatca ttttcagatt gttcatactt	1742
tttcttgagg aagaataagc tttttcaagt tgattttcaa gcttactttt tatattctaa	1802
tctgacaaat gaaaatgtaa aatctgagtt cagtgtatct aagctgcttt acaatttttt	1862
ttcaatgctg tactactgtc tcaagattta aattttaatg cagagtactt tattggtgtg	1922
aggcacacag gtaagaagaa atgtcaacat taaatgtatg acttacttgg tacaaaaatt	1982
ttttaaaaaag ggaactacct tgacattgtg tattaaatgt ttacctaaga ctataatctc	2042
aagtatgatg tttgtttaac atatacctct caaaatttat caccactcaa tgacactgca	2102

tcaaaattga ctataaaact aattcaagaa atatttatat atatttttta atatacaaaa 2162
aatatttagc ctgatggaat ggctttcctt ttcaaacatt attttctaag tttctataca 2222
aatgaaatct ttacctctgc atattaatga gccttgccat aattactgta gagtggcttt 2282
tcaaagatat tttgttgac taaaactgtg gtagtaaact cagtgaacat gatgtgtgga 2342
agagcataat tagctggtca atatttttgt ccaaaatacc tgcaagagta ataaaataca 2402
tacctttcaa acatgaaaaa aaaaaaaa 2430

<210> 177
<211> 1670
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (278)..(658)

<400> 177
ctgcatgag gatgatgtat ataactatct attcgatgat gaagatacc caccaaaccc 60
aaaaaaagag atctctcgag gatccgaatt cgcggccgcg tcgacctagg gtgtgtgag 120
tgtaaattag tgcgatgagt aggggaaggg agcctactag ggtgtagaat aggaagtatg 180
tgctgcgtt caggcgttct ggctggttgc ctcacgggt gatgatagcc aagggtgggga 240
taagtgtggt tgcgaagtgg gctcgtgggt tggcagt atg aga gtt gta atg gcc 295
Met Arg Val Val Met Ala
1

cga ctg ttg agt gag ggg gag cag ggg atc cca acg gct tgc gct gcc 343
Arg Leu Leu Ser Glu Gly Glu Gln Gly Ile Pro Thr Ala Cys Ala Ala
7 12 17 22

ttt gcg cag cag ccg gcg ggc gag cca cgt cgc ggc ctg gct ggg gta 391
Phe Ala Gln Gln Pro Ala Gly Glu Pro Arg Arg Gly Leu Ala Gly Val
23 28 33 38

gga gag ggc ggt ccc cag tgc agt tgg gtg aac tac cgt tgc aca ctg 439
Gly Glu Gly Gly Pro Gln Cys Ser Trp Val Asn Tyr Arg Cys Thr Leu
39 44 49 54

gag ttt ctg gtg tct ttg ctt gga act gac cta gct cgt ggc agg ggg 487
Glu Phe Leu Val Ser Leu Leu Gly Thr Asp Leu Ala Arg Gly Arg Gly
55 60 65 70

aac tcg gct agc ggc ccc aca gcc cct gct gac tca aaa caa cta atg 535
Asn Ser Ala Ser Gly Pro Thr Ala Pro Ala Asp Ser Lys Gln Leu Met
71 76 81 86

aac tct gga agc cca gcc agg gac aat gca cct tca cag aga ttc tgc	583
Asn Ser Gly Ser Pro Ala Arg Asp Asn Ala Pro Ser Gln Arg Phe Cys	
87 92 97 102	
act aat ctg agt gaa ggt cta agg ttt gga atc tcc ccc tca tgg aga	631
Thr Asn Leu Ser Glu Gly Leu Arg Phe Gly Ile Ser Pro Ser Trp Arg	
103 108 113 118	
gaa gct ttg tat ggc tgt cat gct tag acagt gattcctgca acttgacctt	683
Glu Ala Leu Tyr Gly Cys His Ala *	
119 124	
caggctggga gaggtggaga gccatgcctg ttctccttcc ttgctatgga atttgctgac	743
acaatatctt ccgcctgggtg ctgggcatat cctaagaact tacaactttc ctgtattatc	803
ctgtgtgagc agctgtcacc ttattggggg aaaaatgcct gaaaattagg gggcacttca	863
agtagatagc ttctatcttc tatattattc ttactttaa aatgctttat tggaattatt	923
ttgataaaag caaataacttg tatataagac aaatatagga aatagaagct atctacttga	983
agtgccccct aattttcagg catttttccc ccaataagggt gacagctgct cacacaggat	1043
aatacaggaa agttgtaagt tottaggata tgcccagcac caggcggaag atattgtgtc	1103
agcaaattcc atagcaagga aggagaacag gcatggctct ccacctctcc cagcctgaag	1163
gtcaagttgc aggaatcact gtctaagcat gacagccata caaagcttct ctccatgagg	1223
gggagattcc aaaccttaga ccttcactca gattagtgc gaatctctgt gaagggtgcat	1283
tgtccctggc tgggcttcca gagttcattc ttactcaag gataacacgg cgatgaacgt	1343
cttacaactc agttgttttg agtcagcagg ggctgtgggg ccgctagccg agttccccct	1403
gccacgagct aggtcagttc caagcaaaga caccagaaac tccagtgtgc aacggtagtt	1463
cacccaactg cactgggggac cgccctctcc taccacagcc aggccgagac gtggccgccc	1523
gccggctgct gcgcaaaggc agcgcaagcc gttgggatcc cctgctcccc ctactcaac	1583
agtcggggcca ttacaactct catactgcca acccagagc ccactctcgt gccgctcgtg	1643
ccgaattctt ggccctcgagg gccaaat	1670

<210> 178
 <211> 1702
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (167)..(1093)

<400> 178

tatgatgacc gttgtaccgg tccggaattc ccgggtcgac ccacgcgtcc gcgggcccag	60
ccgcctccac ggcccgcgct cgtactggag cgaagagcgg cctcctgaag gaggggaagg	120
gacgtggggg cggccacggc aggattaacc tccatttcag ctaatc atg gga gag	175
Met Gly Glu	
1	
att aaa gtc tct cct gat tat aac tgg ttt aga ggt aca gtt ccc ctt	223
Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu	
4 9 14 19	
aaa aag att att gtg gat gat gat gac agt aag ata tgg tcg ctc tat	271
Lys Lys Ile Ile Val Asp Asp Asp Asp Ser Lys Ile Trp Ser Leu Tyr	
20 25 30 35	
gac gcg ggc ccc cga agt atc agg tgt cct ctc ata ttc ctg ccc cct	319
Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe Leu Pro Pro	
36 41 46 51	
gtc agt gga act gca gat gtc ttt ttc cgg cag att ttg gct ctg act	367
Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu Ala Leu Thr	
52 57 62 67	
gga tgg ggt tac cgg gtt atc gct ttg cag tat cca gtt tat tgg gac	415
Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val Tyr Trp Asp	
68 73 78 83	
cat ctc gag ttc tgt gat gga ttc aga aaa ctt tta gac cat tta caa	463
His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp His Leu Gln	
84 89 94 99	
ttg gat aaa gtt cat ctt ttt ggc gct tct ttg gga ggc ttt ttg gcc	511
Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly Phe Leu Ala	
100 105 110 115	
cag aaa ttt gct gaa tac act cac aaa tct cct aga gtc cat tcc cta	559
Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val His Ser Leu	
116 121 126 131	
atc ctc tgc aat tcc ttc agt gac acc tct atc ttc aac caa act tgg	607
Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn Gln Thr Trp	
132 137 142 147	
act gca aac agc ttt tgg ctg atg cct gca ttt atg ctc aaa aaa ata	655
Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu Lys Lys Ile	
148 153 158 163	
gtt ctt gga aat ttt tca tct ggc ccg gtg gac cct atg atg gct gat	703
Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met Met Ala Asp	
164 169 174 179	
gcc att gat ttc atg gta gac agg cta gaa agt ttg ggt cag agt gaa	751
Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly Gln Ser Glu	

180	185	190	195	
ctg gct tca aga ctt acc ttg aat tgt caa aat tct tat gtg gaa cct				799
Leu Ala Ser Arg Leu Thr Leu Asn Cys Gln Asn Ser Tyr Val Glu Pro				
196	201	206	211	
cat aaa att cgg gac ata cct gta act att atg gat gtg ttt gat cag				847
His Lys Ile Arg Asp Ile Pro Val Thr Ile Met Asp Val Phe Asp Gln				
212	217	222	227	
agt gcg ctt tca act gaa gct aaa gaa gaa atg tac aag ctg tat cct				895
Ser Ala Leu Ser Thr Glu Ala Lys Glu Glu Met Tyr Lys Leu Tyr Pro				
228	233	238	243	
aat gcc cga aga gct cat ctg aaa aca gga ggc aat ttc cca tac ctg				943
Asn Ala Arg Arg Ala His Leu Lys Thr Gly Gly Asn Phe Pro Tyr Leu				
244	249	254	259	
tgc aga agt gca gag gtc aat ctt tat gta cag ata cat ttg ctg caa				991
Cys Arg Ser Ala Glu Val Asn Leu Tyr Val Gln Ile His Leu Leu Gln				
260	265	270	275	
ttc cat gga acc aaa tac gcg gcc att gac cca tca atg gtc agt gcc				1039
Phe His Gly Thr Lys Tyr Ala Ala Ile Asp Pro Ser Met Val Ser Ala				
276	281	286	291	
gag gag ctt gag gtg cag aaa ggc agc ctt ggc atc agc cag gag gag				1087
Glu Glu Leu Glu Val Gln Lys Gly Ser Leu Gly Ile Ser Gln Glu Glu				
292	297	302	307	
cag tag tgtgtctctc gctgtcaatg atgagttgac ccggtgtgtt cttgtatagt				1143
Gln *				
308				
cagtggcattc agcaaccgctc agccggcctt ttccttcagg ttcgctcaggc tcaccggttc				1203
tcactgtgtc tgggaagtag gactgatggt catcttcattg acagggcgga tctccactaa				1263
gcctgtgttaa ctgttccttc tttgggtttc ttagcttttg aatttgaaga agtacttttg				1323
aagactccca ttttaagaac cgtgcaaatt ttgctaccaa aagtcttcac cactgtgttc				1383
ttaagtgaat gttaatttct gaggtttggg actttgtggt ggtttttttc ttcttttctt				1443
ttccattctt ctttctttct ttttatgttg tttgctgtaa atgctgcaca tccagattgc				1503
atatcaggac attggttatt ttatgctttc ttggatataa ccatgatcag agtgccatgg				1563
ccactacccc actgtttgct ctctgcaaa tcaactgctt ttaatttaca cttaaacaaa				1623
ttgttttgag tgtagctac tgcctttcta gatattagtc atttggaata aaaattcaat				1683
ttcaaaaaaa aaaaaaaa				1702

<210> 179
 <211> 2821
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (234)..(2492)

<400> 179

```

atttggccct cgaggccaag aattcggcac gaggcaaagg tttcaccctt cagttcagtc      60
cccaatccct gcttattatt tccctaacag aagaccatcc cccttgccac tccctggttt      120
ttcttctctg gcagcaatga agcagctgct gaccagctc tagttttcgg gaagtcagat      180
gaccttttcc ctcccgcggc tctctacctc tcgccgcccc tagggaggac acc   atg      236
                                   Met
                                   1

ggc cca ctg atg gtt ctt ttt tgc ctg ctg ttc ctg tac cca ggt ctg      284
Gly Pro Leu Met Val Leu Phe Cys Leu Leu Phe Leu Tyr Pro Gly Leu
  2              7              12              17

gca gac tcg gct ccc tcc tgc cct cag aac gtg aat atc tcg ggt ggc      332
Ala Asp Ser Ala Pro Ser Cys Pro Gln Asn Val Asn Ile Ser Gly Gly
  18              23              28              33

acc ttc acc ctc agc cat ggc tgg gct cct ggg agc ctt ctc acc tac      380
Thr Phe Thr Leu Ser His Gly Trp Ala Pro Gly Ser Leu Leu Thr Tyr
  34              39              44              49

tcc tgc ccc cag ggc ctg tac cca tcc cca gca tca cgg ctg tgc aag      428
Ser Cys Pro Gln Gly Leu Tyr Pro Ser Pro Ala Ser Arg Leu Cys Lys
  50              55              60              65

agc agc gga cag tgg cag acc cca gga gcc acc cgg tct ctg tct aag      476
Ser Ser Gly Gln Trp Gln Thr Pro Gly Ala Thr Arg Ser Leu Ser Lys
  66              71              76              81

gcg gtc tgc aaa cct gtg cgc tgt cca gcc cct gtc tcc ttt gag aat      524
Ala Val Cys Lys Pro Val Arg Cys Pro Ala Pro Val Ser Phe Glu Asn
  82              87              92              97

ggc att tat acc cca cgg ctg ggg tcc tat ccc gtg ggt ggc aat gtg      572
Gly Ile Tyr Thr Pro Arg Leu Gly Ser Tyr Pro Val Gly Gly Asn Val
  98              103              108              113

agc ttc gag tgt gag gat ggc ttc ata ttg cgg ggc tcg cct gtg cgt      620
Ser Phe Glu Cys Glu Asp Gly Phe Ile Leu Arg Gly Ser Pro Val Arg
  114              119              124              129

cag tgt cgc ccc aac ggc atg tgg gat gga gaa aca gct gtg tgt gat      668
Gln Cys Arg Pro Asn Gly Met Trp Asp Gly Glu Thr Ala Val Cys Asp
  130              135              140              145

aat ggg gct ggc cac tgc ccc aac cca ggc att tca ctg ggc gca gtg      716

```

Asn Gly Ala Gly His Cys Pro Asn Pro Gly Ile Ser Leu Gly Ala Val	
146 151 156 161	
cgg aca ggc ttc cgc ttt ggt cat ggg gac aag gtc cgc tat cgc tgc	764
Arg Thr Gly Phe Arg Phe Gly His Gly Asp Lys Val Arg Tyr Arg Cys	
162 167 172 177	
tcc tcg aat ctt gtg ctc acg ggg tct tcg gag cgg gag tgc cag ggc	812
Ser Ser Asn Leu Val Leu Thr Gly Ser Ser Glu Arg Glu Cys Gln Gly	
178 183 188 193	
aac ggg gtc tgg agt gga acg gag ccc atc tgc cgc caa ccc tac tct	860
Asn Gly Val Trp Ser Gly Thr Glu Pro Ile Cys Arg Gln Pro Tyr Ser	
194 199 204 209	
tat gac ttc cct gag gac gtg gcc cct gcc ctg ggc act tcc ttc tcc	908
Tyr Asp Phe Pro Glu Asp Val Ala Pro Ala Leu Gly Thr Ser Phe Ser	
210 215 220 225	
cac atg ctt ggg gcc acc aat ccc acc cag aag aca aag gaa agc ctg	956
His Met Leu Gly Ala Thr Asn Pro Thr Gln Lys Thr Lys Glu Ser Leu	
226 231 236 241	
ggc cgt aaa atc caa atc cag cgc tct ggt cat ctg aac ctc tac ctg	1004
Gly Arg Lys Ile Gln Ile Gln Arg Ser Gly His Leu Asn Leu Tyr Leu	
242 247 252 257	
ctc ctg gac tgt tcg cag agt gtg tcg gaa aat gac ttt ctc atc ttc	1052
Leu Leu Asp Cys Ser Gln Ser Val Ser Glu Asn Asp Phe Leu Ile Phe	
258 263 268 273	
aag gag agc gcc tcc ctc atg gtg gac agg atc ttc agc ttt gag atc	1100
Lys Glu Ser Ala Ser Leu Met Val Asp Arg Ile Phe Ser Phe Glu Ile	
274 279 284 289	
aat gtg agc gtt gcc att atc acc ttt gcc tca gag ccc aaa gtc ctc	1148
Asn Val Ser Val Ala Ile Ile Thr Phe Ala Ser Glu Pro Lys Val Leu	
290 295 300 305	
atg tct gtc ctg aac gac aac tcc cgg gat atg act gag gtg atc agc	1196
Met Ser Val Leu Asn Asp Asn Ser Arg Asp Met Thr Glu Val Ile Ser	
306 311 316 321	
agc ctg gaa aat gcc aac tat aaa gat cat gaa aat gga act ggg act	1244
Ser Leu Glu Asn Ala Asn Tyr Lys Asp His Glu Asn Gly Thr Gly Thr	
322 327 332 337	
aac acc tat gcg gcc tta aac agt gtc tat ctc atg atg aac aac caa	1292
Asn Thr Tyr Ala Ala Leu Asn Ser Val Tyr Leu Met Met Asn Asn Gln	
338 343 348 353	
atg cga ctc ctc ggc atg gaa acg atg gcc tgg cag gaa atc cga cat	1340
Met Arg Leu Leu Gly Met Glu Thr Met Ala Trp Gln Glu Ile Arg His	
354 359 364 369	
gcc atc atc ctt ctg aca gat gga aag tcc aat atg ggt ggc tct ccc	1388
Ala Ile Ile Leu Leu Thr Asp Gly Lys Ser Asn Met Gly Gly Ser Pro	

370	375	380	385	
aag aca gct gtt gac cat atc aga gag atc ctg aac atc aac cag aag				1436
Lys Thr Ala Val Asp His Ile Arg Glu Ile Leu Asn Ile Asn Gln Lys				
386	391	396	401	
agg aat gac tat ctg gac atc tat gcc atc ggg gtg ggc aag ctg gat				1484
Arg Asn Asp Tyr Leu Asp Ile Tyr Ala Ile Gly Val Gly Lys Leu Asp				
402	407	412	417	
gtg gac tgg aga gaa ctg aat gag cta ggg tcc aag aag gat ggt gag				1532
Val Asp Trp Arg Glu Leu Asn Glu Leu Gly Ser Lys Lys Asp Gly Glu				
418	423	428	433	
agg cat gcc ttc att ctg cag gac aca aag gct ctg cac cag gtc ttt				1580
Arg His Ala Phe Ile Leu Gln Asp Thr Lys Ala Leu His Gln Val Phe				
434	439	444	449	
gaa cat atg ctg gat gtc tcc aag ctc aca gac acc atc tgc ggg gtg				1628
Glu His Met Leu Asp Val Ser Lys Leu Thr Asp Thr Ile Cys Gly Val				
450	455	460	465	
ggg aac atg tca gca aac gcc tct gac cag gag agg aca ccc tgg cat				1676
Gly Asn Met Ser Ala Asn Ala Ser Asp Gln Glu Arg Thr Pro Trp His				
466	471	476	481	
gtc act att aag ccc aag agc caa gag acc tgc cgg ggg gcc ctc atc				1724
Val Thr Ile Lys Pro Lys Ser Gln Glu Thr Cys Arg Gly Ala Leu Ile				
482	487	492	497	
tcc gac caa tgg gtc ctg aca gca gct cat tgc ttc cgc gat ggc aac				1772
Ser Asp Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asp Gly Asn				
498	503	508	513	
gac cac tcc ctg tgg agg gtc aat gtg gga gac ccc aaa tcc cag tgg				1820
Asp His Ser Leu Trp Arg Val Asn Val Gly Asp Pro Lys Ser Gln Trp				
514	519	524	529	
ggc aaa gaa ttc ctt att gag aag gcg gtg atc tcc cca ggg ttt gat				1868
Gly Lys Glu Phe Leu Ile Glu Lys Ala Val Ile Ser Pro Gly Phe Asp				
530	535	540	545	
gtc ttt gcc aaa aag aac cag gga atc ctg gag ttc tat ggt gat gac				1916
Val Phe Ala Lys Lys Asn Gln Gly Ile Leu Glu Phe Tyr Gly Asp Asp				
546	551	556	561	
ata gct ctg ctg aag ctg gcc cag aaa gta aag atg tcc acc cat gcc				1964
Ile Ala Leu Leu Lys Leu Ala Gln Lys Val Lys Met Ser Thr His Ala				
562	567	572	577	
agg ccc atc tgc ctt ccc tgc acg atg gag gcc aat ctg gct ctg cgg				2012
Arg Pro Ile Cys Leu Pro Cys Thr Met Glu Ala Asn Leu Ala Leu Arg				
578	583	588	593	
aga cct caa ggc agc acc tgt agg gac cat gag aat gaa ctg ctg aac				2060
Arg Pro Gln Gly Ser Thr Cys Arg Asp His Glu Asn Glu Leu Leu Asn				
594	599	604	609	

aaa cag agt gtt cct gct cat ttt gtc gcc ttg aat ggg agc aaa ctg	2108
Lys Gln Ser Val Pro Ala His Phe Val Ala Leu Asn Gly Ser Lys Leu	
610 615 620 625	
aac att aac ctt aag atg gga gtg gag tgg aca agc tgt gcc gag gtt	2156
Asn Ile Asn Leu Lys Met Gly Val Glu Trp Thr Ser Cys Ala Glu Val	
626 631 636 641	
gtc tcc caa gaa aaa acc atg ttc ccc aac ttg aca gat gtc agg gag	2204
Val Ser Gln Glu Lys Thr Met Phe Pro Asn Leu Thr Asp Val Arg Glu	
642 647 652 657	
gtg gtg aca gac cag ttc cta tgc agt ggg acc cag gag gat gag agt	2252
Val Val Thr Asp Gln Phe Leu Cys Ser Gly Thr Gln Glu Asp Glu Ser	
658 663 668 673	
ccc tgc aag gga gaa tct ggg gga gca gtt ttc ctt gag cgg aga ttc	2300
Pro Cys Lys Gly Glu Ser Gly Gly Ala Val Phe Leu Glu Arg Arg Phe	
674 679 684 689	
agg ttt ttt cag gtg ggt ctg gtg agc tgg ggt ctt tac aac ccc tgc	2348
Arg Phe Phe Gln Val Gly Leu Val Ser Trp Gly Leu Tyr Asn Pro Cys	
690 695 700 705	
ctt ggc tct gct gac aaa aac tcc cgc aaa agg gcc cct cgt agc aag	2396
Leu Gly Ser Ala Asp Lys Asn Ser Arg Lys Arg Ala Pro Arg Ser Lys	
706 711 716 721	
gtc ccg ccg cca cga gac ttt cac atc aat ctc ttc cgc atg cag ccc	2444
Val Pro Pro Pro Arg Asp Phe His Ile Asn Leu Phe Arg Met Gln Pro	
722 727 732 737	
tgg ctg agg cag cac ctg ggg gat gtc ctg aat ttt tta ccc ctc tag	2492
Trp Leu Arg Gln His Leu Gly Asp Val Leu Asn Phe Leu Pro Leu *	
738 743 748 753	
ccatggccac tgagccctct gctgccctgc cagaatctgc cgccctcca tttctacct	2552
ctgaatggcc acccttagac cctgtgatcc atcctctctc ctagctgagt aaatccgggt	2612
ctctaggatg ccagaggcag cgcacacaag ctgggaaatc ctcagggctc ctaccagcag	2672
gactgcctcg ctgccccacc tcccgtcct tggcctgtcc ccagattcct tccctgggtg	2732
acttgactca tgcttggttc actttcacat ggaatttccc agttatgaaa ttaataaaaa	2792
tcaatgggtt ccacaaaaaa aaaaaaaaaa	2821

<210> 180
 <211> 1494
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (184)..(498)

<400> 180

ctcccaagtc cagttatttt tcctctctaa tagagacaaa cgagacacat tttatccatg	60
gacccaaaac tctggcgcca gtcaccaact taggaagaca gcctaccctt ggtgtttaat	120
cattgcaggg tgtgcctgct tgattattca cccacacccc attggtgtct gatcaccacg	180
ggg atg cct gcc ttg gtc att cac cca cat tcc ctt ggt ggc aag tca	228
Met Pro Ala Leu Val Ile His Pro His Ser Leu Gly Gly Lys Ser	
1 5 10	
att gtg ggg aca cgt gct ttg gct gct cac cca cat tgc agc cca gga	276
Ile Val Gly Thr Arg Ala Leu Ala Ala His Pro His Cys Ser Pro Gly	
16 21 26 31	
ctg ctc ccc acc cgg ctt ctc cgt gtc tct acc ctt ctc ttt aaa ctt	324
Leu Leu Pro Thr Pro Leu Leu Arg Val Ser Thr Leu Leu Phe Lys Leu	
32 37 42 47	
gcc tcc ttt act atg ggc aac ctt cca ccc tcc att cct cct tct tct	372
Ala Ser Phe Thr Met Gly Asn Leu Pro Pro Ser Ile Pro Pro Ser Ser	
48 53 58 63	
ccc tta gcc tgt gtt ctc aaa aac tta aaa cct ctt caa ctc aca cct	420
Pro Leu Ala Cys Val Leu Lys Asn Leu Lys Pro Leu Gln Leu Thr Pro	
64 69 74 79	
gac cta aaa cct aag tgt ctt att ttc ttc tgc aac acc gct ggg ccc	468
Asp Leu Lys Pro Lys Cys Leu Ile Phe Phe Cys Asn Thr Ala Gly Pro	
80 85 90 95	
caa tac aaa ctc gac aat gat tcc aaa tag c cagaaaacgg cactttcgag	519
Gln Tyr Lys Leu Asp Asn Asp Ser Lys *	
96 101	
ttctccatcc tacaagttct agataattct tgtcataaaa tgggcaaagtg gtctgaggtg	579
cctgacgtcc aggcattctt ttacacattg gtccctccct agtctctgct cccaatgtga	639
ctcatcccaa atctttcttc tttctctcct ttctgttctt tcggtctcca cccaagttc	699
cgagtccctc gaatccttct tttctatgga ctcatctgac ctccccctt ctccccaggc	759
tgctcctcgc caggctgagc cagggtcccaa ttctcactta gcctctgctc ccccacccta	819
taatcctttt atcacctccc ctccctcacac ctgggtccggc ttacagtttc attccgtgac	879
tagccctccc ccacctgccc agcaatttac tcttaaaaag gtggctggag cttaaaggcat	939
agtcaagggt aatgctcctt tttctttatc ccaaatacaga agtggttagg ctctttttca	999
tcaaataataa aaatccagcc cagttcatgg ctcgtttggc agcaaccctg agacacttta	1059

cagccctaga ccctaaaagg tcaaaaggcc gtcttattct caaaatacat tttattaccc 1119
aatctgctcc cgacattaaa taaaactcca aaaattaaat tccggccctc aaaccccaca 1179
acaggattta attaacctcg ccttcaaggt gtacaataat agaaaaaagt tgcaattcct 1239
tgcctccact gtgagacaaa cccagccac atctccagca cacaagaact tccaaacgcc 1299
tgaaccgcag cagccaggcg ttctccaga acctcctccc acaggagctt gctacacgtg 1359
ccggaaatct ggccactggg caagggaatg cccgcagccc gggattcctc ctaagccgcg 1419
tcccatctct ctgggacccc actgaaaatc ggactgttca actcacctgg cagccactcc 1479
cagagcccct ggaag 1494

<210> 181
<211> 1682
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (889) .. (1056)

<400> 181
tccttcgcc atgcttggca cgaggcgag aaggctgcag gccctatagg ggacgacggg 60
ctggggacgc cctgagcttc ctggctgtgt ggcagggtgt ggggaagctc tctgggccat 120
agggacctgg ctcccctctg agaggccgc ctgccctggg acaccaggg ctgtgctggt 180
ggcctgagga tgggaacttg ggttcctggg ctctgctggc gcctgggctt tgtggggggc 240
gaagggtggt gcccgcgcg gcagggggct gtgtggggcc tctggggggc accttcctgt 300
cagtggccga gggacgggtg gacagttgcc cctgcgcaa gggagccac tgccatcccc 360
cgtgggctgg cgctgcagtc ggcaccctg tgttgctgc tgacttgctt atgtctgttt 420
ggaagctgct tctgtttggc cacaggcctg tgttcctggg ctgatggcca cagagctgac 480
acttgggggt tgagttccag acttgacag cctgggatcc gcttactcct ccgcgccacg 540
gctgctgtgc ttccagaggt ggcgtgatgc ctcccggggc cacggtgggg tgaaggatgg 600
cgagccggac ataccattgt tggatgtatt ttttttaaaa cagcaataat tagccatttt 660
aaaggaggga tgtacctgtg tgtgtgcatg tgcacgtgtt tgagcgtgtg tgtgtgtgtg 720
caagtgggtt cttggatatg tgtagtgtga gcatgtgtgc atgtgtgagc ctgtgcacgt 780
gcatgttgta ggtgcataag catgtacacg cgtgagcatg catgtgcgtg tacacgtgta 840

taggtgtaca tgtgcatgag ttgtgtacat gcgtgagcac gtgtatag atg tac gtg	897
Met Tyr Val	
1	

tgt gtg cgc atg tgt gcg tgt aca tgt gtt tgt gtc ttg ggt atg cat	945
Cys Val Arg Met Cys Ala Cys Thr Cys Val Cys Val Leu Gly Met His	
4 9 14 19	

aag cat gca cgt gtg tat gaa tgt gcg tgt gta tgc atg agc acg tat	993
Lys His Ala Arg Val Tyr Glu Cys Ala Cys Val Cys Met Ser Thr Tyr	
20 25 30 35	

gca tgt gtg atg cgc atg ttc ttg tgt act tct ctg agg ggg cac ata	1041
Ala Cys Val Met Arg Met Phe Leu Cys Thr Ser Leu Arg Gly His Ile	
36 41 46 51	

tgt atg agt gta tga gtgcatacat atgcatatgg tgtacgtgtg tgtactttgt	1096
Cys Met Ser Val *	
52	

gtgtgggcat gtatgcgtat gagtacttgt gtgtggctgg tgtatgggtg agcatgcaca	1156
---	------

tgtgtatgga tgcataatgtg agctgtacat gtagagtgt catgtgtgtt gcatgagcat	1216
---	------

gcatgcgtgc gagtgcctgt gtgtgtactt gcatatatgt ggctgtgcag gtacccggcg	1276
---	------

gtggtgggct ggcagtgcc ggggaagcag gtcctgctca cggcttccct gctgggcccc	1336
--	------

agggcccggtg ctgagcctcc ctggccctcc ttgcccctca gtggagcagg gcctgggtgg	1396
--	------

agggcctggg cagctccagg gcaggctcgg ggaggccagg cttggggagc acaggggggtg	1456
--	------

gggttcacct gctgctgttt gttcccgaac ctgtactgtg agcccacggc gggggcagat	1516
---	------

tgttctgagg cccagatgt gccaaaacag ccccagggt gggggcgagc gagttctgag	1576
---	------

gagaggggct gcggggggcg ggggtgggtg tgtgccctc cctgaatgg cccccaatgc	1636
---	------

tgctgttttt caataaaacc agagttgaag gcaaaaaaaaa aaaaaa	1682
---	------

<210> 182

<211> 3526

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (118)..(3159)

<400> 182

agaccaccg ggccggaatt cccgggtcga cgatttcgtc cagcccaagc ctgagcctga	60
--	----

gcccggcccg aggtccccgc cccggccgcc tggtctctct gccgcggagc cgccaag	117
--	-----

atg ggg gac aag aaa gat gac aag gac tca ccc aag aag aac aag ggc	165
---	-----

Met	Gly	Asp	Lys	Lys	Asp	Asp	Lys	Asp	Ser	Pro	Lys	Lys	Asn	Lys	Gly		
1				5					10						15		
aag	gag	cgc	cgg	gac	ctg	gat	gac	ctc	aag	aag	gag	gtg	gct	atg	aca	213	
Lys	Glu	Arg	Arg	Asp	Leu	Asp	Asp	Leu	Lys	Lys	Glu	Val	Ala	Met	Thr		
17					22				27					32			
gag	cac	aag	atg	tca	gtg	gaa	gag	gtc	tgc	cgg	aaa	tac	aac	aca	gac	261	
Glu	His	Lys	Met	Ser	Val	Glu	Glu	Val	Cys	Arg	Lys	Tyr	Asn	Thr	Asp		
33					38				43					48			
tgt	gtg	cag	ggg	ttg	acc	cac	agc	aaa	gcc	cag	gag	atc	ctg	gcc	cgg	309	
Cys	Val	Gln	Gly	Leu	Thr	His	Ser	Lys	Ala	Gln	Glu	Ile	Leu	Ala	Arg		
49					54				59					64			
gat	ggg	cct	aac	gca	ctc	acg	cca	ccg	cct	acc	acc	cca	gag	tgg	gtc	357	
Asp	Gly	Pro	Asn	Ala	Leu	Thr	Pro	Pro	Pro	Thr	Thr	Pro	Glu	Trp	Val		
65					70				75					80			
aag	ttt	tgc	cgg	cag	ctc	ttc	ggg	ggc	ttc	tcc	atc	ctg	ctg	tgg	atc	405	
Lys	Phe	Cys	Arg	Gln	Leu	Phe	Gly	Gly	Phe	Ser	Ile	Leu	Leu	Trp	Ile		
81					86				91					96			
ggg	gct	atc	ctc	tgc	ttc	ctg	gcc	tac	ggg	atc	cag	gcg	ggc	acc	gag	453	
Gly	Ala	Ile	Leu	Cys	Phe	Leu	Ala	Tyr	Gly	Ile	Gln	Ala	Gly	Thr	Glu		
97					102				107					112			
gac	gac	ccc	tct	ggg	gac	aac	ctg	tac	ctg	ggc	atc	gtg	ctg	gcg	gcc	501	
Asp	Asp	Pro	Ser	Gly	Asp	Asn	Leu	Tyr	Leu	Gly	Ile	Val	Leu	Ala	Ala		
113					118				123					128			
gtg	gtg	atc	atc	act	ggc	tgc	ttc	tcc	tac	tac	cag	gag	gcc	aag	agc	549	
Val	Val	Ile	Ile	Thr	Gly	Cys	Phe	Ser	Tyr	Tyr	Gln	Glu	Ala	Lys	Ser		
129					134				139					144			
tcc	aag	atc	atg	gag	tcc	ttc	aag	aac	atg	gtg	ccc	cag	caa	gcc	ctg	597	
Ser	Lys	Ile	Met	Glu	Ser	Phe	Lys	Asn	Met	Val	Pro	Gln	Gln	Ala	Leu		
145					150				155					160			
gtg	atc	cgg	gaa	ggg	gag	aag	atg	cag	gtg	aac	gct	gag	gag	gtg	gtg	645	
Val	Ile	Arg	Glu	Gly	Glu	Lys	Met	Gln	Val	Asn	Ala	Glu	Glu	Val	Val		
161					166				171					176			
gtc	ggg	gac	ctg	gtg	gag	atc	aag	ggg	gga	gac	cga	gtg	cca	gct	gac	693	
Val	Gly	Asp	Leu	Val	Glu	Ile	Lys	Gly	Gly	Asp	Arg	Val	Pro	Ala	Asp		
177					182				187					192			
ctg	cgg	atc	atc	tca	gcc	cac	ggc	tgc	aag	gtg	gac	aac	tcc	tcc	ctg	741	
Leu	Arg	Ile	Ile	Ser	Ala	His	Gly	Cys	Lys	Val	Asp	Asn	Ser	Ser	Leu		
193					198				203					208			
act	ggc	gaa	tcc	gag	ccc	cag	act	cgc	tct	ccc	gac	tgc	acg	cac	gac	789	
Thr	Gly	Glu	Ser	Glu	Pro	Gln	Thr	Arg	Ser	Pro	Asp	Cys	Thr	His	Asp		
209					214				219					224			
aac	ccc	ttg	gag	act	cgg	aac	atc	acc	ttc	ttt	tcc	acc	aac	tgt	gtg	837	
Asn	Pro	Leu	Glu	Thr	Arg	Asn	Ile	Thr	Phe	Phe	Ser	Thr	Asn	Cys	Val		

225	230	235	240	
gaa ggc acg gct cgg ggc gtg gtg gtg gcc acg ggc gac cgc act gtc				885
Glu Gly Thr Ala Arg Gly Val Val Val Ala Thr Gly Asp Arg Thr Val				
241	246	251	256	
atg ggc cgt atc gcc acc ctg gca tca ggg ctg gag gtg ggc aag acg				933
Met Gly Arg Ile Ala Thr Leu Ala Ser Gly Leu Glu Val Gly Lys Thr				
257	262	267	272	
ccc atc gcc atc gag att gag cac ttc atc cag ctc atc acc ggc gtg				981
Pro Ile Ala Ile Glu Ile Glu His Phe Ile Gln Leu Ile Thr Gly Val				
273	278	283	288	
gct gtc ttc ctg ggt gtc tcc ttc ttc atc ctc tcc ctc att ctc gga				1029
Ala Val Phe Leu Gly Val Ser Phe Phe Ile Leu Ser Leu Ile Leu Gly				
289	294	299	304	
tac acc tgg ctt gag gct gtc atc ttc ctc atc ggc atc atc gtg gcc				1077
Tyr Thr Trp Leu Glu Ala Val Ile Phe Leu Ile Gly Ile Ile Val Ala				
305	310	315	320	
aat gtc cca gag ggt ctg ctg gcc act gtc act gtg tgt ctg acg ctg				1125
Asn Val Pro Glu Gly Leu Leu Ala Thr Val Thr Val Cys Leu Thr Leu				
321	326	331	336	
acc gcc aag cgc atg gcc cgg aag aac tgc ctg gtg aag aac ctg gag				1173
Thr Ala Lys Arg Met Ala Arg Lys Asn Cys Leu Val Lys Asn Leu Glu				
337	342	347	352	
gct gta gaa acc ctg ggc tcc acg tcc acc atc tgc tca gat aag aca				1221
Ala Val Glu Thr Leu Gly Ser Thr Ser Thr Ile Cys Ser Asp Lys Thr				
353	358	363	368	
ggg acc ctc act cag aac cgc atg aca gtc gcc cac atg tgg ttt gac				1269
Gly Thr Leu Thr Gln Asn Arg Met Thr Val Ala His Met Trp Phe Asp				
369	374	379	384	
aac cag atc cac gag gct gac acc act gag gac cag tca ggg acc tca				1317
Asn Gln Ile His Glu Ala Asp Thr Thr Glu Asp Gln Ser Gly Thr Ser				
385	390	395	400	
ttt gac aag agt tcg cac acc tgg gtg gcc ctg tct cac atc gct ggg				1365
Phe Asp Lys Ser Ser His Thr Trp Val Ala Leu Ser His Ile Ala Gly				
401	406	411	416	
ctc tgc aat cgc gct gtc ttc aag ggt ggt cag gac aac atc cct gtg				1413
Leu Cys Asn Arg Ala Val Phe Lys Gly Gly Gln Asp Asn Ile Pro Val				
417	422	427	432	
ctc aag agg gat gtg gct ggg gat gcg tct gag tct gcc ctg ctc aag				1461
Leu Lys Arg Asp Val Ala Gly Asp Ala Ser Glu Ser Ala Leu Leu Lys				
433	438	443	448	
tgc atc gag ctg tcc tct ggc tcc gtg aag ctg atg cgt gaa cgc aac				1509
Cys Ile Glu Leu Ser Ser Gly Ser Val Lys Leu Met Arg Glu Arg Asn				
449	454	459	464	

aag aaa gtg gct gag att ccc ttc aat tcc acc aac aaa tac cag ctc	1557
Lys Lys Val Ala Glu Ile Pro Phe Asn Ser Thr Asn Lys Tyr Gln Leu	
465 470 475 480	
tcc atc cat gag acc gag gac ccc aac gac aac cga tac ctg ctg gtg	1605
Ser Ile His Glu Thr Glu Asp Pro Asn Asp Asn Arg Tyr Leu Leu Val	
481 486 491 496	
atg aag ggt gcc ccc gag cgc atc ctg gac cgc tgc tcc acc atc ctg	1653
Met Lys Gly Ala Pro Glu Arg Ile Leu Asp Arg Cys Ser Thr Ile Leu	
497 502 507 512	
cta cag ggc aag gag cag cct ctg gac gag gaa atg aag gag gcc ttc	1701
Leu Gln Gly Lys Glu Gln Pro Leu Asp Glu Glu Met Lys Glu Ala Phe	
513 518 523 528	
cag aat gcc tac ctt gag ctc ggt ggc ctg ggc gag cgc gtg ctt ggt	1749
Gln Asn Ala Tyr Leu Glu Leu Gly Gly Leu Gly Glu Arg Val Leu Gly	
529 534 539 544	
ttc tgc cat tat tac ctg ccc gag gag cag ttc ccc aag ggc ttt gcc	1797
Phe Cys His Tyr Tyr Leu Pro Glu Glu Gln Phe Pro Lys Gly Phe Ala	
545 550 555 560	
ttc gac tgt gat gag gtg aac ttc acc acg gac aac ctc tgc ttt gtg	1845
Phe Asp Cys Asp Asp Val Asn Phe Thr Thr Asp Asn Leu Cys Phe Val	
561 566 571 576	
ggc ctc atg tcc atg atc gac cca ccc cgg gca gcc gtc cct gac gcg	1893
Gly Leu Met Ser Met Ile Asp Pro Pro Arg Ala Ala Val Pro Asp Ala	
577 582 587 592	
gtg ggc aag tgt cgc agc gca ggc atc aag gtc atc atg gtc acc ggc	1941
Val Gly Lys Cys Arg Ser Ala Gly Ile Lys Val Ile Met Val Thr Gly	
593 598 603 608	
gat cac ccc atc acg gcc aag gcc att gcc aag ggt gtg ggc atc atc	1989
Asp His Pro Ile Thr Ala Lys Ala Ile Ala Lys Gly Val Gly Ile Ile	
609 614 619 624	
ttt gag ggc aac gag act gtg gag gac atc gcc gcc cgg ctc aac att	2037
Phe Glu Gly Asn Glu Thr Val Glu Asp Ile Ala Ala Arg Leu Asn Ile	
625 630 635 640	
ccc gtc agc cag gtt aac ccc cgg gat gcc aag gcc tgc gtg atc cac	2085
Pro Val Ser Gln Val Asn Pro Arg Asp Ala Lys Ala Cys Val Ile His	
641 646 651 656	
ggc acc gac ctc aag gac ttc acc tcc gag caa atc gac gag atc ctg	2133
Gly Thr Asp Leu Lys Asp Phe Thr Ser Glu Gln Ile Asp Glu Ile Leu	
657 662 667 672	
cag aat cac acc gag atc gtc ttc gcc cgc aca tcc ccc cag cag aag	2181
Gln Asn His Thr Glu Ile Val Phe Ala Arg Thr Ser Pro Gln Gln Lys	
673 678 683 688	

ctc atc att gtg gag ggc tgt cag aga cag ggt gca att gtg gct gtg	2229
Leu Ile Ile Val Glu Gly Cys Gln Arg Gln Gly Ala Ile Val Ala Val	
689 694 699 704	
acc ggg gat ggt gtg aac gac tcc ccc gct ctg aag aag gcc gac att	2277
Thr Gly Asp Gly Val Asn Asp Ser Pro Ala Leu Lys Lys Ala Asp Ile	
705 710 715 720	
ggg gtg gcc atg ggc atc gct ggc tct gac gtc tcc aag cag gca gct	2325
Gly Val Ala Met Gly Ile Ala Gly Ser Asp Val Ser Lys Gln Ala Ala	
721 726 731 736	
gac atg atc ctg ctg gac gac aac ttt gcc tcc atc gtc aca ggg gtg	2373
Asp Met Ile Leu Leu Asp Asp Asn Phe Ala Ser Ile Val Thr Gly Val	
737 742 747 752	
gag gag ggc cgc ctg atc ttc gac aac cta aag aag tcc att gcc tac	2421
Glu Glu Gly Arg Leu Ile Phe Asp Asn Leu Lys Lys Ser Ile Ala Tyr	
753 758 763 768	
acc ctg acc agc aat atc ccg gag atc acg ccc ttc ctg ctg ttc atc	2469
Thr Leu Thr Ser Asn Ile Pro Glu Ile Thr Pro Phe Leu Leu Phe Ile	
769 774 779 784	
atg gcc aac atc ccg ctg ccc ctg ggc acc atc acc atc ctc tgc atc	2517
Met Ala Asn Ile Pro Leu Pro Leu Gly Thr Ile Thr Ile Leu Cys Ile	
785 790 795 800	
gat ctg ggc act gac atg gtc cct gcc atc tca ctg gcg tac gag gct	2565
Asp Leu Gly Thr Asp Met Val Pro Ala Ile Ser Leu Ala Tyr Glu Ala	
801 806 811 816	
gcc gaa agc gac atc atg aag aga cag ccc agg aac ccg cgg acg gac	2613
Ala Glu Ser Asp Ile Met Lys Arg Gln Pro Arg Asn Pro Arg Thr Asp	
817 822 827 832	
aaa ttg gtc aat gag aga ctc atc agc atg gcc tac ggg cag att gga	2661
Lys Leu Val Asn Glu Arg Leu Ile Ser Met Ala Tyr Gly Gln Ile Gly	
833 838 843 848	
atg atc cag gct ctc ggt ggc ttc ttc tct tac ttt gtg atc ctg gca	2709
Met Ile Gln Ala Leu Gly Gly Phe Phe Ser Tyr Phe Val Ile Leu Ala	
849 854 859 864	
gaa aat ggc ttc ttg ccc ggc aac ctg gtg ggc atc cgg ctg aac tgg	2757
Glu Asn Gly Phe Leu Pro Gly Asn Leu Val Gly Ile Arg Leu Asn Trp	
865 870 875 880	
gat gac cgc acc gtc aat gac ctg gaa gac agt tac ggg cag cag tgg	2805
Asp Asp Arg Thr Val Asn Asp Leu Glu Asp Ser Tyr Gly Gln Gln Trp	
881 886 891 896	
aca tac gag cag agg aag gtg gtg gag ttc acc tgc cac acg gcc ttc	2853
Thr Tyr Glu Gln Arg Lys Val Val Glu Phe Thr Cys His Thr Ala Phe	
897 902 907 912	
ttt gtg agc atc gtt gtc gtc cag tgg gcc gat ctg atc atc tgc aag	2901

Phe Val Ser Ile Val Val Val Gln Trp Ala Asp Leu Ile Ile Cys Lys	
913 918 923 928	
acc cgg agg aac tcg gtc ttc cag cag ggc atg aag aac aag atc ctg	2949
Thr Arg Arg Asn Ser Val Phe Gln Gln Gly Met Lys Asn Lys Ile Leu	
929 934 939 944	
atc ttc ggg ctg ttt gag gag acg gcc ctg gct gcc ttc ctg tcc tac	2997
Ile Phe Gly Leu Phe Glu Glu Thr Ala Leu Ala Ala Phe Leu Ser Tyr	
945 950 955 960	
tgc ccc ggc atg gac gtg gcc ctg cgc atg tac cct ctc aag ccc agc	3045
Cys Pro Gly Met Asp Val Ala Leu Arg Met Tyr Pro Leu Lys Pro Ser	
961 966 971 976	
tgg tgg ttc tgt gcc ttc ccc tac agt ttc ctc atc ttc gtc tac gac	3093
Trp Trp Phe Cys Ala Phe Pro Tyr Ser Phe Leu Ile Phe Val Tyr Asp	
977 982 987 992	
gaa atc cgc aaa ctc atc ctg cgc agg aac cca ggg ggt tgg gtg gag	3141
Glu Ile Arg Lys Leu Ile Leu Arg Arg Asn Pro Gly Gly Trp Val Glu	
993 998 1003 1008	
aag gaa acc tac tac tga cctcag cccaccaca tcgcccattc cttccccgtc	3195
Lys Glu Thr Tyr Tyr *	
1009 1014	
ccgcaggccc aggaccgccc ctgtcagtc ccccaatttt gtattctggg gggaggagcc	3255
ctctcttctt gtggccccac cttggcccc accccctcca ctatctcctg ccgccccac	3315
tctggctggc ttctctcccc tgccccaaac ctctctcttc tctcttttct gtgtcagttt	3375
ctctccctct cctcaccct ctatccattc ctcccgcccc agccacctcc ctgggctctt	3435
ttttactccc cttcagcccc ccggctgatg ccattctctgg ttctggacaa ttatcaaata	3495
tatcagtggg gagagagaaa aaaaaaaaaa a	3526

<210> 183
 <211> 1428
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (38)..(1306)

<220>
 <221> misc_feature
 <222> (1)..(1428)
 <223> n = a,t,c or g

<400> 183

gcacgaggcg ccggcccagg cgctggacgg cagcagg atg ggg aag gcg aag gtc	55
Met Gly Lys Ala Lys Val	
1	
ccc gcc tcc aag cgc gcc ccg agc agc ccc gtg gct aag ccg ggt cct	103
Pro Ala Ser Lys Arg Ala Pro Ser Ser Pro Val Ala Lys Pro Gly Pro	
7 12 17 22	
gtc aag acg ctc act cgg aag aaa aac aag aag aaa aaa agg ttt tgg	151
Val Lys Thr Leu Thr Arg Lys Lys Asn Lys Lys Lys Lys Arg Phe Trp	
23 28 33 38	
aaa agc aag gcg cgg gaa gta agc aag aag cca gca agc ggc ccc ggt	199
Lys Ser Lys Ala Arg Glu Val Ser Lys Lys Pro Ala Ser Gly Pro Gly	
39 44 49 54	
gct gtg gtg cga cct cca aag gca cca gaa gac ttt tct caa aac tgg	247
Ala Val Val Arg Pro Pro Lys Ala Pro Glu Asp Phe Ser Gln Asn Trp	
55 60 65 70	
aag gcg ctg caa gag tgg ctg ctg aaa caa aaa tct cag gcc cca gaa	295
Lys Ala Leu Gln Glu Trp Leu Leu Lys Gln Lys Ser Gln Ala Pro Glu	
71 76 81 86	
aag cct ctt gtc atc tct cag atg ggt tcc aaa aag aag ccc aaa att	343
Lys Pro Leu Val Ile Ser Gln Met Gly Ser Lys Lys Lys Pro Lys Ile	
87 92 97 102	
atc cag caa aac aaa aaa gag acc tcg cct caa gtg aag gga gag gag	391
Ile Gln Gln Asn Lys Lys Glu Thr Ser Pro Gln Val Lys Gly Glu Glu	
103 108 113 118	
atg ccg gca gga aaa gac cag gag gcc agc agg ggc tct gtt cct tca	439
Met Pro Ala Gly Lys Asp Gln Glu Ala Ser Arg Gly Ser Val Pro Ser	
119 124 129 134	
ggg tcc aag atg gac agg agg gcg cca gta cct cgc acc aag gcc agt	487
Gly Ser Lys Met Asp Arg Arg Ala Pro Val Pro Arg Thr Lys Ala Ser	
135 140 145 150	
gga aca gag cac aat aag aaa gga acc aag gaa agg aca aat ggt gat	535
Gly Thr Glu His Asn Lys Lys Gly Thr Lys Glu Arg Thr Asn Gly Asp	
151 156 161 166	
att gtt cca gaa cga ggg gac atc gag cat aag aag cgg aaa gct aag	583
Ile Val Pro Glu Arg Gly Asp Ile Glu His Lys Lys Arg Lys Ala Lys	
167 172 177 182	
gag gca gcc cca gcc cca ccc acc gag gaa gac atc tgg ttt gac gac	631
Glu Ala Ala Pro Ala Pro Pro Thr Glu Glu Asp Ile Trp Phe Asp Asp	
183 188 193 198	
gtg gac cca gcg gat atc gaa gct gcc ata ggt cca gag gcg gcc aag	679
Val Asp Pro Ala Asp Ile Glu Ala Ala Ile Gly Pro Glu Ala Ala Lys	
199 204 209 214	
ata gcg agg aaa cag ttg ggt cag agc gag ggc agc gtc agc ctc agc	727

ttaagatt

1428

<210> 184
<211> 2086
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (212)..(1561)

<400> 184

aattgatacg cctgtcaggt actaggtcgg gaattcccgg gtcgacccac gcgtccgccc	60
acgggtccgg ggggectcat gcttggtcct gctggcgctg tgtctgctgc tgccgctgct	120
gctgctggga ggatggaagc gctggcgccg gggggcgggcg gcccggcacg tagtagcggg	180
ggtgctgggc gacgtgggcc gcagcccccg t atg cag tac cac gcg ctg tgc	232
Met Gln Tyr His Ala Leu Ser	
1 5	
ttg gcc atg cac ggc ttc tgc gtg acc ctc ctg ggg ttc tgc aac tcc	280
Leu Ala Met His Gly Phe Ser Val Thr Leu Leu Gly Phe Cys Asn Ser	
8 13 18 23	
aaa ccc cat gat gag ctc ttg cag aac aac aga att cag att gtg ggg	328
Lys Pro His Asp Glu Leu Leu Gln Asn Asn Arg Ile Gln Ile Val Gly	
24 29 34 39	
ttg aca gaa ctt cag agt ctt gca gtt ggg ccc cga gtt ttc cag tac	376
Leu Thr Glu Leu Gln Ser Leu Ala Val Gly Pro Arg Val Phe Gln Tyr	
40 45 50 55	
gga gtc aaa gtt gta ctt cag gct atg tac ttg ctg tgg aag ttg atg	424
Gly Val Lys Val Val Leu Gln Ala Met Tyr Leu Leu Trp Lys Leu Met	
56 61 66 71	
tgg agg gag cca ggt gcc tat atc ttt ctc cag aac ccc cca ggt ctg	472
Trp Arg Glu Pro Gly Ala Tyr Ile Phe Leu Gln Asn Pro Pro Gly Leu	
72 77 82 87	
cct agc att gct gtc tgc tgg ttc gtg ggc tgc ctt tgt gga agc aag	520
Pro Ser Ile Ala Val Cys Trp Phe Val Gly Cys Leu Cys Gly Ser Lys	
88 93 98 103	
ctc gtc att gac tgg cac aac tat ggc tac tcc atc atg ggt ctg gtg	568
Leu Val Ile Asp Trp His Asn Tyr Gly Tyr Ser Ile Met Gly Leu Val	
104 109 114 119	
cat ggc ccc aac cat ccc ctc gtt ctg ctg gcc aag tgg tgc aca tcc	616
His Gly Pro Asn His Pro Leu Val Leu Leu Ala Lys Trp Cys Thr Ser	
120 125 130 135	

agc ctc cgt gtg cat gtc cag ctg ctg cgt gta ctt ccg gcc ttg ggc	664
Ser Leu Arg Val His Val Gln Leu Leu Arg Val Leu Pro Ala Leu Gly	
136 141 146 151	
cat tgg ctg gct gtg gcc ttc gcc ctg ata gtt tgt tca ctg gca gtg	712
His Trp Leu Ala Val Ala Phe Ala Leu Ile Val Cys Ser Leu Ala Val	
152 157 162 167	
gtg aca gca gca gca aac agc tta gtt gag caa atg gag cag aat ggt	760
Val Thr Ala Ala Ala Asn Ser Leu Val Glu Gln Met Glu Gln Asn Gly	
168 173 178 183	
caa tgg tac gag aag ttc ttt ggg cgc ctg tcc cac ctg aac ctg tgt	808
Gln Trp Tyr Glu Lys Phe Phe Gly Arg Leu Ser His Leu Asn Leu Cys	
184 189 194 199	
gtt acc aat gct atg cga gaa gac ctg gcg gat aac tgg cac atc agg	856
Val Thr Asn Ala Met Arg Glu Asp Leu Ala Asp Asn Trp His Ile Arg	
200 205 210 215	
gct gtg acc gtc tac gac aag ccc gca tct ttc ttt aaa gag aca cct	904
Ala Val Thr Val Tyr Asp Lys Pro Ala Ser Phe Phe Lys Glu Thr Pro	
216 221 226 231	
ctg gac ctg cag cac cgg ctc ttc atg aag ctg ggc agc atg cac tct	952
Leu Asp Leu Gln His Arg Leu Phe Met Lys Leu Gly Ser Met His Ser	
232 237 242 247	
ccg ttc agg gcc cgc tca gaa cct gag gac cca gtc acg gag cgg tcg	1000
Pro Phe Arg Ala Arg Ser Glu Pro Glu Asp Pro Val Thr Glu Arg Ser	
248 253 258 263	
gcc ttc acg gag cgg gat gct ggg agc ggg ctg gtg acg cgt ctc cgt	1048
Ala Phe Thr Glu Arg Asp Ala Gly Ser Gly Leu Val Thr Arg Leu Arg	
264 269 274 279	
gag cgg cca gcc ctg ctg gtc agc agc acg agc tgg aca gag gac gaa	1096
Glu Arg Pro Ala Leu Leu Val Ser Ser Thr Ser Trp Thr Glu Asp Glu	
280 285 290 295	
gac ttc tcc atc ctg ctg gca gct tta gaa agc aaa ggg cct ctg agg	1144
Asp Phe Ser Ile Leu Leu Ala Ala Leu Glu Ser Lys Gly Pro Leu Arg	
296 301 306 311	
gag tat tat agc cgc ctc atc cac cag aag cac ttc cag cac atc cag	1192
Glu Tyr Tyr Ser Arg Leu Ile His Gln Lys His Phe Gln His Ile Gln	
312 317 322 327	
gtc tgc acc ccc tgg ctg gag gcc gag gac tac ccc ctg ctt cta ggg	1240
Val Cys Thr Pro Trp Leu Glu Ala Glu Asp Tyr Pro Leu Leu Leu Gly	
328 333 338 343	
tcg gcg gac ctg ggt gtc tgt ctg cac acg tcc tcc agt ggc ctg gac	1288
Ser Ala Asp Leu Gly Val Cys Leu His Thr Ser Ser Ser Gly Leu Asp	
344 349 354 359	
ctg ccc atg aag gtg gtg gac atg ttc ggg tgc tgt ttg cct gtg tgt	1336

```

Leu Pro Met Lys Val Val Asp Met Phe Gly Cys Cys Leu Pro Val Cys
360                               365                               370                               375

gct gtg aac ttc aag tgt tta cat gag ctg gtg aaa cat gaa gaa aat      1384
Ala Val Asn Phe Lys Cys Leu His Glu Leu Val Lys His Glu Glu Asn
376                               381                               386                               391

ggc ctg gtc ttt gag gac tca gag gaa ctg gca gct cag ctg cag atg      1432
Gly Leu Val Phe Glu Asp Ser Glu Glu Leu Ala Ala Gln Leu Gln Met
392                               397                               402                               407

ctt ttc tca aac ttt cct gat cct gcg ggc aag cta aac cag ttc cgg      1480
Leu Phe Ser Asn Phe Pro Asp Pro Ala Gly Lys Leu Asn Gln Phe Arg
408                               413                               418                               423

aag aac ctg cgg gag tcg cag cag ctc cga tgg gat gag agc tgg gtg      1528
Lys Asn Leu Arg Glu Ser Gln Gln Leu Arg Trp Asp Glu Ser Trp Val
424                               429                               434                               439

cag act gtg ctc cct ttg gtt atg gac aca taa ctctctggg ccagaggcta      1579
Gln Thr Val Leu Pro Leu Val Met Asp Thr *
440                               445                               450

aaaccccagg acccctgctg tccttcccgc agcttcttct tggagtctca gggcaaaccc      1639

tttcgagcag cacctcccag tggccagaag ctgaaatgac agcagtggta ctgcctggta      1699

aaagaattgg ttctgtgacc cgggaagctt tgggtggcct tgatttcttc tctggaggct      1759

tggaacgct tcctctcttc ttctgttctt cacgccccat gccctgcta gcgtattact      1819

gttctgtgac ttccctgtga cctctgcaga actcctcatc ctgcgttttg totccagggt      1879

tcccctttct gccgtgttcc taacattttg attcctgtct tgaaaaaagc acctgctgca      1939

ccgtaagccc agggatgtgg cagctgcagt gggcttggct ttgtgaggaa ctgagtgtgt      1999

ccacgttggg ggaacatcat acttgataca cacgttttta ttgcacaaa gaaaatgcta      2059

tttttgagc cagaaaaaaaa aaaaaaa      2086

```

<210> 185
 <211> 1927
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (212)..(1402)

```

<400> 185
aattgatagc cctgtcaggt actaggtccg gaattcccgg gtcgaccac gcgtccgccc      60
acgcgtccgg gcggcctcat gcttggtcct gctggcgctg tgtctgctgc tgccgctgct      120

```


gacctctgca gaactcctca tctctcgcttt ggtctccagg tgtccccctt ctgccgtgtt 1738
cctaacattt tgattcctgt cttgaaaaaa gcacctgctg caccgtaagc ccagggatgt 1798
ggcagctgca gtgggcttgg ctttctgagg aactgagtgt gtccacgttg ggggaacatc 1858
atacttgata cacacgtttt tatttgcaca aagaaaatgc tatttttggga gccagaaaaa 1918
aaaaaaaaa 1927

<210> 186
<211> 2146
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (212) .. (1621)

<400> 186
aattgatacg cctgtcaggt actaggtccg gaattccqgg gtcgacccac gcgtccgccc 60
acgcgtccgg ggggcctcat gcttggctct gctggcgctg tgtctgctgc tgccgctgct 120
gctgctggga ggatggaagc gctggcgccg ggggcgggcg gcccggcattg tagtagcggt 180
ggtgctgggc gacgtgggccc gcagcccccg t atg cag tac cac gcg ctg tgc 232
Met Gln Tyr His Ala Leu Ser
1 5
ttg gcc atg cac ggc ttc tgc gtg acc ctc ctg ggg ttc tgc aac tcc 280
Leu Ala Met His Gly Phe Ser Val Thr Leu Leu Gly Phe Cys Asn Ser
8 13 18 23
aaa ccc cat gat gag ctc ttg cag aac aac aga att cag att gtg ggg 328
Lys Pro His Asp Glu Leu Leu Gln Asn Asn Arg Ile Gln Ile Val Gly
24 29 34 39
ttg aca gaa ctt cag agt ctt gca gtt ggg ccc cga gtt ttc cag tac 376
Leu Thr Glu Leu Gln Ser Leu Ala Val Gly Pro Arg Val Phe Gln Tyr
40 45 50 55
gga gtc aaa gtt gta ctt cag gct atg tac ttg ctg tgg aag ttg atg 424
Gly Val Lys Val Val Leu Gln Ala Met Tyr Leu Leu Trp Lys Leu Met
56 61 66 71
tgg agg gag cca ggt gcc tat atc ttt ctc cag aac ccc cca ggt ctg 472
Trp Arg Glu Pro Gly Ala Tyr Ile Phe Leu Gln Asn Pro Pro Gly Leu
72 77 82 87
cct agc att gct gtc tgc tgg ttc gtg ggc tgc ctt tgt gga agc aag 520
Pro Ser Ile Ala Val Cys Trp Phe Val Gly Cys Leu Cys Gly Ser Lys
88 93 98 103

ctc gtc att gac tgg cac aac tat ggc tac tcc atc atg ggt ctg gtg	568
Leu Val Ile Asp Trp His Asn Tyr Gly Tyr Ser Ile Met Gly Leu Val	
104 109 114 119	
cat ggc ccc aac cat ccc ctc gtt ctg ctg gcc aag tgg tgc aca tcc	616
His Gly Pro Asn His Pro Leu Val Leu Leu Ala Lys Trp Cys Thr Ser	
120 125 130 135	
agc ctc cgt gtg cat gtc cag ctg ctg cgt gta ctt ccg gcc ttg ggc	664
Ser Leu Arg Val His Val Gln Leu Leu Arg Val Leu Pro Ala Leu Gly	
136 141 146 151	
cat tgg ctg gct gtg gcc ttc gcc ctg ata gtt tgt tca ctg gca gtg	712
His Trp Leu Ala Val Ala Phe Ala Leu Ile Val Cys Ser Leu Ala Val	
152 157 162 167	
gtg aca gca gca gca aac agc tta gtt gag caa atg gag cag aat ggt	760
Val Thr Ala Ala Ala Asn Ser Leu Val Glu Gln Met Glu Gln Asn Gly	
168 173 178 183	
caa tgg tac gag aag ttc ttt ggg cgc ctg tcc cac ctg aac ctg tgt	808
Gln Trp Tyr Glu Lys Phe Phe Gly Arg Leu Ser His Leu Asn Leu Cys	
184 189 194 199	
gtt acc aat gct atg cga gaa gac ctg gcg gat aac tgg cac atc agg	856
Val Thr Asn Ala Met Arg Glu Asp Leu Ala Asp Asn Trp His Ile Arg	
200 205 210 215	
gct gtg acc gtc tac gac aag ccc gca tct ttc ttt aaa gag aca cct	904
Ala Val Thr Val Tyr Asp Lys Pro Ala Ser Phe Phe Lys Glu Thr Pro	
216 221 226 231	
ctg gac ctg cag cac cgg ctc ttc atg aag ctg ggc agc atg cac tct	952
Leu Asp Leu Gln His Arg Leu Phe Met Lys Leu Gly Ser Met His Ser	
232 237 242 247	
ccg ttc agg gcc cgc tca gaa cct gag gac cca gtc acg gag cgg tcg	1000
Pro Phe Arg Ala Arg Ser Glu Pro Glu Asp Pro Val Thr Glu Arg Ser	
248 253 258 263	
gcc ttc acg gag cgg gat gct ggg agc ggg ctg gtg acg cgt ctc cgt	1048
Ala Phe Thr Glu Arg Asp Ala Gly Ser Gly Leu Val Thr Arg Leu Arg	
264 269 274 279	
gag cgg cca gcc ctg ctg gtc agc agc acg agc tgg aca gag gac gaa	1096
Glu Arg Pro Ala Leu Leu Val Ser Ser Thr Ser Trp Thr Glu Asp Glu	
280 285 290 295	
gac ttc tcc atc ctg ctg gca gct tta gaa aag ttt gaa caa ctg act	1144
Asp Phe Ser Ile Leu Leu Ala Ala Leu Glu Lys Phe Glu Gln Leu Thr	
296 301 306 311	
ctt gat gga cac aac ctt cct tct ctc gtc tgt gtg ata aca ggc aaa	1192
Leu Asp Gly His Asn Leu Pro Ser Leu Val Cys Val Ile Thr Gly Lys	
312 317 322 327	

ggg cct ctg agg gag tat tat agc cgc ctc atc cac cag aag cac ttc	1240
Gly Pro Leu Arg Glu Tyr Tyr Ser Arg Leu Ile His Gln Lys His Phe	
328 333 338 343	
cag cac atc cag gtc tgg acc ccc tgg ctg gag gcc gag gac tac ccc	1288
Gln His Ile Gln Val Cys Thr Pro Trp Leu Glu Ala Glu Asp Tyr Pro	
344 349 354 359	
ctg ctt cta ggg tgc gcg gac ctg ggt gtc tgt ctg cac acg tcc tcc	1336
Leu Leu Leu Gly Ser Ala Asp Leu Gly Val Cys Leu His Thr Ser Ser	
360 365 370 375	
agt ggc ctg gac ctg ccc atg aag gtg gtg gac atg ttc ggg tgc tgt	1384
Ser Gly Leu Asp Leu Pro Met Lys Val Val Asp Met Phe Gly Cys Cys	
376 381 386 391	
ttg cct gtg tgt gct gtg aac ttc aag tgt tta cat gag ctg gtg aaa	1432
Leu Pro Val Cys Ala Val Asn Phe Lys Cys Leu His Glu Leu Val Lys	
392 397 402 407	
cat gaa gaa aat ggc ctg gtc ttt gag gac tca gag gaa ctg gca gct	1480
His Glu Glu Asn Gly Leu Val Phe Glu Asp Ser Glu Glu Leu Ala Ala	
408 413 418 423	
cag ctg cag atg ctt ttc tca aac ttt cct gat cct gcg ggc aag cta	1528
Gln Leu Gln Met Leu Phe Ser Asn Phe Pro Asp Pro Ala Gly Lys Leu	
424 429 434 439	
aac cag ttc cgg aag aac ctg cgg gag tgc cag cag ctc cga tgg gat	1576
Asn Gln Phe Arg Lys Asn Leu Arg Glu Ser Gln Gln Leu Arg Trp Asp	
440 445 450 455	
gag agc tgg gtg cag act gtg ctc cct ttg gtt atg gac aca taa ctc	1624
Glu Ser Trp Val Gln Thr Val Leu Pro Leu Val Met Asp Thr *	
456 461 466	
ctggggccaga ggctaaaacc ccaggacccc tgctgtcctt cccgcagctt cttcttggag	1684
tctcagggca aacccttttcg agcagcacct cccagtggcc agaagctgaa atgacagcag	1744
tggtactgcc tggtaaaaga attggttctg tgaccgggga agctttgggtt ggccttgatt	1804
tcttctctgg aggcttggaa acgcttcttc tcttcttctg ttcttcacgc cccatgcccc	1864
tgctagcgta ttactgttct gtgacttccc tgtgacctct gcagaactcc tcatcctgcg	1924
tttggtctcc aggtgtcccc tttctgccgt gttcctaaca ttttgattcc tgtcttgaaa	1984
aaagcacctg ctgcaccgta agcccaggga tgtggcagct gcagtgggct tggctttgtg	2044
aggaactgag tgtgtccacg ttgggggaac atcatacttg atacacacgt ttttatttgc	2104
acaaagaaaa tgctatTTTTT ggagccagaa aaaaaaaaaa aa	2146

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100

1000

60
120
170
218
266
314
362
410
458
506
554
602
650

ctt cag ata aat gca gtg tca ctt tat ctc ctt tac ctt gtg gaa atg	698
Leu Gln Ile Asn Ala Val Ser Leu Tyr Leu Leu Tyr Leu Val Glu Met	
170 175 180 185	
att tcc tca gga ctc cag att atc tac aac act gat gag gtc tct ttt	746
Ile Ser Ser Gly Leu Gln Ile Ile Tyr Asn Thr Asp Glu Val Ser Phe	
186 191 196 201	
att caa aac ctt gta ttt tgt gtg gaa aga gtt tac cgt gtg cct gac	794
Ile Gln Asn Leu Val Phe Cys Val Glu Arg Val Tyr Arg Val Pro Asp	
202 207 212 217	
ttt ggt gtc tgg gaa aga gga agc aaa tat aat aat ggc agc aca gag	842
Phe Gly Val Trp Glu Arg Gly Ser Lys Tyr Asn Asn Gly Ser Thr Glu	
218 223 228 233	
cta cat tcg agc tcg gtt ggt tta gca aaa gca gct cta gaa gca att	890
Leu His Ser Ser Ser Val Gly Leu Ala Lys Ala Ala Leu Glu Ala Ile	
234 239 244 249	
aat gga ttc aac ctt ttt ggc aac cag ggc tgt tcg tgg tca gtt ata	938
Asn Gly Phe Asn Leu Phe Gly Asn Gln Gly Cys Ser Trp Ser Val Ile	
250 255 260 265	
ttt gtg gat ctc gat gct cac aat cgc aac agg caa act ttg tgc tcg	986
Phe Val Asp Leu Asp Ala His Asn Arg Asn Arg Gln Thr Leu Cys Ser	
266 271 276 281	
ctg tta ccc aga gaa tca aga tca cat aat aca gat gct gcc ctg ctc	1034
Leu Leu Pro Arg Glu Ser Arg Ser His Asn Thr Asp Ala Ala Leu Leu	
282 287 292 297	
ccc tgc atc agt tat cct gca ttt gcc ctg gat gat gaa gtt ctt ttt	1082
Pro Cys Ile Ser Tyr Pro Ala Phe Ala Leu Asp Asp Glu Val Leu Phe	
298 303 308 313	
agc cag aca ctt gat aaa gtg gtt aga aaa tta aaa gga aaa tat gga	1130
Ser Gln Thr Leu Asp Lys Val Val Arg Lys Leu Lys Gly Lys Tyr Gly	
314 319 324 329	
ttt aaa cgt ttc ttg aga gat ggg tat aga aca tca ttg gaa gat ccc	1178
Phe Lys Arg Phe Leu Arg Asp Gly Tyr Arg Thr Ser Leu Glu Asp Pro	
330 335 340 345	
aac aga tgc tac tac aag cca gct gaa att aag cta ttt gat ggc att	1226
Asn Arg Cys Tyr Tyr Lys Pro Ala Glu Ile Lys Leu Phe Asp Gly Ile	
346 351 356 361	
gaa tgt gaa ttt ccc ata ttt ttc ctt tat atg atg att gat gga gtt	1274
Glu Cys Glu Phe Pro Ile Phe Phe Leu Tyr Met Met Ile Asp Gly Val	
362 367 372 377	
ttt aga ggc aat cct aag caa gta cag gaa tat cag gat ctt ttg act	1322
Phe Arg Gly Asn Pro Lys Gln Val Gln Glu Tyr Gln Asp Leu Leu Thr	
378 383 388 393	

cca gta ctt cat cat acc aca gaa gga tat cct gtt gta cca aag tac	1370
Pro Val Leu His His Thr Thr Glu Gly Tyr Pro Val Val Pro Lys Tyr	
394 399 404 409	
tat tat gtg cca gct gac ttt gta gaa tat gaa aaa aat aac cct ggt	1418
Tyr Tyr Val Pro Ala Asp Phe Val Glu Tyr Glu Lys Asn Asn Pro Gly	
410 415 420 425	
agt caa aaa cga ttt cct agc aac tgt ggc cgt gat gga aaa ctg ttt	1466
Ser Gln Lys Arg Phe Pro Ser Asn Cys Gly Arg Asp Gly Lys Leu Phe	
426 431 436 441	
ctt tgg gga caa gca ctt tat atc atc gca aaa ctc ctg gct gat gaa	1514
Leu Trp Gly Gln Ala Leu Tyr Ile Ile Ala Lys Leu Leu Ala Asp Glu	
442 447 452 457	
ctt att agt cct aaa gac att gat cct gtc cag cgc tat gtc cca cta	1562
Leu Ile Ser Pro Lys Asp Ile Asp Pro Val Gln Arg Tyr Val Pro Leu	
458 463 468 473	
aag gat caa cgt aac gtg agc atg agg ttt tcc aat cag ggc cca ctg	1610
Lys Asp Gln Arg Asn Val Ser Met Arg Phe Ser Asn Gln Gly Pro Leu	
474 479 484 489	
gaa aat gac ttg gta gtt cat gtg gca ctt ata gca gaa agc caa aga	1658
Glu Asn Asp Leu Val Val His Val Ala Leu Ile Ala Glu Ser Gln Arg	
490 495 500 505	
ctt caa gtt ttt ctg aac aca tat ggt att caa act caa act cct caa	1706
Leu Gln Val Phe Leu Asn Thr Tyr Gly Ile Gln Thr Gln Thr Pro Gln	
506 511 516 521	
caa gta gaa ccc att cag ata tgg cct cag cag gag ctt gtg aaa gct	1754
Gln Val Glu Pro Ile Gln Ile Trp Pro Gln Gln Glu Leu Val Lys Ala	
522 527 532 537	
tat ttg cag ctg ggt atc aat gaa aag tta gga ctc tct gga agg cca	1802
Tyr Leu Gln Leu Gly Ile Asn Glu Lys Leu Gly Leu Ser Gly Arg Pro	
538 543 548 553	
gac agg ccc att ggc tgc ctc ggg aca tca aag att tat cgc att cta	1850
Asp Arg Pro Ile Gly Cys Leu Gly Thr Ser Lys Ile Tyr Arg Ile Leu	
554 559 564 569	
gga aag act gtg gtt tgt tac ccg att att ttc gac cta agt gat ttc	1898
Gly Lys Thr Val Val Cys Tyr Pro Ile Ile Phe Asp Leu Ser Asp Phe	
570 575 580 585	
tac atg tct cag gat gtt ttc ctg ctg ata gat gac ata aag aat gcg	1946
Tyr Met Ser Gln Asp Val Phe Leu Leu Ile Asp Asp Ile Lys Asn Ala	
586 591 596 601	
ctg cag ttc att aaa caa tat tgg aaa atg cat gga cgt cca ctt ttc	1994
Leu Gln Phe Ile Lys Gln Tyr Trp Lys Met His Gly Arg Pro Leu Phe	
602 607 612 617	
ctt gtt ctc atc cgg gaa gac aat ata aga ggt agc cgg ttc aac ccc	2042

842	847	852	857	
ggc tgg atc atc tcc aat aac cct gag tta ttc agt ggc acg ctg aaa				2762
Gly Trp Ile Ile Ser Asn Asn Pro Glu Leu Phe Ser Gly Thr Leu Lys				
858	863	868	873	
ata cga atc ggg tgg atc atc cat gcc atg gag tat gaa ctt cag atc				2810
Ile Arg Ile Gly Trp Ile Ile His Ala Met Glu Tyr Glu Leu Gln Ile				
874	879	884	889	
cgt ggc gga gac aag cca gcc ttg gac ttg tat cag ctg tca cct agt				2858
Arg Gly Gly Asp Lys Pro Ala Leu Asp Leu Tyr Gln Leu Ser Pro Ser				
890	895	900	905	
gaa gtt aaa cag ctt ctg ctg ggt ata ctg cag cct caa cag aat gga				2906
Glu Val Lys Gln Leu Leu Leu Gly Ile Leu Gln Pro Gln Gln Asn Gly				
906	911	916	921	
aga tgt tgg ctg aac agg cgt cag atc gat ggg tct ttg aat aga act				2954
Arg Cys Trp Leu Asn Arg Arg Gln Ile Asp Gly Ser Leu Asn Arg Thr				
922	927	932	937	
ccc acc ggg ttc tat gac cga gtg tgg cag att ctg gag cgc acg ccc				3002
Pro Thr Gly Phe Tyr Asp Arg Val Trp Gln Ile Leu Glu Arg Thr Pro				
938	943	948	953	
aat ggg atc att gtt gct ggg aag cat ttg cct cag caa cca acc ctg				3050
Asn Gly Ile Ile Val Ala Gly Lys His Leu Pro Gln Gln Pro Thr Leu				
954	959	964	969	
tca gat atg acc atg tat gag atg aat ttc tct ctc ctt gtt gaa gac				3098
Ser Asp Met Thr Met Tyr Glu Met Asn Phe Ser Leu Leu Val Glu Asp				
970	975	980	985	
acg ttg gga aat att gac cag cca cag tac aga cag atc gtt gta gag				3146
Thr Leu Gly Asn Ile Asp Gln Pro Gln Tyr Arg Gln Ile Val Val Glu				
986	991	996	1001	
tta ctt atg gtt gta tcc att gta ctg gaa aga aac ccc gag cta gaa				3194
Leu Leu Met Val Val Ser Ile Val Leu Glu Arg Asn Pro Glu Leu Glu				
1002	1007	1012	1017	
ttt caa gac aaa gta gat cta gac aga ctg gtc aaa gaa gca ttt aat				3242
Phe Gln Asp Lys Val Asp Leu Asp Arg Leu Val Lys Glu Ala Phe Asn				
1018	1023	1028	1033	
gaa ttt caa aaa gat cag agt cgg cta aag gaa att gaa aaa caa gat				3290
Glu Phe Gln Lys Asp Gln Ser Arg Leu Lys Glu Ile Glu Lys Gln Asp				
1034	1039	1044	1049	
gac atg act tcc ttt tac aac act cct ccc ctg gga aaa aga gga aca				3338
Asp Met Thr Ser Phe Tyr Asn Thr Pro Pro Leu Gly Lys Arg Gly Thr				
1050	1055	1060	1065	
tgc agc tat ttg aca aag gcg gtg atg aat ctg ctg ctg gaa gga gaa				3386
Cys Ser Tyr Leu Thr Lys Ala Val Met Asn Leu Leu Leu Glu Gly Glu				
1066	1071	1076	1081	

gtc aag cca aac aat gat gac ccg tgt ctg att agc tag tggggaaggt	3435
Val Lys Pro Asn Asn Asp Asp Pro Cys Leu Ile Ser *	
1082 / 1087 1092	
gtaggaagct ctgttgagac acatgttctg aagtgtgttg tgtttcatgt tcaagcttaa	3495
tcaaggcagc cattaatata cgaactgagc atgctgggga ggtgaatgcc acatccttgg	3555
cggggttatg gacctcttgc atgtcatagc caatctaacg gtaatggtaa atgcttttaa	3615
tcaagcagga aaaagttctc atgattatgc caactataat agtaatcctc actgagtgat	3675
aaaaatagtt tatgaattga aaatttgccg ctgcatgttg tatgatcaaa tagttcatca	3735
aaatgaatct ttgctctttg gactgaattc ttaccatact gccattaaaa taaatttgcc	3795
aactagtaat gcatactgga aatcaaaaga tactgaaaga atggatgaact tctcttagtg	3855
gtattgtcat gctaaaagat gttaatatat atcataaaag caaagtcagc cagctgatat	3915
tttggttctc aaaaactgca ttattaataa tatttttagta tacagagcta ttctacagtt	3975
tttacattgt aaacatgact gtggttttgt atttgctaaa tataggggtt ggactaaaat	4035
ataataaatc tgtaccttat caaacatttt ctttgagctc ctgctaaaaa taggacatgt	4095
ctatgattgt tcaaaaatat gttaaattta ggctcagcac agtagctcac acctgaaatc	4155
ttagcacttc gggaggctga ggcagggtga tcacttgagg ttaggagttc aagaccagcc	4215
cagccaacat ggtgaaaacc ctgtctctac taaaaatata aaaattagcc aggcattgat	4275
gtgcatgctt ttaaaccag ctactgagga ggctgaggca tgagaattgc ttgaaccagg	4335
agacggaggt tgcagtgagc tgaaatcctg ccactgcaca ccagcctggg tgacagagcg	4395
agactccatc tcaaaaaaaaa aaaa	4419

<210> 188
 <211> 1521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (595) .. (1083)

<220>
 <221> misc_feature
 <222> (1) ... (1521)
 <223> n = a,t,c or g

<400> 188

ttttttaaat aaaatagaat gtattttctct ccatacgaca atcttaggat agtccagggc	60
aggtaggcaa ttccgttcca caaggtcata aggagaacag gctagaggag cagccctctc	120
ttccttaaca tgtaatttct gaatttttggc cccagtgggt cctgtacttt tcatcatttc	180
cgagccagag agaagaggga aaaagaatag aagacaggca aatttctcat aaaaataaaa	240
tccagaaggc acacatttca cttctgctaa catctcattg gccaaaactt agaacctggc	300
tatagttacc tgcaaaggag gctggaaatg cagtctctag ctaagcaatc atatgtcaga	360
aattggcatt tccaaatacc cagtggatat tcatcaggat atacaaatga gaagttggaa	420
ncctgggaat tcttagaaat ttctgaaata ataagttatc cttttaaaaa aaaaaacttt	480
tatttttaggt tcagggatac atgtataggt ttgttataaa gataaactcg tgttattctg	540
aaaagacttc catttgcaga catcgctgct gcccagaact ccctgccacc agcc atg	597
	Met
	1
gcc aac ccc act gtg ttc ttc aac att gca att gat agt gag tcc ttg	645
Ala Asn Pro Thr Val Phe Phe Asn Ile Ala Ile Asp Ser Glu Ser Leu	
2 7 12 17	
ggc tgc atc tcc ttc aag cta ttt gca gac aaa gtt cta aag atg gaa	693
Gly Cys Ile Ser Phe Lys Leu Phe Ala Asp Lys Val Leu Lys Met Glu	
18 23 28 33	
gaa aat ttt tgt gct ctg aac act gga gag aaa gta ttt ggt gat aaa	741
Glu Asn Phe Cys Ala Leu Asn Thr Gly Glu Lys Val Phe Gly Asp Lys	
34 39 44 49	
ggc ccc tgc ttt tac aga att att ccg ggg tgt tgt cag ggt ggt gac	789
Gly Pro Cys Phe Tyr Arg Ile Ile Pro Gly Cys Cys Gln Gly Gly Asp	
50 55 60 65	
ttc aca cac cat aat ggc act ggt ggc aag tcc ctc tac agc aag gaa	837
Phe Thr His His Asn Gly Thr Gly Gly Lys Ser Leu Tyr Ser Lys Glu	
66 71 76 81	
ttt gat gat gag aac ttc atc cta aag cat aca gct cct ggc gtc ttg	885
Phe Asp Asp Glu Asn Phe Ile Leu Lys His Thr Ala Pro Gly Val Leu	
82 87 92 97	
tcc acg gca aat gct gga ccc acc aca aat ggt tcc cag ttt ttc atc	933
Ser Thr Ala Asn Ala Gly Pro Thr Thr Asn Gly Ser Gln Phe Phe Ile	
98 103 108 113	
tgt act gcc aag aca gag gat gga tgc cag cat gtg gtc ttt ggc aag	981
Cys Thr Ala Lys Thr Glu Asp Gly Cys Gln His Val Val Phe Gly Lys	
114 119 124 129	
gtg aaa gat ggc atg agt att gtg gaa gcc ctg gaa cgc tct ggg tcc	1029
Val Lys Asp Gly Met Ser Ile Val Glu Ala Leu Glu Arg Ser Gly Ser	
130 135 140 145	

agg aat ggt aag acc agc aag aag atc aca gct gct aac tgt gga caa 1077
 Arg Asn Gly Lys Thr Ser Lys Lys Ile Thr Ala Ala Asn Cys Gly Gln
 146 151 156 161

ctc taa taaatttgat tgttttatct gaaccaccag atcgttcctt ctatagotca 1133
 Leu *
 162

ggaaagcatg cttccacccc atttgctcac agcatcctat aatctttgca cagtcccttg 1193

ggttccatat tttccttata ctcttccatg tctagctgga tcgcagagtt aagtttataa 1253

ttacaaaatg aaaactaagt aacaagaaga aaataaaaga cttccagcaa tttttataact 1313

ctttagtcac tactgtggat atctaaaaga aattgggtta ataaataaga aatattacat 1373

ttagcaaatt tataaacaac tatagcctga gattnnngnn gntcaaactt tagaaaatac 1433

cagtgaacat ttttgggtaa tattcaaaga atgtgacatt cagatctcnt ggnttccncg 1493

acggttcttc aggtctctaa ngggacct 1521

<210> 189
 <211> 2413
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (258) .. (1922)

<400> 189
 aagctggtac gcctgcaggt accggtccgg aattcccggg tcgacgattt cgtcccagcc 60

cctccccagg ccgcgagcgc ccctgccgcg gtgcctggcc tcccctccca gactgcaggg 120

acagcaccocg gtaactgcga gtggagcgga ggaccocgag ggctgaggag agaggaggcg 180

gcggcttagc tgctacgggg tccggccggc gccctcccga ggggggctca ggaggaggaa 240

ggaggaccocg tgcgaga atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg 290
 Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu
 1 5

ctg ctc tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg 338
 Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg
 12 17 22 27

cat cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgt cac tat 386
 His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr
 28 33 38 43

gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc aag gga 434

Gly	Thr	Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	
44					49					54					59	
gtc	tgt	gaa	gct	aca	tgc	gaa	cct	gga	tgt	aag	ttt	ggg	gag	tgc	gtg	482
Val	Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
60					65					70					75	
gga	cca	aac	aaa	tgc	aga	tgc	ttt	cca	gga	tac	acc	ggg	aaa	acc	tgc	530
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	
76					81					86					91	
agt	caa	gat	gtg	aat	gag	tgt	gga	atg	aaa	ccc	cgg	cca	tgc	caa	cac	578
Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	
92					97					102					107	
aga	tgt	gtg	aat	aca	cac	gga	agc	tac	aag	tgc	ttt	tgc	ctc	agt	ggc	626
Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	
108					113					118					123	
cac	atg	ctc	atg	cca	gat	gct	acg	tgt	gtg	aac	tct	agg	aca	tgt	gcc	674
His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	
124					129					134					139	
atg	ata	aac	tgt	cag	tac	agc	tgt	gaa	gac	aca	gaa	gaa	ggg	cca	cag	722
Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	
140					145					150					155	
tgc	ctg	tgt	cca	tcc	tca	gga	ctc	cgc	ctg	gcc	cca	aat	gga	aga	gac	770
Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	
156					161					166					171	
tgt	cta	gat	att	gat	gaa	tgt	gcc	tct	ggg	aaa	gtc	atc	tgt	ccc	tac	818
Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	
172					177					182					187	
aat	cga	aga	tgt	gtg	aac	aca	ttt	gga	agc	tac	tac	tgc	aaa	tgt	cac	866
Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	
188					193					198					203	
att	ggg	ttc	gaa	ctg	caa	tat	atc	agt	gga	cga	tat	gac	tgt	ata	gat	914
Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	
204					209					214					219	
ata	aat	gaa	tgt	act	atg	gat	agc	cat	acg	tgc	agc	cac	cat	gcc	aat	962
Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	
220					225					230					235	
tgc	ttc	aat	acc	caa	ggg	tcc	ttc	aag	tgt	aaa	tgc	aag	cag	gga	tat	1010
Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	
236					241					246					251	
aaa	ggc	aat	gga	ctt	cgg	tgt	tct	gct	atc	cct	gaa	aat	tct	gtg	aag	1058
Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	
252					257					262					267	
gaa	gtc	ctc	aga	gca	cct	ggg	acc	atc	aaa	gac	aga	atc	aag	aag	ttg	1106
Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	

268	273	278	283	
ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa aat gtt				1154
Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn Val				
284	289	294	299	
acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg cag ccc				1202
Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro				
300	305	310	315	
ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat gga ggt				1250
Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly				
316	321	326	331	
aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat gag aaa				1298
Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys				
332	337	342	347	
aga gaa gag aaa gcc ctg aag aat gac ata gag gag cga agc ctg cga				1346
Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg				
348	353	358	363	
gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc ggc ctg				1394
Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu				
364	369	374	379	
att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat aaa gca				1442
Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Ala				
380	385	390	395	
gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt gac				1490
Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp				
396	401	406	411	
tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat cga				1538
Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg				
412	417	422	427	
gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt cac				1586
Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His				
428	433	438	443	
aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa ccc				1634
Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro				
444	449	454	459	
caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac aaa				1682
Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys				
460	465	470	475	
gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg gca				1730
Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala				
476	481	486	491	
tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa att				1778
Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile				
492	497	502	507	

Ala Lys Arg Tyr His Met Asp Ala Ser Gly Glu Ala Val Ser Glu Thr	
19 24 29 34	
ctt cag ttt aaa gct caa gat ctc tta agg gca gtc cca aga tcc aga	319
Leu Gln Phe Lys Ala Gln Asp Leu Leu Arg Ala Val Pro Arg Ser Arg	
35 40 45 50	
gca gag atg tat gat gac gtc cac agc gat ggc aga tac tcc ctc agt	367
Ala Glu Met Tyr Asp Asp Val His Ser Asp Gly Arg Tyr Ser Leu Ser	
51 56 61 66	
gga tct gta gct cac tct aga gat gcc gga aga gaa ggc ctg aga agt	415
Gly Ser Val Ala His Ser Arg Asp Ala Gly Arg Glu Gly Leu Arg Ser	
67 72 77 82	
gac gta ttt cca ggg cct tcc ttc aga tca agc aac cct tcc atc agt	463
Asp Val Phe Pro Gly Pro Ser Phe Arg Ser Ser Asn Pro Ser Ile Ser	
83 88 93 98	
gat gac agc tac ttt cgc aaa gaa tgt ggc cgg gat ctg gaa ttt tct	511
Asp Asp Ser Tyr Phe Arg Lys Glu Cys Gly Arg Asp Leu Glu Phe Ser	
99 104 109 114	
cac tct gat tct cgg gac cag gtc att ggc cac cgg aaa ttg ggg cat	559
His Ser Asp Ser Arg Asp Gln Val Ile Gly His Arg Lys Leu Gly His	
115 120 125 130	
ttc cgt tct cag gac tgg aaa ttt gcg ctc cgt ggt tct tgg gaa caa	607
Phe Arg Ser Gln Asp Trp Lys Phe Ala Leu Arg Gly Ser Trp Glu Gln	
131 136 141 146	
gac ttt ggc cat cca gtt tct caa gag tcc tct tgg tca cag gag tat	655
Asp Phe Gly His Pro Val Ser Gln Glu Ser Ser Trp Ser Gln Glu Tyr	
147 152 157 162	
agt ttt ggt ccc tct gca gtt ttg ggg gac ttt gga tct tcc agg ctg	703
Ser Phe Gly Pro Ser Ala Val Leu Gly Asp Phe Gly Ser Ser Arg Leu	
163 168 173 178	
att gag aaa gag tgt ttg gag aag gag agt cgg gat tat gac gtg gac	751
Ile Glu Lys Glu Cys Leu Glu Lys Glu Ser Arg Asp Tyr Asp Val Asp	
179 184 189 194	
cat cct ggg gag gct gac tct gtg ctt agg ggc agc agt caa gtc cag	799
His Pro Gly Glu Ala Asp Ser Val Leu Arg Gly Ser Ser Gln Val Gln	
195 200 205 210	
gcc aga ggt cga gct cta aac atc gtt gac cag gaa ggt tcc ctc cta	847
Ala Arg Gly Arg Ala Leu Asn Ile Val Asp Gln Glu Gly Ser Leu Leu	
211 216 221 226	
gga aag ggg gag act cag ggc ctg ctc aca gct aag ggg ggt gtt ggg	895
Gly Lys Gly Glu Thr Gln Gly Leu Leu Thr Ala Lys Gly Gly Val Gly	
227 232 237 242	
aaa ctt gtc aca ttg aga aat gtg agc aca aaa aaa ata ccc acc gtg	943
Lys Leu Val Thr Leu Arg Asn Val Ser Thr Lys Lys Ile Pro Thr Val	

243	248	253	258	
aat cgt att act ccc aaa act cag ggc act aac caa atc cag aaa aac				991
Asn Arg Ile Thr Pro Lys Thr Gln Gly Thr Asn Gln Ile Gln Lys Asn				
259	264	269	274	
act cca agt cct gat gtg acc ctg ggg aca aac cca ggg aca gaa gat				1039
Thr Pro Ser Pro Asp Val Thr Leu Gly Thr Asn Pro Gly Thr Glu Asp				
275	280	285	290	
atc cag ttc ccc att cag aag atc cct ctg ggg ctg gat ctg aag aat				1087
Ile Gln Phe Pro Ile Gln Lys Ile Pro Leu Gly Leu Asp Leu Lys Asn				
291	296	301	306	
ctt cgg ctc ccc aga aga aag atg agc ttt gac atc ata gat aag tct				1135
Leu Arg Leu Pro Arg Arg Lys Met Ser Phe Asp Ile Ile Asp Lys Ser				
307	312	317	322	
gat gtt ttt tca aga ttt ggg ata gaa ata atc aaa tgg gca gga ttc				1183
Asp Val Phe Ser Arg Phe Gly Ile Glu Ile Ile Lys Trp Ala Gly Phe				
323	328	333	338	
cac acc ata aaa gat gat att aaa ttt tcc caa ctt ttc cag act ctc				1231
His Thr Ile Lys Asp Asp Ile Lys Phe Ser Gln Leu Phe Gln Thr Leu				
339	344	349	354	
ttt gaa ctt gaa aca gaa acc tgt gct aaa atg ctt gcc tca ttc aaa				1279
Phe Glu Leu Glu Thr Glu Thr Cys Ala Lys Met Leu Ala Ser Phe Lys				
355	360	365	370	
tgt tcc tta aaa cca gag cac aga gat ttt tgc ttt ttt act atc aaa				1327
Cys Ser Leu Lys Pro Glu His Arg Asp Phe Cys Phe Phe Thr Ile Lys				
371	376	381	386	
ttt tta aag cac tct gct ttg aaa aca ccc aga gtt gat aat gag ttt				1375
Phe Leu Lys His Ser Ala Leu Lys Thr Pro Arg Val Asp Asn Glu Phe				
387	392	397	402	
tta aac atg ctt tta gac aaa ggt gct gtg aag acc aaa aat tgc ttt				1423
Leu Asn Met Leu Leu Asp Lys Gly Ala Val Lys Thr Lys Asn Cys Phe				
403	408	413	418	
ttt gaa atc ata aag cct ttt gac aag tac ata atg aga ctt caa gac				1471
Phe Glu Ile Ile Lys Pro Phe Asp Lys Tyr Ile Met Arg Leu Gln Asp				
419	424	429	434	
cgg ctt ctg aag agt gtc aca cct ttg ctt atg gcc tgc aat gcc tac				1519
Arg Leu Leu Lys Ser Val Thr Pro Leu Leu Met Ala Cys Asn Ala Tyr				
435	440	445	450	
gag cta agt gtc aag atg aag acc ctc agt aac ccc ctg gac ttg gct				1567
Glu Leu Ser Val Lys Met Lys Thr Leu Ser Asn Pro Leu Asp Leu Ala				
451	456	461	466	
ctt gcc cta gaa acc acc aac tct ctc tgc cgg aag tct ttg gcc ctt				1615
Leu Ala Leu Glu Thr Thr Asn Ser Leu Cys Arg Lys Ser Leu Ala Leu				
467	472	477	482	

ttg gga cag aca ttt tcc ttg gcc tct tct ttc cgg cag gag aaa atc	1663
Leu Gly Gln Thr Phe Ser Leu Ala Ser Ser Phe Arg Gln Glu Lys Ile	
483 488 493 498	
tta gaa gct gtc ggc ctg caa gat ata gct ccc tca cct gct gcg ttt	1711
Leu Glu Ala Val Gly Leu Gln Asp Ile Ala Pro Ser Pro Ala Ala Phe	
499 504 509 514	
cca aac ttc gaa gac tcc act ttg ttt ggg cga gag tac ata gac cac	1759
Pro Asn Phe Glu Asp Ser Thr Leu Phe Gly Arg Glu Tyr Ile Asp His	
515 520 525 530	
ctg aag gcc tgg cta gtc agc agc gga tgt ccc ctg cag gtt aag aaa	1807
Leu Lys Ala Trp Leu Val Ser Ser Gly Cys Pro Leu Gln Val Lys Lys	
531 536 541 546	
gcc gaa cca gag ccg atg cga gag gag gag aaa atg att cct cct acg	1855
Ala Glu Pro Glu Pro Met Arg Glu Glu Glu Lys Met Ile Pro Pro Thr	
547 552 557 562	
aaa cct gaa att cag gcc aag gct cca agt agt ctg agt gat gct gtc	1903
Lys Pro Glu Ile Gln Ala Lys Ala Pro Ser Ser Leu Ser Asp Ala Val	
563 568 573 578	
ccc cag cga gca gat cac agg gta gtg ggc acc atc gac cag ctt gtg	1951
Pro Gln Arg Ala Asp His Arg Val Val Gly Thr Ile Asp Gln Leu Val	
579 584 589 594	
aaa cgt gtc atc gaa ggc agc ctg tct ccc aaa gag aga act ctt ctc	1999
Lys Arg Val Ile Glu Gly Ser Leu Ser Pro Lys Glu Arg Thr Leu Leu	
595 600 605 610	
aaa gag gac cct gct tac tgg ttt ttg tot gat gaa aat agt ctg gag	2047
Lys Glu Asp Pro Ala Tyr Trp Phe Leu Ser Asp Glu Asn Ser Leu Glu	
611 616 621 626	
tat aaa tat tac aag ctg aag ttg gca gaa atg cag cgg atg agc gag	2095
Tyr Lys Tyr Tyr Lys Leu Lys Leu Ala Glu Met Gln Arg Met Ser Glu	
627 632 637 642	
aac ttg cga gga gcc gac cag aag ccg acc tca gca gac tgt gca gtg	2143
Asn Leu Arg Gly Ala Asp Gln Lys Pro Thr Ser Ala Asp Cys Ala Val	
643 648 653 658	
agg gcc atg ctg tac tcc cgg gct gtc cgc aac ctc aag aag aaa ctc	2191
Arg Ala Met Leu Tyr Ser Arg Ala Val Arg Asn Leu Lys Lys Lys Leu	
659 664 669 674	
ctt ccg tgg cag cgg cgg ggg ctc ctc cgt gct caa ggg ctc cgg ggc	2239
Leu Pro Trp Gln Arg Arg Gly Leu Leu Arg Ala Gln Gly Leu Arg Gly	
675 680 685 690	
tgg aag gcg agg aga gcg acc acc ggg acc cag acc ctc cta tcc tca	2287
Trp Lys Ala Arg Arg Ala Thr Thr Gly Thr Gln Thr Leu Leu Ser Ser	
691 696 701 706	

ggc acc agg ctg aaa cac cac ggc cgg cag gct cca ggc ctc tca cag	2335
Gly Thr Arg Leu Lys His His Gly Arg Gln Ala Pro Gly Leu Ser Gln	
707 712 717 722	
gca aaa cca tcc ctg cca gac aga aat gat gct gcc aag gac tgc ccg	2383
Ala Lys Pro Ser Leu Pro Asp Arg Asn Asp Ala Ala Lys Asp Cys Pro	
723 728 733 738	
cca gac cca gtt gga cct tct cct cag gac ccc agc tta gaa gcc tca	2431
Pro Asp Pro Val Gly Pro Ser Pro Gln Asp Pro Ser Leu Glu Ala Ser	
739 744 749 754	
ggc cca tcc ccc aag cca gca gga gtg gac atc tct gaa gca cct cag	2479
Gly Pro Ser Pro Lys Pro Ala Gly Val Asp Ile Ser Glu Ala Pro Gln	
755 760 765 770	
acc tct tct ccc tgc cca tct gct gac att gac atg aag aca atg gag	2527
Thr Ser Ser Pro Cys Pro Ser Ala Asp Ile Asp Met Lys Thr Met Glu	
771 776 781 786	
act gca gag aaa ctg gct aga ttt gtt gct cag gtg gga cca gag atc	2575
Thr Ala Glu Lys Leu Ala Arg Phe Val Ala Gln Val Gly Pro Glu Ile	
787 792 797 802	
gaa caa ttc agc ata gaa aac agc acc gat aac cct gac ctg tgg ttt	2623
Glu Gln Phe Ser Ile Glu Asn Ser Thr Asp Asn Pro Asp Leu Trp Phe	
803 808 813 818	
cta cat gac caa aat agt tct gct ttc aaa ttc tat cga aag aaa gtg	2671
Leu His Asp Gln Asn Ser Ser Ala Phe Lys Phe Tyr Arg Lys Lys Val	
819 824 829 834	
ttt gaa cta tgt cca tca att tgt ttc acg tca tct ccg cac aac ctt	2719
Phe Glu Leu Cys Pro Ser Ile Cys Phe Thr Ser Ser Pro His Asn Leu	
835 840 845 850	
cac act ggt ggt ggt gac acc acg ggt tct cag gag agc ccc gtg gac	2767
His Thr Gly Gly Gly Asp Thr Thr Gly Ser Gln Glu Ser Pro Val Asp	
851 856 861 866	
ctc atg gaa ggg gaa gca gag ttt gaa gac gag ccc cct ccg cgg gag	2815
Leu Met Glu Gly Glu Ala Glu Phe Glu Asp Glu Pro Pro Pro Arg Glu	
867 872 877 882	
gct gag ctg gag agc cca gag gtg atg cct gag gag gag gac gag gac	2863
Ala Glu Leu Glu Ser Pro Glu Val Met Pro Glu Glu Glu Asp Glu Asp	
883 888 893 898	
gat gag gat ggg gga gag gag gcc ccc gct cct gga ggg gcg ggc aag	2911
Asp Glu Asp Gly Gly Glu Glu Ala Pro Ala Pro Gly Gly Ala Gly Lys	
899 904 909 914	
tct gag ggc agc acc cct gcc gac ggc ctt ccc ggc gag gct gcc gag	2959
Ser Glu Gly Ser Thr Pro Ala Asp Gly Leu Pro Gly Glu Ala Ala Glu	
915 920 925 930	
gac gac ctg gct gga gca cct gcc ttg tca cag gcc tcc tca ggt acc	3007

ggctcaggtg	cacaactgac	tctctttttc	actccctagg	ggaacccccct	cggaagggga	3975
agggttgggt	gctgacgggc	aggagcacia	agaagacaca	ttcgatgtgt	tccgacagag	4035
gatgatgcag	atgtacagac	acaagcgggc	caacaaatag	gtatgttcac	aggccagtgt	4095
gtaaggccgt	ctgccctcgc	tggcgtgctg	gtatgcagag	aaatttcccc	caacaaagtt	4155
gatgttcctt	gctcccccaa	aaatgccaca	cacaaaaaaa	atcacaaaat	tctgtgaggg	4215
aaacaaaagg	gtctatggat	gtggatatgc	cccattctta	ccttccaggt	ttgctgaagg	4275
agcaaacctc	acactggcca	agggcagatg	cgcattggcct	gcctgggtgcc	cggcctgtga	4335
gcccccaag	gcctccaggc	cagcctccgt	ggatgtgcgt	gtggaaatag	gccacgcctg	4395
tctctttctt	tgctcaagtt	ttctctcaca	gatgacagcc	acctaccaca	taacatgacc	4455
agcaaacgga	ctgttcctag	tccagagggc	cttgccatca	tgcaagtgga	agggcgactg	4515
tgacagccac	tgccacagag	gatggcagtt	ggctgtgtcc	ctttgtgagg	gtcttcaaat	4575
ccttttcttt	ctgcaggggc	ttgggcctgt	aaatatcctc	atctttctat	tctttttttt	4635
tttttagttg	ccccctcacc	taattttcac	ctcagttttg	aacaaaatcg	ttctcttctt	4695
gaatagatca	aaaccactga	tgtgaaagat	aagccttgaa	gcagcaattg	cccttaaaac	4755
atcatccctg	ccctggatcg	gcctggagcc	agtgcccaag	tacggtttgg	tgtgtacatg	4815
aaaacaaaacg	tctctgcagt	ctctggggcg	gaggtttcgc	tggtttttct	ttctctcaaa	4875
gaaaaaaaaca	tgcaccattt	tcaatgtgct	tttgctctc	ctctctgttc	acatgctttt	4935
agcagcaagt	cccccccaaa	tctgtcttgg	ttccccctca	gaagggtggcg	ctgccccoga	4995
aaggcacctc	agcctgtgag	tgctgaggaa	ccagctcctc	tggttgattt	tccagttgga	5055
ctggccattg	ctctccagaa	gtgctctggt	agcaaacgtg	atgtggaaac	gatcacagat	5115
ggtgtttttct	cgttggttcgc	cagaatttat	acgggggaga	caaattcccg	gtaattacca	5175
agtctgcact	cggttaccaa	agctctgaag	ctctctgaac	agttgccata	cttgagttga	5235
tgaatgtggt	attcatgggt	tctcatctca	tcaatgcata	ttgagagact	taatgaaatt	5295
ttagcaacag	tatagaatag	ctctatcggg	tggggagtaa	tcattaaaca	gatgaaatcg	5355
gccccagatt	tacatgtctc	tttagaatcc	acagtgtgaa	caaactacag	ttacaaaggg	5415
atggggggttg	taaaccctct	gagactctgc	acttttcgca	cgtatggcat	cgtcaagtgc	5475
tgtcttatta	cagcctttgt	aaggagaggc	aggctcctcc	tgggggtgggc	tctgcagctg	5535
ctctattttcc	aggcatgtga	tcgccccgc	tctccagatt	ccccagcact	ctgctgcgtg	5595
taactccact	caattctcca	ctcatccttc	cttgtgaagc	aggatcgttg	aagttttaag	5655

tatgggcaaa aatctggaaa acttaggatc cctctgacac cccaggatta ggggacacag 5715
cagtggctag ggcacagcc acagaactga gcgggaaatg ccacttgat tggctgtaaa 5775
gaaatcctgg ctttgggcca ggcacagtgg ctcaagcctg taatcccagc acttttaggag 5835
gttgaggcgg atggatcacc tgaggtcagg agtttgagac cagcctggcc aacatggtgt 5895
aaccccgctct ctactaaaaa tacaaaaaaa ttagccaggc gtggtagcgg gcacctgtaa 5955
tcccagctac tcaggaggct gaggcaggag aatcacttga accggggagg cagaggttgc 6015
agtgagctga gatcatgcc a cccactcca gcctgggcca cagagcaaga ctccatctcc 6075
aaaaaaaaaaa aaa 6088

<210> 191
<211> 1915
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (179)..(1522)

<400> 191
acggggcccca tagaacgcct gaggtaccgc tccggaattc ccgggtcgac ccacgcgtcc 60
ggttcaggca gtgacgtaac ttgctgcctt aggtggcctt ccgctctggc ggctgtcgcg 120
acgggggttc agggaaatatt tactgggctt ctccgctccc tctgctcttg gaggtgcc 178
atg agg tca gtt agc tac gtg cag cgc gtg gcg ctg gag ttc agc ggg 226
Met Arg Ser Val Ser Tyr Val Gln Arg Val Ala Leu Glu Phe Ser Gly
1 5 10 15
agc ctc ttc ccg cac gca atc tgc ctc gga gac gtt gat aac gat acg 274
Ser Leu Phe Pro His Ala Ile Cys Leu Gly Asp Val Asp Asn Asp Thr
17 22 27 32
tta aat gaa ctg gtg gtg gga gac acc agc ggg aag gtg tct gtg tat 322
Leu Asn Glu Leu Val Val Gly Asp Thr Ser Gly Lys Val Ser Val Tyr
33 38 43 48
aaa aat gat gac agt cgg cca tgg ctc acc tgt tcc tgc cag gga atg 370
Lys Asn Asp Asp Ser Arg Pro Trp Leu Thr Cys Ser Cys Gln Gly Met
49 54 59 64
ctg act tgc gtt ggg gtt gga gac gtg tgt aat aaa gga aag aac ctg 418
Leu Thr Cys Val Gly Val Gly Asp Val Cys Asn Lys Gly Lys Asn Leu
65 70 75 80
ttg gtg gca gtg agt gct gaa ggc tgg ttt cat ttg ttt gac ctg aca 466
Leu Val Ala Val Ser Ala Glu Gly Trp Phe His Leu Phe Asp Leu Thr

81	86	91	96	
cct gcc aag gtg ttg gat gct tct ggg cac cac gag aca cta atc gga				514
Pro Ala Lys Val Leu Asp Ala Ser Gly His His Glu Thr Leu Ile Gly				
97	102	107	112	
gag gag cag cgt cca gtc ttc aag cag cac atc cct gcc aac acc aag				562
Glu Glu Gln Arg Pro Val Phe Lys Gln His Ile Pro Ala Asn Thr Lys				
113	118	123	128	
gtc atg ctg atc agc gac atc gat gga gat ggg tgt cgt gag ctg gtg				610
Val Met Leu Ile Ser Asp Ile Asp Gly Asp Gly Cys Arg Glu Leu Val				
129	134	139	144	
gtg ggc tac aca gac cgt gtg gtg cga gct ttc cgc tgg gag gag cta				658
Val Gly Tyr Thr Asp Arg Val Val Arg Ala Phe Arg Trp Glu Glu Leu				
145	150	155	160	
ggt gag ggt cct gaa cat ctg aca ggg cag ctg gtg tcc ctc aag aaa				706
Gly Glu Gly Pro Glu His Leu Thr Gly Gln Leu Val Ser Leu Lys Lys				
161	166	171	176	
tgg atg ctg gag ggt cag gtg gac agc ctc tca gtg act ctg ggg cca				754
Trp Met Leu Glu Gly Gln Val Asp Ser Leu Ser Val Thr Leu Gly Pro				
177	182	187	192	
ctg ggt ctt cct gaa ctg atg gtg tct cag cca ggt tgt gcg tat gca				802
Leu Gly Leu Pro Glu Leu Met Val Ser Gln Pro Gly Cys Ala Tyr Ala				
193	198	203	208	
att cta ctg tgt acc tgg aaa aag gac act ggg tcc cct cct gcc tct				850
Ile Leu Leu Cys Thr Trp Lys Lys Asp Thr Gly Ser Pro Pro Ala Ser				
209	214	219	224	
gaa ggg ccc acg gat ggt agt agg gag acc cca gct gcc cga gac gtg				898
Glu Gly Pro Thr Asp Gly Ser Arg Glu Thr Pro Ala Ala Arg Asp Val				
225	230	235	240	
gtg ctg cac cag aca tct ggc cgt atc cac aac aag aat gtc tcc act				946
Val Leu His Gln Thr Ser Gly Arg Ile His Asn Lys Asn Val Ser Thr				
241	246	251	256	
cac cta att ggc aac atc aaa caa ggc cac ggc act gag agt agt ggc				994
His Leu Ile Gly Asn Ile Lys Gln Gly His Gly Thr Glu Ser Ser Gly				
257	262	267	272	
tct ggc ctc ttt gcc ctg tgc acc ctg gat ggg aca ctg aag ctc atg				1042
Ser Gly Leu Phe Ala Leu Cys Thr Leu Asp Gly Thr Leu Lys Leu Met				
273	278	283	288	
gaa gaa atg gaa gaa gca gac aag ctg ctg tgg tca gtg cag gtg gat				1090
Glu Glu Met Glu Glu Ala Asp Lys Leu Leu Trp Ser Val Gln Val Asp				
289	294	299	304	
cac cag ctc ttt gcc ctg gag aaa ctg gat gtc acc ggc aac ggg cat				1138
His Gln Leu Phe Ala Leu Glu Lys Leu Asp Val Thr Gly Asn Gly His				
305	310	315	320	

gag gag gta gtt gca tgc gcc tgg gat gga cag aca tat atc att gat	1186
Glu Glu Val Val Ala Cys Ala Trp Asp Gly Gln Thr Tyr Ile Ile Asp	
321 326 331 336	
cac aac cgc acc gtc gtc cgc ttc caa gtg gat gaa aat atc cgt gcc	1234
His Asn Arg Thr Val Val Arg Phe Gln Val Asp Glu Asn Ile Arg Ala	
337 342 347 352	
ttc tgt gca ggc ctg tac gcc tgc aaa gag ggc cgc aac agc ccc tgc	1282
Phe Cys Ala Gly Leu Tyr Ala Cys Lys Glu Gly Arg Asn Ser Pro Cys	
353 358 363 368	
ctc gta tat gtc act ttc aac cag aag atc tat gtg tac tgg gag gtg	1330
Leu Val Tyr Val Thr Phe Asn Gln Lys Ile Tyr Val Tyr Trp Glu Val	
369 374 379 384	
cag ctg gag cgg atg gag tct acc aat ctg gtg aaa ctg ctg gag acc	1378
Gln Leu Glu Arg Met Glu Ser Thr Asn Leu Val Lys Leu Leu Glu Thr	
385 390 395 400	
aag ccg gag tac cac agc ctg ctg cag gag ctg ggc gtg gat cct gac	1426
Lys Pro Glu Tyr His Ser Leu Leu Gln Glu Leu Gly Val Asp Pro Asp	
401 406 411 416	
gac ctc cct gtg act cgt gcc ctg ctt cac caa acg ctc tac cat cca	1474
Asp Leu Pro Val Thr Arg Ala Leu Leu His Gln Thr Leu Tyr His Pro	
417 422 427 432	
gac cag cca cca cag tgt gct ccc tca agc ctc cag gat ccc acc tag	1522
Asp Gln Pro Pro Gln Cys Ala Pro Ser Ser Leu Gln Asp Pro Thr *	
433 438 443 448	
ctgtacttgc ctcatagctg gtgaaggatt cttctgaacc cccaccctac cccctaaagg	1582
cgtcttttga tcacactgcg cggctgctgg ctccatcaca aaacaatgaa ggagggaagtg	1642
ggacgcagag agaaacgcac atggggagaa cgccacgtga aggctgaggt cgggataatg	1702
catctgcaag ccaaggaaca cctaagagga ccagcaaacc accagaagcc aggggagagg	1762
cgtggaacag accctgcctt acagctgtca gaaggaacca accctgcca caccttcctg	1822
ttgtactttc agcttcocaga actgtgcctg cagggcttga gagaaatgga gacaaagaag	1882
gccgtgggca ggaggccaag agaagcccag cag	1915

<210> 192
 <211> 1136
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (82)..(918)

<400> 192

atttggccct cgaggcaaga aattcggcac gaggcgcac tcccgcctagg agttcctagt	60
aaagtggcgg gagccgcagc t atg gag ccg cag gag gag aga gaa acg cag	111
Met Glu Pro Gln Glu Glu Arg Glu Thr Gln	
1 5	
gtt gct gcg tgg tta aaa aaa ata ttt gga gat cat cct att cca cag	159
Val Ala Ala Trp Leu Lys Lys Ile Phe Gly Asp His Pro Ile Pro Gln	
11 16 21 26	
tat gag gtg aac cca cgg acc aca gag att tta cat cac ctt tca gaa	207
Tyr Glu Val Asn Pro Arg Thr Thr Glu Ile Leu His His Leu Ser Glu	
27 32 37 42	
cgc aac agg gtc cgg gac agg gat gtc tac ctg gta ata gag gac ttg	255
Arg Asn Arg Val Arg Asp Arg Asp Val Tyr Leu Val Ile Glu Asp Leu	
43 48 53 58	
aag cag aaa gca agt gaa tac gag tca gaa gcc aag tat ctt caa gac	303
Lys Gln Lys Ala Ser Glu Tyr Glu Ser Glu Ala Lys Tyr Leu Gln Asp	
59 64 69 74	
ctt ctc atg gag agt gtg aat ttt tcc ccc gcc aat ctc tct agc act	351
Leu Leu Met Glu Ser Val Asn Phe Ser Pro Ala Asn Leu Ser Ser Thr	
75 80 85 90	
ggt tcc agg tat ctg aat gct ttg gtt gac agt gcg gtg gcc ctt gaa	399
Gly Ser Arg Tyr Leu Asn Ala Leu Val Asp Ser Ala Val Ala Leu Glu	
91 96 101 106	
aca aag gat acc tcg cta gct agt ttt atc cct gca gtg aat gat ttg	447
Thr Lys Asp Thr Ser Leu Ala Ser Phe Ile Pro Ala Val Asn Asp Leu	
107 112 117 122	
acc tct gat ctc ttt cgt acc aaa tcc aaa agt gaa gaa atc aag att	495
Thr Ser Asp Leu Phe Arg Thr Lys Ser Lys Ser Glu Glu Ile Lys Ile	
123 128 133 138	
gaa ctg gaa aaa ctt gaa aaa aat tta act gca act tta gta tta gaa	543
Glu Leu Glu Lys Leu Glu Lys Asn Leu Thr Ala Thr Leu Val Leu Glu	
139 144 149 154	
aaa tgt cta caa gag gat gtc aag aaa gca gag ttg cat ctg tct aca	591
Lys Cys Leu Gln Glu Asp Val Lys Lys Ala Glu Leu His Leu Ser Thr	
155 160 165 170	
gaa agg gcc aaa gtt gat aat cgt cgt cag aac atg gac ttt cta aaa	639
Glu Arg Ala Lys Val Asp Asn Arg Arg Gln Asn Met Asp Phe Leu Lys	
171 176 181 186	
gca aag tca gag gaa ttc aga ttt gga atc aag gct gca gag gag caa	687
Ala Lys Ser Glu Glu Phe Arg Phe Gly Ile Lys Ala Ala Glu Glu Gln	
187 192 197 202	

ctt tca gcc aga ggc atg gat gct tct ctg tct cat cag tcc tta gta 735
 Leu Ser Ala Arg Gly Met Asp Ala Ser Leu Ser His Gln Ser Leu Val
 203 208 213 218

gca cta tca gag aaa ctg gca aga tta aag caa cag act ata cct ttg 783
 Ala Leu Ser Glu Lys Leu Ala Arg Leu Lys Gln Gln Thr Ile Pro Leu
 219 224 229 234

aag aaa aaa ttg gag tcc tat tta gac tta atg ccg aat ccg tct ctt 831
 Lys Lys Lys Leu Glu Ser Tyr Leu Asp Leu Met Pro Asn Pro Ser Leu
 235 240 245 250

gct caa gtg aaa att gaa gaa gca aag cga gaa cta gat agc att gaa 879
 Ala Gln Val Lys Ile Glu Glu Ala Lys Arg Glu Leu Asp Ser Ile Glu
 251 256 261 266

gct gaa ctt aca aga aga gta gac atg atg gaa ctg tga caaaagccaa 928
 Ala Glu Leu Thr Arg Arg Val Asp Met Met Glu Leu *
 267 272 277

ataaacatcc ttttccctaa caaagtaaat tgaataggac tttacagagt tcttttttct 988

cttggcatttt cctaataaca aaactttctg tgttcttaga ttacagaata tcataattga 1048

tagaatatgg tttcttactg tgtgttgcac ttttgtgcc aaatacatag ttttcatatt 1108

aaaaagcctt ttctcttaaa aaaaaaaaa 1136

<210> 193
 <211> 1486
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (103)..(915)

<400> 193
 atcgtatagg cagtaccag ctggctagcg tttaactta agcttggtac cgagctcgga 60

tccactagtc cagtgtggtg gaattccggg actctgggga aa atg gct gcg tct 114
 Met Ala Ala Ser
 1

tcg agt ggt gag aag gag aag gag cgg ctg gga ggc ggt ttg gga gtg 162
 Ser Ser Gly Glu Lys Glu Lys Glu Arg Leu Gly Gly Gly Leu Gly Val
 5 10 15 20

gcg ggt ggt aac agc aca cga gag cgg ctg ctg tct gcg ctt gag gac 210
 Ala Gly Gly Asn Ser Thr Arg Glu Arg Leu Leu Ser Ala Leu Glu Asp
 21 26 31 36

ttg gag gtc ctg tct agg gaa ctt ata gaa atg ctg gca att tca aga 258
 Leu Glu Val Leu Ser Arg Glu Leu Ile Glu Met Leu Ala Ile Ser Arg

37	42	47	52	
aac caa aag ttg tta cag gct gga gag gaa aac cag gtc ctg gag ttg				306
Asn Gln Lys Leu Leu Gln Ala Gly Glu Glu Asn Gln Val Leu Glu Leu				
53	58	63	68	
tta att cac cga gat ggg gaa ttt caa gaa cta atg aaa ttg gca ctt				354
Leu Ile His Arg Asp Gly Glu Phe Gln Glu Leu Met Lys Leu Ala Leu				
69	74	79	84	
aat cag gga aaa att cat cat gaa atg caa gtt tta gaa aaa gaa gta				402
Asn Gln Gly Lys Ile His His Glu Met Gln Val Leu Glu Lys Glu Val				
85	90	95	100	
gag aag aga gac agt gat att cag cag cta caa aaa cag cta aag gaa				450
Glu Lys Arg Asp Ser Asp Ile Gln Gln Leu Gln Lys Gln Leu Lys Glu				
101	106	111	116	
gca gaa caa ata ctg gca aca gct gtt tac caa gcg aag gag aaa ctc				498
Ala Glu Gln Ile Leu Ala Thr Ala Val Tyr Gln Ala Lys Glu Lys Leu				
117	122	127	132	
aag tca ata gaa aaa gca aga aaa ggt gct atc tcc tct gaa gaa ata				546
Lys Ser Ile Glu Lys Ala Arg Lys Gly Ala Ile Ser Ser Glu Glu Ile				
133	138	143	148	
att aag tat gca cat agg atc agt gca agt aat gct gta tgt gct cca				594
Ile Lys Tyr Ala His Arg Ile Ser Ala Ser Asn Ala Val Cys Ala Pro				
149	154	159	164	
ctg acc tgg gtt cca ggg gac ccc cgg aga ccc tac cca act gat tta				642
Leu Thr Trp Val Pro Gly Asp Pro Arg Arg Pro Tyr Pro Thr Asp Leu				
165	170	175	180	
gag atg aga agt ggg tta ctg ggt cag atg aac aat cct tcc act aat				690
Glu Met Arg Ser Gly Leu Leu Gly Gln Met Asn Asn Pro Ser Thr Asn				
181	186	191	196	
ggc gtg aat ggc cat tta cca gga gat gca ctt gca gca gga aga ttg				738
Gly Val Asn Gly His Leu Pro Gly Asp Ala Leu Ala Ala Gly Arg Leu				
197	202	207	212	
cca gat gtc ctt gct cca cag tat cca tgg cag tca aat gac atg tgc				786
Pro Asp Val Leu Ala Pro Gln Tyr Pro Trp Gln Ser Asn Asp Met Ser				
213	218	223	228	
atg aat atg tta cca cca aat cat agt agt gac ttt ttg ttg gaa cct				834
Met Asn Met Leu Pro Pro Asn His Ser Ser Asp Phe Leu Leu Glu Pro				
229	234	239	244	
cct ggg cat aat aaa gaa aat gaa gat gat gta gag att atg tca acg				882
Pro Gly His Asn Lys Glu Asn Glu Asp Asp Val Glu Ile Met Ser Thr				
245	250	255	260	
gac tcc tca agc agt agt agt gag tct gat tga aaaacctt aaaagacaat				933
Asp Ser Ser Ser Ser Ser Ser Ser Glu Ser Asp *				
261	266	271		

atacagaatt gaatactgta gaattctgtt tctttaacag tagcagggaa atgtaaacta 993
 caggtgacaa aaaataccca ggtaaact ggctttggta gaattgtgca gtcattaaaa 1053
 gtcaaaat tttgaactttc tttttaaagc caaagaccat agtttttagtt ttaagccact 1113
 aggtagatat ttaggggaat agtcaaaatt tactgttgaa aaagcagttg ctatgtgctt 1173
 tcttaccctg ttctgttcca gttttgctgg atttgtacat agccattcta gaaatagagt 1233
 tgagggaaat tatccatata catatcacta ataggcttct tggaattatt tagaaaagca 1293
 tttttaaaact ggcagtgat gactgaatag gcatcatatt tctttttgtg tgtcatttaa 1353
 aagtaacaaa aactgccatt tgacagtaaa ggctcttggc ttctgttgga ggcattggaa 1413
 attgtctcaa tttgtacagt ttgtaattgt aatttttgta aataaatttg tttgtacatt 1473
 gaaaaaaaaa aaa 1486

<210> 194
 <211> 2353
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (153) .. (2309)

<400> 194
 ccggaattcc cgggtcgacg atttcgtgcg gaggtcgcg cgagccgggc cgagcagtga 60
 gggccctagc gggggccgag cggggcccg ggcccctaag ccattcctga agtcatgggc 120
 tggccaggac atcgggtgacc cgccaatccg gt atg gac gac tgg aag ccc agc 173
 Met Asp Asp Trp Lys Pro Ser
 1 5
 ccc ctc atc aag ccc ttt ggg gct cgg aag aag cgg agc tgg tac ctt 221
 Pro Leu Ile Lys Pro Phe Gly Ala Arg Lys Lys Arg Ser Trp Tyr Leu
 8 13 18 23
 acc tgg aag tat aaa ctg aca aac cag cgg gcc ctg cgg aga ttc tgt 269
 Thr Trp Lys Tyr Lys Leu Thr Asn Gln Arg Ala Leu Arg Arg Phe Cys
 24 29 34 39
 cag aca ggg gcc gtg ctt ttc ctg ctg gtg act gtc att gtc aat atc 317
 Gln Thr Gly Ala Val Leu Phe Leu Leu Val Thr Val Ile Val Asn Ile
 40 45 50 55
 aag ttg atc ctg gac act cgg cga gcc atc agt gaa gcc aat gaa gac 365
 Lys Leu Ile Leu Asp Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp
 56 61 66 71

cca gag cca gag caa gac tat gat gag gcc cta ggc cgc ctg gag ccc	413
Pro Glu Pro Glu Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro	
72 77 82 87	
cca cgg cgc aga ggc agt ggt ccc cgg cgg gtc ctg gac gta gag gtg	461
Pro Arg Arg Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val	
88 93 98 103	
tat tca agt cgc agc aaa gta tat gtg gca gtg gat ggc acc acg gtg	509
Tyr Ser Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val	
104 109 114 119	
ctg gag gat gag gcc cgg gag cag ggc cgg ggc atc cat gtc att gtc	557
Leu Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val	
120 125 130 135	
ctc aac cag gcc acg ggc cac gtg atg gca aaa cgt gtg ttt gac acg	605
Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp Thr	
136 141 146 151	
tac tca cct cat gag gat gag gcc atg gtg cta ttc ctc aac atg gta	653
Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn Met Val	
152 157 162 167	
gcg ccc ggc cga gtg ctc atc tgc act gtc aag gat gag ggc tcc ttc	701
Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu Gly Ser Phe	
168 173 178 183	
cac ctc aag gac aca gcc aag gct ctg ctg agg agc ctg ggc agc cag	749
His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser Leu Gly Ser Gln	
184 189 194 199	
gct ggc cct gcc ctg ggc tgg agg gac aca tgg gcc ttc gtg gga cga	797
Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp Ala Phe Val Gly Arg	
200 205 210 215	
aaa gga ggt cct gtc ttc ggg gag aaa cat tct aaa tca cct gcc ctc	845
Lys Gly Gly Pro Val Phe Gly Glu Lys His Ser Lys Ser Pro Ala Leu	
216 221 226 231	
tct tcc tgg ggg gac cca gtc ctg ctg aag aca gat gtg cca ttg agc	893
Ser Ser Trp Gly Asp Pro Val Leu Leu Lys Thr Asp Val Pro Leu Ser	
232 237 242 247	
tca gca gaa gag gca gag tgc cac tgg gca gac aca gag ctg aac cgt	941
Ser Ala Glu Glu Ala Glu Cys His Trp Ala Asp Thr Glu Leu Asn Arg	
248 253 258 263	
cgc cgc cgg cgc ttc tgc agc aaa gtt gag ggc tat gga agt gta tgc	989
Arg Arg Arg Arg Phe Cys Ser Lys Val Glu Gly Tyr Gly Ser Val Cys	
264 269 274 279	
agc tgc aag gac ccc aca ccc atc gag ttc agc cct gac cca ctc cca	1037
Ser Cys Lys Asp Pro Thr Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro	
280 285 290 295	

gac aac aag gtc ctc aat gtg cct gtg gct gtc att gca ggg aac cga	1085
Asp Asn Lys Val Leu Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg	
296 301 306 311	
ccc aat tac ctg tac agg atg ctg cgc tct ctg ctt tca gcc cag ggg	1133
Pro Asn Tyr Leu Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly	
312 317 322 327	
gtg tct cct cag atg ata aca gtt ttc att gac ggc tac tat gag gaa	1181
Val Ser Pro Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu	
328 333 338 343	
ccc atg gat gtg gtg gca ctg ttt ggt ctg agg ggc atc cag cat act	1229
Pro Met Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr	
344 349 354 359	
ccc atc agc atc aag aat gcc cgc gtg tct cag cac tac aag gcc agc	1277
Pro Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser	
360 365 370 375	
ctc act gcc act ttc aac ctg ttt ccg gag gcc aag ttt gct gtg gtt	1325
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val Val	
376 381 386 391	
ctg gaa gag gac ctg gac att gct gtg gat ttt ttc agt ttc ctg agc	1373
Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe Leu Ser	
392 397 402 407	
caa tcc atc cac cta ctg gag gag gat gac agc ctg tac tgc atc tct	1421
Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr Cys Ile Ser	
408 413 418 423	
gcc tgg aat gac cag ggg tat gaa cac acg gct gag gac cca gca cta	1469
Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu Asp Pro Ala Leu	
424 429 434 439	
ctg tac cgt gtg gag acc atg cct ggg ctg ggc tgg gtg ctc agg agg	1517
Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly Trp Val Leu Arg Arg	
440 445 450 455	
tcc ttg tac aag gag gag ctt gag ccc aag tgg cct aca ccg gaa aag	1565
Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys Trp Pro Thr Pro Glu Lys	
456 461 466 471	
ctc tgg gat tgg gac atg tgg atg cgg atg cct gaa caa cgc cgg ggc	1613
Leu Trp Asp Trp Asp Met Trp Met Arg Met Pro Glu Gln Arg Arg Gly	
472 477 482 487	
cga gag tgc atc atc cct gac gtt tcc cga tcc tac cac ttt ggc atc	1661
Arg Glu Cys Ile Ile Pro Asp Val Ser Arg Ser Tyr His Phe Gly Ile	
488 493 498 503	
gtc ggc ctc aac atg aat ggc tac ttt cac gag gcc tac ttc aag aag	1709
Val Gly Leu Asn Met Asn Gly Tyr Phe His Glu Ala Tyr Phe Lys Lys	
504 509 514 519	
cac aag ttc aac acg gtt cca ggt gtc cag ctc agg aat gtg gac agt	1757

His	Lys	Phe	Asn	Thr	Val	Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser		
520					525					530					535		
ctg	aag	aaa	gaa	gct	tat	gaa	gtg	gaa	gtt	cac	agg	ctg	ctc	agt	gag	1805	
Leu	Lys	Lys	Glu	Ala	Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu		
536					541					546					551		
gct	gag	gtt	ctg	gac	cac	agc	aag	aac	cct	tgt	gaa	gac	tct	ttc	ctg	1853	
Ala	Glu	Val	Leu	Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu		
552					557					562					567		
cca	gac	aca	gag	ggc	cac	acc	tac	gtg	gcc	ttt	att	cga	atg	gag	aaa	1901	
Pro	Asp	Thr	Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys		
568					573					578					583		
gat	gat	gac	ttc	acc	acc	tgg	acc	cag	ctt	gcc	aag	tgc	ctc	cat	atc	1949	
Asp	Asp	Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile		
584					589					594					599		
tgg	gac	ctg	gat	gtg	cgt	ggc	aac	cat	cgg	ggc	ctg	tgg	aga	ttg	ttt	1997	
Trp	Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe		
600					605					610					615		
cgg	aag	aag	aac	cac	ttc	ctg	gtg	gtg	ggg	gtc	ccg	gct	tcc	ccc	tac	2045	
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro	Tyr		
616					621					626					631		
tgc	cct	ggc	tca	gaa	tct	aac	cta	ttt	att	gac	tgt	cct	gag	ggc	ctt	2093	
Ser	Pro	Gly	Ser	Glu	Ser	Asn	Leu	Phe	Ile	Asp	Cys	Pro	Glu	Gly	Leu		
632					637					642					647		
gaa	aac	agg	ccg	aac	ctg	gag	ggc	ctg	gat	ttc	ttt	ttg	ggc	tgg	aat	2141	
Glu	Asn	Arg	Pro	Asn	Leu	Glu	Gly	Leu	Asp	Phe	Phe	Leu	Gly	Trp	Asn		
648					653					658					663		
gct	gcc	ctg	agg	gtg	ggg	ctg	gct	ctt	act	cag	gaa	act	gct	gtg	ccc	2189	
Ala	Ala	Leu	Arg	Val	Gly	Leu	Ala	Leu	Thr	Gln	Glu	Thr	Ala	Val	Pro		
664					669					674					679		
aac	cca	tgg	aca	ggc	cca	gct	ggg	gcc	cac	atg	ctg	aca	cag	act	cac	2237	
Asn	Pro	Trp	Thr	Gly	Pro	Ala	Gly	Ala	His	Met	Leu	Thr	Gln	Thr	His		
680					685					690					695		
tca	gag	acc	ctt	aga	cac	tgg	acc	agg	cct	cct	ctc	agc	ctt	ctc	ttt	2285	
Ser	Glu	Thr	Leu	Arg	His	Trp	Thr	Arg	Pro	Pro	Leu	Ser	Leu	Leu	Phe		
696					701					706					711		
gtc	cag	att	tcc	aaa	gct	gga	taa	gttggtcatt	gattaaaaaa	ggagaagccc	2339						
Val	Gln	Ile	Ser	Lys	Ala	Gly	*										
712					717												
tcaaaaaaaaa	aaaa															2353	

<211> 3996
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (52)..(3996)

<400> 195

```

gccgacagtc cctccttgct tgtctccggg attcaggcct ccctccctga c atg gag      57
                                     Met Glu
                                     1

agt aac ctg tct ggc ctg gtg cct gct gcc ggg ctg gtg cct gcg ctg      105
Ser Asn Leu Ser Gly Leu Val Pro Ala Ala Gly Leu Val Pro Ala Leu
  3                               8                               13                               18

cca cct gct gtg acc ctg ggg ctg aca gct gcc tac acc acc ctg tat      153
Pro Pro Ala Val Thr Leu Gly Leu Thr Ala Ala Tyr Thr Thr Leu Tyr
  19                               24                               29                               34

gcc ctg ctc ttc ttc tcc gtc tat gcc cag ctc tgg ctg gtg ctt ctg      201
Ala Leu Leu Phe Phe Ser Val Tyr Ala Gln Leu Trp Leu Val Leu Leu
  35                               40                               45                               50

tat ggg cac aag cgt ctc agc tat cag acg gtg ttc ctg gcc ctc tgt      249
Tyr Gly His Lys Arg Leu Ser Tyr Gln Thr Val Phe Leu Ala Leu Cys
  51                               56                               61                               66

ctg ctc tgg gcc gcc ttg cgt acc acc ctc ttc tcc ttc tac ttc cga      297
Leu Leu Trp Ala Ala Leu Arg Thr Thr Leu Phe Ser Phe Tyr Phe Arg
  67                               72                               77                               82

gat act ccc cgc gcc aac cgc ctg ggg ccc ttg ccc ttc tgg ctt ctc      345
Asp Thr Pro Arg Ala Asn Arg Leu Gly Pro Leu Pro Phe Trp Leu Leu
  83                               88                               93                               98

tac tgc tgc ccc gtc tgc ctg cag ttc ttc acc ttg acg ctt atg aac      393
Tyr Cys Cys Pro Val Cys Leu Gln Phe Phe Thr Leu Thr Leu Met Asn
  99                               104                               109                               114

ctc tac ttt gcc cag gtg gtg ttc aag gcc aag gtg aag cgt cgg ccg      441
Leu Tyr Phe Ala Gln Val Val Phe Lys Ala Lys Val Lys Arg Arg Pro
  115                               120                               125                               130

gag atg agc cga ggc ttg ctc gct gtc cga ggg gcc ttt gtg ggg gcc      489
Glu Met Ser Arg Gly Leu Leu Ala Val Arg Gly Ala Phe Val Gly Ala
  131                               136                               141                               146

tcg ctg ctc ttt ctg ctg gtg aac gtg ctg tgt gct gtg ctc tcc cat      537
Ser Leu Leu Phe Leu Leu Val Asn Val Leu Cys Ala Val Leu Ser His
  147                               152                               157                               162

cgg cgc cgg gca cag ccc tgg gcc ctg ctg ctt gtc cgc gtc ctg gtg      585
Arg Arg Arg Ala Gln Pro Trp Ala Leu Leu Leu Val Arg Val Leu Val
  163                               168                               173                               178

```

agc gac tcc ctg ttc gtc atc tgc gcg ctg tct ctt gct gcc tgc ctc	633
Ser Asp Ser Leu Phe Val Ile Cys Ala Leu Ser Leu Ala Ala Cys Leu	
179 184 189 194	
tgc ctc gtc gcc agg cgg gcg ccc tcc act agc atc tac ctg gag gcc	681
Cys Leu Val Ala Arg Arg Ala Pro Ser Thr Ser Ile Tyr Leu Glu Ala	
195 200 205 210	
aag ggg acc agt gtg tgc cag gcg gcc gcg atg ggt ggc gcc atg gtc	729
Lys Gly Thr Ser Val Cys Gln Ala Ala Ala Met Gly Gly Ala Met Val	
211 216 221 226	
ctg ctc tat gcc agc cgg gcc tgc tac aac ctg aca gca ctg gcc ttg	777
Leu Leu Tyr Ala Ser Arg Ala Cys Tyr Asn Leu Thr Ala Leu Ala Leu	
227 232 237 242	
gcc ccc cag agc cgg ctg gac acc ttc gat tac gac tgg tac aat gtg	825
Ala Pro Gln Ser Arg Leu Asp Thr Phe Asp Tyr Asp Trp Tyr Asn Val	
243 248 253 258	
tct gac cag gcg gac ctg gtg aat gac ctg ggg aac aaa ggc tac ctg	873
Ser Asp Gln Ala Asp Leu Val Asn Asp Leu Gly Asn Lys Gly Tyr Leu	
259 264 269 274	
gta ttt ggc ctc atc ctc ttc gtg tgg gag cta ctg ccc acc acc ctg	921
Val Phe Gly Leu Ile Leu Phe Val Trp Glu Leu Leu Pro Thr Thr Leu	
275 280 285 290	
ctg gtg ggc ttc ttc cgg gtg cac cgg ccc cca cag gac ctg agc acc	969
Leu Val Gly Phe Phe Arg Val His Arg Pro Pro Gln Asp Leu Ser Thr	
291 296 301 306	
agc cac atc ctc aat ggg cag gtc ttt gcc tct cgg tcc tac ttc ttt	1017
Ser His Ile Leu Asn Gly Gln Val Phe Ala Ser Arg Ser Tyr Phe Phe	
307 312 317 322	
gac cgg gct ggg cac tgt gaa gat gag ggc tgc tcc tgg gag cac agc	1065
Asp Arg Ala Gly His Cys Glu Asp Glu Gly Cys Ser Trp Glu His Ser	
323 328 333 338	
cgg ggt gag agc acc agc tct tgt gac tgt ggc cct ggt cac tgt cct	1113
Arg Gly Glu Ser Thr Ser Ser Cys Asp Cys Gly Pro Gly His Cys Pro	
339 344 349 354	
gag act gac cct gtt tct ctg ctg cag tat gtc ggg cag tct agg ctc	1161
Glu Thr Asp Pro Val Ser Leu Leu Gln Tyr Val Gly Gln Ser Arg Leu	
355 360 365 370	
tgg gag ctg aat acc cag gcc cca gtc ccc ctc acc cta ggc ccc tgt	1209
Trp Glu Leu Asn Thr Gln Ala Pro Val Pro Leu Thr Leu Gly Pro Cys	
371 376 381 386	
gcc aag ttt gtc tgc cgc ttc ttg ccc agg atc ctg ggg gtc gtg gct	1257
Ala Lys Phe Val Cys Arg Phe Leu Pro Arg Ile Leu Gly Val Val Ala	
387 392 397 402	
acc ccc tcc tct ggc cgg ctc ctt gct gct cct gtc ata gac tca ggg	1305

Thr	Pro	Ser	Ser	Gly	Arg	Leu	Leu	Ala	Ala	Pro	Val	Ile	Asp	Ser	Gly		
403					408					413					418		
gca	ggg	acg	ccc	cag	ggg	cga	ctg	gcc	ggg	cgg	ggt	gcc	cac	ctc	tcg		1353
Ala	Gly	Thr	Pro	Gln	Gly	Arg	Leu	Ala	Gly	Arg	Gly	Ala	His	Leu	Ser		
419					424					429					434		
cgc	gtg	ggc	gcc	tcc	ggg	agt	ggt	gtg	gcc	gcc	ggt	ccc	gcc	gcc	cgc		1401
Arg	Val	Gly	Ala	Ser	Gly	Ser	Gly	Val	Ala	Ala	Gly	Pro	Ala	Ala	Arg		
435					440					445					450		
cac	gct	ccg	agg	cgt	cgc	tgt	gcg	gac	gcg	ggg	gag	gcg	gtg	gga	gcg		1449
His	Ala	Pro	Arg	Arg	Arg	Cys	Ala	Asp	Ala	Gly	Glu	Ala	Val	Gly	Ala		
451					456					461					466		
agc	tgc	ggg	cgc	tgc	gcg	gtg	gcc	ctg	ctg	tct	ggc	gtg	tgc	acg	cta		1497
Ser	Cys	Gly	Arg	Cys	Ala	Val	Ala	Leu	Leu	Ser	Gly	Val	Cys	Thr	Leu		
467					472					477					482		
gtg	tcc	aca	cac	gtg	tgc	gtg	ggc	tct	ggg	tgc	cct	ggc	gcg	gcc	ggc		1545
Val	Ser	Thr	His	Val	Cys	Val	Gly	Ser	Gly	Cys	Pro	Gly	Ala	Ala	Gly		
483					488					493					498		
acg	ccc	atg	ggg	gcc	ggg	gat	gcc	ggg	gcg	tct	gcg	gag	agt	gca	gtg		1593
Thr	Pro	Met	Gly	Ala	Gly	Asp	Ala	Gly	Ala	Ser	Ala	Glu	Ser	Ala	Val		
499					504					509					514		
acg	aca	gct	ccc	cag	gag	ccc	ccc	gcc	cgg	ccc	ctc	cag	gcg	ggc	agt		1641
Thr	Thr	Ala	Pro	Gln	Glu	Pro	Pro	Ala	Arg	Pro	Leu	Gln	Ala	Gly	Ser		
515					520					525					530		
gga	gct	ggc	ccg	gcg	cct	ggg	cgc	gcc	atg	cgc	agc	acc	acg	ctc	ctg		1689
Gly	Ala	Gly	Pro	Ala	Pro	Gly	Arg	Ala	Met	Arg	Ser	Thr	Thr	Leu	Leu		
531					536					541					546		
gcc	ctg	ctg	gcg	ctg	gtc	ttg	ctt	tac	ttg	gtg	tct	ggt	gcc	ctg	gtg		1737
Ala	Leu	Leu	Ala	Leu	Val	Leu	Leu	Tyr	Leu	Val	Ser	Gly	Ala	Leu	Val		
547					552					557					562		
ttc	cgg	gcc	ctg	gag	cag	ccc	cac	gag	cag	cag	gcc	cag	agg	gag	ctg		1785
Phe	Arg	Ala	Leu	Glu	Gln	Pro	His	Glu	Gln	Gln	Ala	Gln	Arg	Glu	Leu		
563					568					573					578		
ggg	gag	gtc	cga	gag	aag	ttc	ctg	agg	gcc	cat	ccg	tgt	gtg	agc	gac		1833
Gly	Glu	Val	Arg	Glu	Lys	Phe	Leu	Arg	Ala	His	Pro	Cys	Val	Ser	Asp		
579					584					589					594		
cag	gag	ctg	ggc	ctc	ctc	atc	aag	gag	gtg	gct	gat	gcc	ctg	gga	ggg		1881
Gln	Glu	Leu	Gly	Leu	Leu	Ile	Lys	Glu	Val	Ala	Asp	Ala	Leu	Gly	Gly		
595					600					605					610		
ggt	gcg	gac	cca	gaa	acc	aac	tcg	acc	agc	aac	agc	agc	cac	tca	gcc		1929
Gly	Ala	Asp	Pro	Glu	Thr	Asn	Ser	Thr	Ser	Asn	Ser	Ser	His	Ser	Ala		
611					616					621					626		
tgg	gac	ctg	ggc	agc	gcc	ttc	ttt	ttc	tca	ggg	acc	atc	atc	acc	acc		1977
Trp	Asp	Leu	Gly	Ser	Ala	Phe	Phe	Phe	Ser	Gly	Thr	Ile	Ile	Thr	Thr		

627	632	637	642	
atc ggc tat ggc aat gtg gcc ctg cgc aca gat gcc ggg cgc ctc ttc				2025
Ile Gly Tyr Gly Asn Val Ala Leu Arg Thr Asp Ala Gly Arg Leu Phe				
643	648	653	658	
tgc atc ttt tat gcg ctg gtg ggg att ccg ctg ttt ggg atc cta ctg				2073
Cys Ile Phe Tyr Ala Leu Val Gly Ile Pro Leu Phe Gly Ile Leu Leu				
659	664	669	674	
gca ggg gtc ggg gac cgg ctg ggc tcc tcc ctg cgc cat ggc atc ggt				2121
Ala Gly Val Gly Asp Arg Leu Gly Ser Ser Leu Arg His Gly Ile Gly				
675	680	685	690	
cac att gaa gcc atc ttc ttg aag tgg cac gtg cca ccg gag cta gta				2169
His Ile Glu Ala Ile Phe Leu Lys Trp His Val Pro Pro Glu Leu Val				
691	696	701	706	
aga gtg ctg tcg gcg atg ctt ttc ctg ctg atc ggc tgc ctg ctc ttt				2217
Arg Val Leu Ser Ala Met Leu Phe Leu Leu Ile Gly Cys Leu Leu Phe				
707	712	717	722	
gtc ctc acg ccc acg ttc gtg ttc tgc tat atg gag gac tgg agc aag				2265
Val Leu Thr Pro Thr Phe Val Phe Cys Tyr Met Glu Asp Trp Ser Lys				
723	728	733	738	
ctg gag gcc atc tac ttt gtc ata gtg acg ctt acc acc gtg ggc ttt				2313
Leu Glu Ala Ile Tyr Phe Val Ile Val Thr Leu Thr Thr Val Gly Phe				
739	744	749	754	
ggc gac tat gtg gcc ggc gcg gac ccc agg cag gac tcc ccg gcc tat				2361
Gly Asp Tyr Val Ala Gly Ala Asp Pro Arg Gln Asp Ser Pro Ala Tyr				
755	760	765	770	
cag ccg ctg gtg tgg ttc tgg atc ctg ctc ggc ctg gct tac ttc gcc				2409
Gln Pro Leu Val Trp Phe Trp Ile Leu Leu Gly Leu Ala Tyr Phe Ala				
771	776	781	786	
tca gtg ctc acc acc atc ggg aac tgg ctg cga gta gtg tcc cgc cgc				2457
Ser Val Leu Thr Thr Ile Gly Asn Trp Leu Arg Val Val Ser Arg Arg				
787	792	797	802	
act cgg gca gag atg ggc ggc ctc acg gct cag gct gcc agc tgg act				2505
Thr Arg Ala Glu Met Gly Gly Leu Thr Ala Gln Ala Ala Ser Trp Thr				
803	808	813	818	
ggc aca gtg aca gcg cgc gtg acc cag cga gcc ggg ccc gcc gcc ccg				2553
Gly Thr Val Thr Ala Arg Val Thr Gln Arg Ala Gly Pro Ala Ala Pro				
819	824	829	834	
ccg ccg gag aag gag cag cca ctg ctg cct cca ccg ccc tgt cca gcg				2601
Pro Pro Glu Lys Glu Gln Pro Leu Leu Pro Pro Pro Pro Cys Pro Ala				
835	840	845	850	
cag ccg ctg ggc agg ccc cga tcc cct tcg ccc ccc gag aag gct cag				2649
Gln Pro Leu Gly Arg Pro Arg Ser Pro Ser Pro Pro Glu Lys Ala Gln				
851	856	861	866	

ccg cct tcc ccg ccc acg gcc tcg gcc ctg gat tat ccc agc gag aac	2697
Pro Pro Ser Pro Pro Thr Ala Ser Ala Leu Asp Tyr Pro Ser Glu Asn	
867 872 877 882	
ctg gcc ttc atc gac gag tcc tcg gat acg cag agc gag cgc ggc tgc	2745
Leu Ala Phe Ile Asp Glu Ser Ser Asp Thr Gln Ser Glu Arg Gly Cys	
883 888 893 898	
ccg ctg ccc cgc gcg ccg aga ggt cgc cgc cgc cca aat ccc ccc agg	2793
Pro Leu Pro Arg Ala Pro Arg Gly Arg Arg Arg Pro Asn Pro Pro Arg	
899 904 909 914	
aag ccc gtg cgg ccc cgc ggc ccc ggg cgt ccc cga gac aaa ggc gtg	2841
Lys Pro Val Arg Pro Arg Gly Pro Gly Arg Pro Arg Asp Lys Gly Val	
915 920 925 930	
ccg acc ccc cca agg ctt tct gtg tcg ctg ccc cgg gcg ggt gta tcc	2889
Pro Thr Pro Pro Arg Leu Ser Val Ser Leu Pro Arg Ala Gly Val Ser	
931 936 941 946	
ctc aca gca cct cac gac tgt gcc tca aag cct gca tca ata aat gaa	2937
Leu Thr Ala Pro His Asp Cys Ala Ser Lys Pro Ala Ser Ile Asn Glu	
947 952 957 962	
aac ggt ctg cac cgc tgc ggg cgt gac gct ccc gga cgc gag tgg gtg	2985
Asn Gly Leu His Arg Cys Gly Arg Asp Ala Pro Gly Arg Glu Trp Val	
963 968 973 978	
tgg aat tgc ttt cct cgg gcc acc gtg ggg gca cct ctg gcc tcc cgt	3033
Trp Asn Cys Phe Pro Arg Ala Thr Val Gly Ala Pro Leu Ala Ser Arg	
979 984 989 994	
gac ccc cag gcc gag ggt ccc cgg gca ccc agc ctt ggc tgc ccg cag	3081
Asp Pro Gln Ala Glu Gly Pro Arg Ala Pro Ser Leu Gly Cys Pro Gln	
995 1000 1005 1010	
ccc cca ccc aac ccc acg ttc tac ggg atc ccc aac ccg gcc cgg ctc	3129
Pro Pro Pro Asn Pro Thr Phe Tyr Gly Ile Pro Asn Pro Ala Arg Leu	
1011 1016 1021 1026	
agt tcc cca gcc cgc tct tcc ttc ccg ctc cag cca tcc gcg acc ctt	3177
Ser Ser Pro Ala Arg Ser Ser Phe Pro Leu Gln Pro Ser Ala Thr Leu	
1027 1032 1037 1042	
ggc tcc ctc ctt gta tgt ggc cca cag gtg tcg ctc aag tct tcc gac	3225
Gly Ser Leu Leu Val Cys Gly Pro Gln Val Ser Leu Lys Ser Ser Asp	
1043 1048 1053 1058	
cgc caa ggc tcg gac gag gag agc gtg cat agc gac act cgg gac ctg	3273
Arg Gln Gly Ser Asp Glu Glu Ser Val His Ser Asp Thr Arg Asp Leu	
1059 1064 1069 1074	
tgg acc acg acc acg ctg tcc cag gca cag ctg aac atg ccg ctg tcc	3321
Trp Thr Thr Thr Thr Ser Gln Ala Gln Leu Asn Met Pro Leu Ser	
1075 1080 1085 1090	

gag gtc tgc gag ggc ttc gac gat gag ggc cgc aac att agc aag acc	3369
Glu Val Cys Glu Gly Phe Asp Asp Glu Gly Arg Asn Ile Ser Lys Thr	
1091 1096 1101 1106	
cgc ggg tgg cac agc ccg ggg cgg ggc tgc ttg gac gag ggg tac aag	3417
Arg Gly Trp His Ser Pro Gly Arg Gly Ser Leu Asp Glu Gly Tyr Lys	
1107 1112 1117 1122	
gcc agc cac aag ccg gag gaa ctg gac gag cac gcg ctg gtg gag ctg	3465
Ala Ser His Lys Pro Glu Glu Leu Asp Glu His Ala Leu Val Glu Leu	
1123 1128 1133 1138	
gag ttg cac cgc ggc agc tcc atg gaa atc aat ctg ggg gag aag gac	3513
Glu Leu His Arg Gly Ser Ser Met Glu Ile Asn Leu Gly Glu Lys Asp	
1139 1144 1149 1154	
act gca tcc cag atc gag gcc gaa aag tct tcc tca atg tca tca ctc	3561
Thr Ala Ser Gln Ile Glu Ala Glu Lys Ser Ser Ser Met Ser Ser Leu	
1155 1160 1165 1170	
aat att gcg aag cac atg ccc cat cga gcc tac tgg gca gag cag cag	3609
Asn Ile Ala Lys His Met Pro His Arg Ala Tyr Trp Ala Glu Gln Gln	
1171 1176 1181 1186	
agc agg gtt gga ggg gct ggg gag act ggg cgt ttc ggt ggg ctg cca	3657
Ser Arg Val Gly Gly Ala Gly Glu Thr Gly Arg Phe Gly Gly Leu Pro	
1187 1192 1197 1202	
ctg ccc ctg atg gaa ctc atg gag aat gaa gct ctg gaa atc ctc acc	3705
Leu Pro Leu Met Glu Leu Met Glu Asn Glu Ala Leu Glu Ile Leu Thr	
1203 1208 1213 1218	
aaa gcc ctc cgg agt aag ctc ccc gcc aac ccc caa gaa ctc cca cga	3753
Lys Ala Leu Arg Ser Lys Leu Pro Ala Asn Pro Gln Glu Leu Pro Arg	
1219 1224 1229 1234	
cag att ctg gtg gat ttt gca ggg ctg ggg ccc agg ggg aga tgc aaa	3801
Gln Ile Leu Val Asp Phe Ala Gly Leu Gly Pro Arg Gly Arg Cys Lys	
1235 1240 1245 1250	
gtt ccc cag gct aac aca gac ctg agt gcc ctg cgc tac tgc tac ctc	3849
Val Pro Gln Ala Asn Thr Asp Leu Ser Ala Leu Arg Tyr Cys Tyr Leu	
1251 1256 1261 1266	
gaa tca tct gcg gtt cct cga atc aca cat gcg gcg ccc cct ggc tac	3897
Glu Ser Ser Ala Val Pro Arg Ile Thr His Ala Ala Pro Pro Gly Tyr	
1267 1272 1277 1282	
cag tta ggg atc ggc agg gac cac ttc ctg act aag gag ctg cag cga	3945
Gln Leu Gly Ile Gly Arg Asp His Phe Leu Thr Lys Glu Leu Gln Arg	
1283 1288 1293 1298	
tac atc gaa ggg ctc aag aag cgc cgg agc aag agg ctg tac gtg aat	3993
Tyr Ile Glu Gly Leu Lys Lys Arg Arg Ser Lys Arg Leu Tyr Val Asn	
1299 1304 1309 1314	
taa	3996

*
1315

<210> 196
<211> 1332
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (171)..(920)

<400> 196
actctggaac gcctgcaggt accggtccgg aattcccggg tcgacccacg cgtccggggc 60
gcctgcagga agcggcggca gcgggcagcg gctctcgggc tgcaggctgg gcaggggtccc 120
ctcccacgct cctgccgctg tctcccacgt ccccaggtg cgcggccacc atg gcg 176
Met Ala
1
tcc agc gac gag gac ggc acc aac ggc ggc gcc tcg gag gcc ggc gag 224
Ser Ser Asp Glu Asp Gly Thr Asn Gly Gly Ala Ser Glu Ala Gly Glu
3 8 13 18
gac cgg gag gct ccc ggc aag cgg agg cgc ctg ggg ttc ttg gcc acc 272
Asp Arg Glu Ala Pro Gly Lys Arg Arg Arg Leu Gly Phe Leu Ala Thr
19 24 29 34
gcc tgg ctc acc ttc tac gac atc gcc atg acc gcg ggg tgg ttg gtt 320
Ala Trp Leu Thr Phe Tyr Asp Ile Ala Met Thr Ala Gly Trp Leu Val
35 40 45 50
cta gct att gcc atg gta cgt ttt tat atg gaa aaa gga aca cac aga 368
Leu Ala Ile Ala Met Val Arg Phe Tyr Met Glu Lys Gly Thr His Arg
51 56 61 66
ggg tta tat aaa agt att cag aag aca ctt aaa ttt ttc cag aca ttt 416
Gly Leu Tyr Lys Ser Ile Gln Lys Thr Leu Lys Phe Phe Gln Thr Phe
67 72 77 82
gcc ttg ctt gag ata gtt cac tgt tta att gga att gta cct act tct 464
Ala Leu Leu Glu Ile Val His Cys Leu Ile Gly Ile Val Pro Thr Ser
83 88 93 98
gtg att gtg act ggg gtc caa gtg agt tca aga atc ttt atg gtg tgg 512
Val Ile Val Thr Gly Val Gln Val Ser Ser Arg Ile Phe Met Val Trp
99 104 109 114
ctc att act cac agt ata aaa cca atc cag aat gaa gag agt gtg gtg 560
Leu Ile Thr His Ser Ile Lys Pro Ile Gln Asn Glu Glu Ser Val Val
115 120 125 130

ctt ttt ctg gtc gcg tgg act gtg aca gag atc act cgc tat tcc ttc	608
Leu Phe Leu Val Ala Trp Thr Val Thr Glu Ile Thr Arg Tyr Ser Phe	
131 136 141 146	
tac aca ttc agc ctt ctt gac cac ttg cca tac ttc att aaa tgg gcc	656
Tyr Thr Phe Ser Leu Leu Asp His Leu Pro Tyr Phe Ile Lys Trp Ala	
147 152 157 162	
aga tat aat ttt ttt atc atc tta tat cct gtt gga gtt gct ggt gaa	704
Arg Tyr Asn Phe Phe Ile Ile Leu Tyr Pro Val Gly Val Ala Gly Glu	
163 168 173 178	
ctt ctt aca ata tac gct gcc ttg ccg tat gtg aag aaa aca gga atg	752
Leu Leu Thr Ile Tyr Ala Ala Leu Pro Tyr Val Lys Lys Thr Gly Met	
179 184 189 194	
ttt tca ata aga ctt cct aac aaa tac aat gtc tct ttt gac tac tat	800
Phe Ser Ile Arg Leu Pro Asn Lys Tyr Asn Val Ser Phe Asp Tyr Tyr	
195 200 205 210	
tat ttt ctt ctt ata acc atg gca tca tat ata cct ttg ttt cca caa	848
Tyr Phe Leu Leu Ile Thr Met Ala Ser Tyr Ile Pro Leu Phe Pro Gln	
211 216 221 226	
ctc tat ttt cat atg tta cgt caa aga aga aag gtg ctt cat gga gag	896
Leu Tyr Phe His Met Leu Arg Gln Arg Arg Lys Val Leu His Gly Glu	
227 232 237 242	
gtg att gta gaa aag gat gat taa atgatctctg caaacaagggt gctttttcca	950
Val Ile Val Glu Lys Asp Asp *	
243 248	
gaataaccaa gattacctga gtccaagttt taataacaag aataaacaac tttgtgaaat	1010
atcatggatt gtatggtttc ttaaaatata acttgagaca cgtgggtatctt gccagtatctt	1070
gtgttcctct tgtgccagat ctatcttttta caagaactgt gcaaatatca gtaacttttg	1130
ggtaggtatt gattattagg aaaataatta ggtgtattat ctgggggaaa aaaaaacttt	1190
tgctaagttt tttttgaaac atgctcaaag ctttttaaata caatatttag aaattagttt	1250
aacgattttac tattatacct gctagtataatattatgtgat atttataaat gaaaataaat	1310
gcaaaattat aaaaaaaaaa aa	1332

<210> 197
 <211> 2128
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (42)..(1031)

<400> 197

taagcttgcg gccgcgcggc ctcccgggcg gccctacagc c	atg tcc cgg gac	53
	Met Ser Arg Asp	
	1	
ccg ggg tcg ggc ggc tgg gag gag gcc ccg cgc gca gct gcc gcg ctc		101
Pro Gly Ser Gly Gly Trp Glu Glu Ala Pro Arg Ala Ala Ala Ala Leu		
5 10 15 20		
tgc acc ctg tac cac gag gcc gga cag cgg ctg cgc cgc ctg cag gac		149
Cys Thr Leu Tyr His Glu Ala Gly Gln Arg Leu Arg Arg Leu Gln Asp		
21 26 31 36		
cag ctc gct gcc cgc gac gcc ctc atc gct cgc ctc cgc gcc cgc ctg		197
Gln Leu Ala Ala Arg Asp Ala Leu Ile Ala Arg Leu Arg Ala Arg Leu		
37 42 47 52		
gcc gcg ctg gag ggg gac gcc gcg ccg tcc cta gtg gac gcg ctg ctg		245
Ala Ala Leu Glu Gly Asp Ala Ala Pro Ser Leu Val Asp Ala Leu Leu		
53 58 63 68		
gag cag gtt gcg cgc ttc cgg gag cag ctg cga agg cag gag ggc ggc		293
Glu Gln Val Ala Arg Phe Arg Glu Gln Leu Arg Arg Gln Glu Gly Gly		
69 74 79 84		
gcc gcc gag gcc cag atg cgc cag gaa att gag agg ctg act gag cga		341
Ala Ala Glu Ala Gln Met Arg Gln Glu Ile Glu Arg Leu Thr Glu Arg		
85 90 95 100		
cta gaa gaa aaa gag agg gag atg cag cag ctg ctg agc cag ccc caa		389
Leu Glu Glu Lys Glu Arg Glu Met Gln Gln Leu Leu Ser Gln Pro Gln		
101 106 111 116		
cac gag cga gag aag gaa gtc gtc ctg cta cgg agg agc atg gca gaa		437
His Glu Arg Glu Lys Glu Val Val Leu Leu Arg Arg Ser Met Ala Glu		
117 122 127 132		
ggg gag cgc gcc cgg gcc gcc agt gac gtc ctg tgc cgc tcc ttg gcc		485
Gly Glu Arg Ala Arg Ala Ala Ser Asp Val Leu Cys Arg Ser Leu Ala		
133 138 143 148		
aac gag acc cat cag ctg cgg agg acg ctg acc gcc acc gcc cac atg		533
Asn Glu Thr His Gln Leu Arg Arg Thr Leu Thr Ala Thr Ala His Met		
149 154 159 164		
tgt cag cat ctg gcc aag tgt ctg gat gaa cga cag cat gca caa agg		581
Cys Gln His Leu Ala Lys Cys Leu Asp Glu Arg Gln His Ala Gln Arg		
165 170 175 180		
aat gtg ggg gag aga agt cct gac cag tcg gaa cac aca gat ggg cac		629
Asn Val Gly Glu Arg Ser Pro Asp Gln Ser Glu His Thr Asp Gly His		
181 186 191 196		
acc tct gtc cag agt gtt att gag aag ttg cag gaa gaa aat cga ctg		677
Thr Ser Val Gln Ser Val Ile Glu Lys Leu Gln Glu Glu Asn Arg Leu		
197 202 207 212		

tta aaa cag aag gtg act cac gtt gaa gac ctc aat gcc aag tgg cag	725
Leu Lys Gln Lys Val Thr His Val Glu Asp Leu Asn Ala Lys Trp Gln	
213 218 223 228	
cgc tac aac gcc agc agg gac gaa tac gtg agg ggg ctc cat gcg cag	773
Arg Tyr Asn Ala Ser Arg Asp Glu Tyr Val Arg Gly Leu His Ala Gln	
229 234 239 244	
ctc agg ggg ctg cag atc ccc cac gag ccc gag ctg atg agg aag gag	821
Leu Arg Gly Leu Gln Ile Pro His Glu Pro Glu Leu Met Arg Lys Glu	
245 250 255 260	
atc tcc cgg ctc aac aga cag ttg gaa gag aaa ata aat gac tgt gcc	869
Ile Ser Arg Leu Asn Arg Gln Leu Glu Glu Lys Ile Asn Asp Cys Ala	
261 266 271 276	
gaa gtg aag cag gag ctg gcg gcc tcc agg acg gcc cgg gat gct gcg	917
Glu Val Lys Gln Glu Leu Ala Ala Ser Arg Thr Ala Arg Asp Ala Ala	
277 282 287 292	
ttg gag cgg gtg cag atg ctg gaa cag cag gtg tct gtc cct cgg gct	965
Leu Glu Arg Val Gln Met Leu Glu Gln Gln Val Ser Val Pro Arg Ala	
293 298 303 308	
ccg gac ggc act gac cag atg tct gct ggc cgg tgg tgg ccg aaa tca	1013
Pro Asp Gly Thr Asp Gln Met Ser Ala Gly Arg Trp Trp Pro Lys Ser	
309 314 319 324	
tgg gac agg ctg ggc tga aggcctt ggtggcactg agtgggcagt ggtcactgtg	1067
Trp Asp Arg Leu Gly *	
325 330	
gggggtgggag aagcctgggg gggcgcttcc tccttccttg agcagaaatg tgtgtctcgc	1127
ctctcttcag attctcgctt acaaggatga cttcatgtca gaaagggccg atcggaacg	1187
ggctcaaagt aggattcaag aactggagga aaaggctgcc tctttgctgc accaggtgtc	1247
ctggagacag gattctcgag agccagacgc cggccggatt cacgctggga gcaaaactgc	1307
caagtatttg gccgccgacg cattagagct tatggtgcct ggtggctgga ggctgggac	1367
tgggtcccag cagccagaac cccctgcaga gggcgggcat cctggcgccg ccagagagg	1427
ccagggggac cttcagtgcc ctactgcct gcagtgcctc agtgacgagc aaggggaaga	1487
gctcctcagg catgtggccg agtgctgcca gtgaccgaga ctcacccgtg cccttgccgc	1547
ctcctggccc ggtgcagctg cctcagga caggggtgggt gctctcagat gccatgggtt	1607
gagctctact gagagccaag gccctagaa tagttgcggg gcactctgat cgttcacttt	1667
ggtccttttg gctatggaac aggtctgggtc acagggaaact gccagtgagg ctggaggctg	1727
gaggtggaga tggggtcagg aacatctggc agaggagggt cccagtctgt gtctccatca	1787

ggcttaagcc agagctatct ggtgctggtg tgccagcccc tccccagcc tgcctagaaa 1847
 ggggtggctg cctgagggag tcaactgtat ggtccccagg gtgggagccc catcctgttc 1907
 tatggaataa agcgtcgcct ctctgcctcg aaccagtcaa atggagtatt gcggctgcac 1967
 gtcacactag ggtggccacc cccgccattg cgagccacat gtctgcactg agaaactgca 2027
 ttccagtagc atttgtcatc cagccggaag ttaaagcaca cttattttat tcacctattt 2087
 ttataataaa cgttcttgct gctgtgaaaa aaaaaaaaaa a 2128

<210> 198
 <211> 668
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (136)..(498)

<400> 198
 aggctcgatg tatataacta tctattcgat gatgaagata cccacacaaa ccaaaaaaaaa 60
 gagatctctc gaggatccga attcgcggcc gcgtcgacct cccctacaga agcccccaga 120
 gcgcagcacc tcacc atg gac tgc acc tgg agg atc ctc ttc ttg gtg gca 171
 Met Asp Cys Thr Trp Arg Ile Leu Phe Leu Val Ala
 1 5 10
 gca gct aca ggc acc cac gcc cag gtc cag ctg gta cag tct ggg gct 219
 Ala Ala Thr Gly Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Ala
 13 18 23 28
 gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gtt tcc 267
 Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Val Ser
 29 34 39 44
 gga tac acc ctc act gaa tta tcc atg cac tgg gtg cga cag gct cct 315
 Gly Tyr Thr Leu Thr Glu Leu Ser Met His Trp Val Arg Gln Ala Pro
 45 50 55 60
 gga aaa ggg ctt gag tgg atg gga gct ttt gat cct gaa gat ggt gaa 363
 Gly Lys Gly Leu Glu Trp Met Gly Ala Phe Asp Pro Glu Asp Gly Glu
 61 66 71 76
 aca atc tac gca cag aag ttc cag ggc aga gtc acc atg acc gag gac 411
 Thr Ile Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Glu Asp
 77 82 87 92
 aca tct aca gac aca ggc tac atg ggg ctg agc agc ctg aga tct gag 459
 Thr Ser Thr Asp Thr Gly Tyr Met Gly Leu Ser Ser Leu Arg Ser Glu
 93 98 103 108

gac acg gcc gtg tat tat tgt gca aca gac aca gtg tga aaacccacat 508
 Asp Thr Ala Val Tyr Tyr Cys Ala Thr Asp Thr Val *
 109 114 119

cctgagagcg tcagaaaccc tgaggaatga ggcagctgtg ctgaggctga ggagatgaca 568

ggatttatga agtttaaate tgtttagaaa atgggttgag taattgagta aaacagcaat 628

ggaaaaaac gaaatcgga cagcgaagtc gacccgggaa 668

<210> 199
 <211> 2310
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (201)..(2105)

<400> 199
 gggcatgctg taccgctccg gaattaccgg gtcgacgatc tcgagtggct agagctgaaa 60

ggcgaccgct ggtgtcaaac atcttagctc aaatatctgg gaacgattgc gcgctgagga 120

agaccctttg ggactttag ctccactccg gggaaacggac tcgcggggac tgacagttgc 180

cggaaagtgag gctgcgggga atg gcc gcc gct gcg acc atg gcg gct gcg 230
 Met Ala Ala Ala Ala Thr Met Ala Ala Ala
 1 5

gcc cgg gaa ctg gtg ttg cgg gct ggg acc tca gat atg gag gag gaa 278
 Ala Arg Glu Leu Val Leu Arg Ala Gly Thr Ser Asp Met Glu Glu Glu
 11 16 21 26

gag ggc ccg ctg gcg ggt ggt cct ggg ctc cag gaa cca ctg caa ctt 326
 Glu Gly Pro Leu Ala Gly Gly Pro Gly Leu Gln Glu Pro Leu Gln Leu
 27 32 37 42

ggg gag ttg gat atc act tct gat gaa ttc atc ctg gat gaa gtg gat 374
 Gly Glu Leu Asp Ile Thr Ser Asp Glu Phe Ile Leu Asp Glu Val Asp
 43 48 53 58

gtt cac att cag gca aat ctg gag gat gag tta gta aag gaa gct ctt 422
 Val His Ile Gln Ala Asn Leu Glu Asp Glu Leu Val Lys Glu Ala Leu
 59 64 69 74

aaa acg ggt gta gat ctc cgt cac tat tca aag caa gtt gag ctg gag 470
 Lys Thr Gly Val Asp Leu Arg His Tyr Ser Lys Gln Val Glu Leu Glu
 75 80 85 90

cta cag cag att gaa cag aaa tcc att cgg gat tat att caa gag agt 518
 Leu Gln Gln Ile Glu Gln Lys Ser Ile Arg Asp Tyr Ile Gln Glu Ser
 91 96 101 106

gag aat ata gca tct cta cac aac cag atc aca gcc tgt gat gct gtc	566
Glu Asn Ile Ala Ser Leu His Asn Gln Ile Thr Ala Cys Asp Ala Val	
107 112 117 122	
ctg gag cga atg gag cag atg ttg gga gct ttt cag agt gac ctc agc	614
Leu Glu Arg Met Glu Gln Met Leu Gly Ala Phe Gln Ser Asp Leu Ser	
123 128 133 138	
tcc atc agc tct gag atc cgg aca ctg cag gaa cag tca gga gcc atg	662
Ser Ile Ser Ser Glu Ile Arg Thr Leu Gln Glu Gln Ser Gly Ala Met	
139 144 149 154	
aac att cga ctt cga aat cgc cag gca gtt cgg ggg aaa ctt ggg gag	710
Asn Ile Arg Leu Arg Asn Arg Gln Ala Val Arg Gly Lys Leu Gly Glu	
155 160 165 170	
ctt gtt gat ggt ctg gtg gtg cct tct gct ctg gtc acg gca att ctg	758
Leu Val Asp Gly Leu Val Val Pro Ser Ala Leu Val Thr Ala Ile Leu	
171 176 181 186	
gag gct cca gtg aca gag ccc agg ttc ttg gag cag cta cag gag ctg	806
Glu Ala Pro Val Thr Glu Pro Arg Phe Leu Glu Gln Leu Gln Glu Leu	
187 192 197 202	
gat gcc aag gca gcc gca gtc aga gag cag gaa gct aga ggc aca gca	854
Asp Ala Lys Ala Ala Ala Val Arg Glu Gln Glu Ala Arg Gly Thr Ala	
203 208 213 218	
gcc tgc gca gat gtc aga ggc gtg ctc gat cgg ctc cgg gtc aag gca	902
Ala Cys Ala Asp Val Arg Gly Val Leu Asp Arg Leu Arg Val Lys Ala	
219 224 229 234	
gtg acg aag atc cga gag ttt atc ctc cag aag att tat tcc ttc agg	950
Val Thr Lys Ile Arg Glu Phe Ile Leu Gln Lys Ile Tyr Ser Phe Arg	
235 240 245 250	
aaa ccc atg acc aac tat cag atc ccc cag acg gcc ctg ctg aag tac	998
Lys Pro Met Thr Asn Tyr Gln Ile Pro Gln Thr Ala Leu Leu Lys Tyr	
251 256 261 266	
agg ttc ttc tat cag ttt ctg ctg ggc aat gaa cga gca aca gca aag	1046
Arg Phe Phe Tyr Gln Phe Leu Leu Gly Asn Glu Arg Ala Thr Ala Lys	
267 272 277 282	
gag atc agg gat gaa tat gtg gag acg ctg agc aag att tac ctg tct	1094
Glu Ile Arg Asp Glu Tyr Val Glu Thr Leu Ser Lys Ile Tyr Leu Ser	
283 288 293 298	
tac tac cgc tct tac ctg ggg cgg ctc atg aag gtg cag tat gag gaa	1142
Tyr Tyr Arg Ser Tyr Leu Gly Arg Leu Met Lys Val Gln Tyr Glu Glu	
299 304 309 314	
gtc gct gag aaa gat gat cta atg ggt gtg gaa gat aca gca aag aaa	1190
Val Ala Glu Lys Asp Asp Leu Met Gly Val Glu Asp Thr Ala Lys Lys	
315 320 325 330	
gga ttc ttc tca aag cca tcg ctc cgc agc agg aac acc att ttc acc	1238

Gly Phe Phe Ser Lys Pro Ser Leu Arg Ser Arg Asn Thr Ile Phe Thr	
331 336 341 346	
cta gga acc cgc ggc tct gtc atc tcc ccc act gaa ctt gag gcc ccc	1286
Leu Gly Thr Arg Gly Ser Val Ile Ser Pro Thr Glu Leu Glu Ala Pro	
347 352 357 362	
atc ctg gtg cct cac aca gcg cag cgc gga gag cag agg tat cca ttt	1334
Ile Leu Val Pro His Thr Ala Gln Arg Gly Glu Gln Arg Tyr Pro Phe	
363 368 373 378	
gag gcc ctc ttc cgc agc cag cac tac gcc ctc cta gac aat tcc tgc	1382
Glu Ala Leu Phe Arg Ser Gln His Tyr Ala Leu Leu Asp Asn Ser Cys	
379 384 389 394	
cgc gaa tac ctt ttc atc tgt gaa ttt ttt gtt gtg tct ggc cca gct	1430
Arg Glu Tyr Leu Phe Ile Cys Glu Phe Phe Val Val Ser Gly Pro Ala	
395 400 405 410	
gca cac gac ctg ttc cat gct gtc atg ggc cgt aca ctc agc atg acc	1478
Ala His Asp Leu Phe His Ala Val Met Gly Arg Thr Leu Ser Met Thr	
411 416 421 426	
ctg aaa cac ctg gat tct tat cta gct gac tgc tac gat gcc att gct	1526
Leu Lys His Leu Asp Ser Tyr Leu Ala Asp Cys Tyr Asp Ala Ile Ala	
427 432 437 442	
gtt ttt ctc tgt atc cac att gtt ctc cgg ttc cgt aac att gca gca	1574
Val Phe Leu Cys Ile His Ile Val Leu Arg Phe Arg Asn Ile Ala Ala	
443 448 453 458	
aag agg gat gtt cct gcc ctg gac agg tac tgg gaa cag gtg ctt gcc	1622
Lys Arg Asp Val Pro Ala Leu Asp Arg Tyr Trp Glu Gln Val Leu Ala	
459 464 469 474	
ttg cta tgg cca cgg ttt gaa ctg atc ctg gag atg aat gtt cag agc	1670
Leu Leu Trp Pro Arg Phe Glu Leu Ile Leu Glu Met Asn Val Gln Ser	
475 480 485 490	
gtc cga agc act gac ccc cag cgc cta ggg ggg ttg gat act cgg ccc	1718
Val Arg Ser Thr Asp Pro Gln Arg Leu Gly Gly Leu Asp Thr Arg Pro	
491 496 501 506	
cac tat atc aca cgc cgc tat gca gag ttc tcc tcc gct ctt gtc agt	1766
His Tyr Ile Thr Arg Arg Tyr Ala Glu Phe Ser Ser Ala Leu Val Ser	
507 512 517 522	
atc aac cag aca att cct aat gaa cgg acc atg caa ttg ctg gga cag	1814
Ile Asn Gln Thr Ile Pro Asn Glu Arg Thr Met Gln Leu Leu Gly Gln	
523 528 533 538	
ctg cag gtg gag gtg gag aat ttt gtc ctc cga gtg gca gct gag ttc	1862
Leu Gln Val Glu Val Glu Asn Phe Val Leu Arg Val Ala Ala Glu Phe	
539 544 549 554	
tcc tca agg aag gag cag ott gtg ttt ctg atc aac aac tat gac atg	1910
Ser Ser Arg Lys Glu Gln Leu Val Phe Leu Ile Asn Asn Tyr Asp Met	

555	560	565	570	
atg ctg ggt gtg ctg atg gag cgg gct gca gat gac agc aaa gag gtt				1958
Met Leu Gly Val Leu Met Glu Arg Ala Ala Asp Asp Ser Lys Glu Val				
571	576	581	586	
gag agc ttc cag cag ctg ctc aat gct cgg aca cag aga cca agg atg				2006
Glu Ser Phe Gln Gln Leu Leu Asn Ala Arg Thr Gln Arg Pro Arg Met				
587	592	597	602	
ctg cta aag atg ctc ggg atc aga aat gtt tca gat ttt gat ttt ttt				2054
Leu Leu Lys Met Leu Gly Ile Arg Asn Val Ser Asp Phe Asp Phe Phe				
603	608	613	618	
cgg att ttg gat tcc ttg cat tat ttt tac tgg tta gca tct gta gtc				2102
Arg Ile Leu Asp Ser Leu His Tyr Phe Tyr Trp Leu Ala Ser Val Val				
619	624	629	634	
tga aaat ctgaaatctg aaatgctcca aagagcatta cctttgagca tcatgttgat				2159
*				
635				
actcaaaaac ttccggattt tggagcattt tggatttcag attattggat tagggatact				2219
caacctgtat ttcagtgggt tttatttgta attttctgat tactaataac attgagcatc				2279
atttcaaatg tttagtaact atatgtaggg g				2310

<210> 200
 <211> 1835
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (32)..(1603)

<400> 200				
ggaattcccg ggtcgacgat ttcgtgcggt c	atg gag gcg ggc gcc gga gcc	52		
	Met Glu Ala Gly Ala Gly Ala			
	1 5			
ggc gcg gga gcc gcg ggc tgg agc tgc ccg ggc cca gga ccc aca gtg				100
Gly Ala Gly Ala Ala Gly Trp Ser Cys Pro Gly Pro Gly Pro Thr Val				
8 13 18 23				
acc act cta ggc tcc tat gag gct tcc gag ggc tgt gag agg aag aag				148
Thr Thr Leu Gly Ser Tyr Glu Ala Ser Glu Gly Cys Glu Arg Lys Lys				
24 29 34 39				
ggc caa cgc tgg ggg tcc ctg gaa cga cgg ggg atg caa gct atg gag				196
Gly Gln Arg Trp Gly Ser Leu Glu Arg Arg Gly Met Gln Ala Met Glu				
40 45 50 55				

ggg gag gtg tta ctc cca gct ctc tat gag gag gaa gag gaa gag gaa	244
Gly Glu Val Leu Leu Pro Ala Leu Tyr Glu Glu Glu Glu Glu Glu Glu	
56 61 66 71	
gag gag gaa gaa gag gtg gaa gaa gaa gaa gaa caa gtg cag aaa ggt	292
Glu Glu Glu Glu Glu Val Glu Glu Glu Glu Glu Gln Val Gln Lys Gly	
72 77 82 87	
ggc agt gtt ggc tct ctg tca gtc aac aag cac cgg gga ctg agc ctc	340
Gly Ser Val Gly Ser Leu Ser Val Asn Lys His Arg Gly Leu Ser Leu	
88 93 98 103	
acg gag aca gag ctg gag gag ctg cgg gct cag gtg ctg cag ctg gtg	388
Thr Glu Thr Glu Leu Glu Glu Leu Arg Ala Gln Val Leu Gln Leu Val	
104 109 114 119	
gca gaa ctg gag gag acc cgg gaa ctg gca ggg cag cat gag gat gac	436
Ala Glu Leu Glu Glu Thr Arg Glu Leu Ala Gly Gln His Glu Asp Asp	
120 125 130 135	
tcc ttg gag cta cag ggg ctc ctg gag gat gaa cgg cta gcc agc gcc	484
Ser Leu Glu Leu Gln Gly Leu Leu Glu Asp Glu Arg Leu Ala Ser Ala	
136 141 146 151	
cag cag gca gag gtg ttc acc aag cag atc cag cag ctc caa ggt gag	532
Gln Gln Ala Glu Val Phe Thr Lys Gln Ile Gln Gln Leu Gln Gly Glu	
152 157 162 167	
ctg cgt tct cta cgg gag gag att tcc ctg tta gag cat gag aaa gaa	580
Leu Arg Ser Leu Arg Glu Glu Ile Ser Leu Leu Glu His Glu Lys Glu	
168 173 178 183	
agc gaa ctt aag gaa ata gaa cag gaa ttg cat ttg gcc cag gct gag	628
Ser Glu Leu Lys Glu Ile Glu Gln Glu Leu His Leu Ala Gln Ala Glu	
184 189 194 199	
atc cag agt ctg cgg caa gca gca gag gat tcc gca act gaa cat gag	676
Ile Gln Ser Leu Arg Gln Ala Ala Glu Asp Ser Ala Thr Glu His Glu	
200 205 210 215	
agt gac ata gca tcc ctg cag gag gat ctc tgc cgg atg cag aat gaa	724
Ser Asp Ile Ala Ser Leu Gln Glu Asp Leu Cys Arg Met Gln Asn Glu	
216 221 226 231	
ctt gaa gac atg gaa cgc att cgg gga gat tat gag atg gag atc gcc	772
Leu Glu Asp Met Glu Arg Ile Arg Gly Asp Tyr Glu Met Glu Ile Ala	
232 237 242 247	
tcc ctc cgt gca gaa atg gaa atg aag agc tct gaa cca tcc ggt agt	820
Ser Leu Arg Ala Glu Met Glu Met Lys Ser Ser Glu Pro Ser Gly Ser	
248 253 258 263	
tta ggt ctc tca gat tac tct ggg tta caa gaa gaa ctg cag gag ctg	868
Leu Gly Leu Ser Asp Tyr Ser Gly Leu Gln Glu Glu Leu Gln Glu Leu	
264 269 274 279	
cgg gaa cgc tac cat ttc ctg aat gag gaa tac cgg gcc ctg cag gag	916

Arg Glu Arg Tyr His Phe Leu Asn Glu Glu Tyr Arg Ala Leu Gln Glu	
280 285 290 295	
agc aac agc agc ctc acg ggg cag ctt gca gat ctg gag agt gag agg	964
Ser Asn Ser Ser Leu Thr Gly Gln Leu Ala Asp Leu Glu Ser Glu Arg	
296 301 306 311	
aca cag aga gca aca gag aga tgg ctg cag tcc caa aca ctg agt atg	1012
Thr Gln Arg Ala Thr Glu Arg Trp Leu Gln Ser Gln Thr Leu Ser Met	
312 317 322 327	
acg tca gca gag tct cag act tca gaa atg gat ttc tta gag cct gat	1060
Thr Ser Ala Glu Ser Gln Thr Ser Glu Met Asp Phe Leu Glu Pro Asp	
328 333 338 343	
cct gaa atg cag ttg tta cgg cag cag cta cgg gat gct gaa gag cag	1108
Pro Glu Met Gln Leu Leu Arg Gln Gln Leu Arg Asp Ala Glu Glu Gln	
344 349 354 359	
atg cat ggc atg aag aac aag tgt cag gaa ttg tgt tgt gag ttg gaa	1156
Met His Gly Met Lys Asn Lys Cys Gln Glu Leu Cys Cys Glu Leu Glu	
360 365 370 375	
gag cta cag cat cat cgc cag gtc agt gag gag gag cag agg cgg ctg	1204
Glu Leu Gln His His Arg Gln Val Ser Glu Glu Glu Gln Arg Arg Leu	
376 381 386 391	
cag agg gag ctc aag tgt gct cag aat gag gtg ctt cgg ttt cag acc	1252
Gln Arg Glu Leu Lys Cys Ala Gln Asn Glu Val Leu Arg Phe Gln Thr	
392 397 402 407	
tcc cac agt gtc acc cag cgc ttt gag gaa atg gtt gtg aaa gtg ctg	1300
Ser His Ser Val Thr Gln Arg Phe Glu Glu Met Val Val Lys Val Leu	
408 413 418 423	
atc aag ctg cag gcg gtg cag gcc atg tac cag ata agc cag gag gaa	1348
Ile Lys Leu Gln Ala Val Gln Ala Met Tyr Gln Ile Ser Gln Glu Glu	
424 429 434 439	
cac agc cag ctg caa gag cag atg gaa aag tta ctg gcc aag cag aaa	1396
His Ser Gln Leu Gln Glu Gln Met Glu Lys Leu Leu Ala Lys Gln Lys	
440 445 450 455	
gac ctg aag gaa gag ctg gat gcc tgt gaa agg gag ttc aag gag tgc	1444
Asp Leu Lys Glu Glu Leu Asp Ala Cys Glu Arg Glu Phe Lys Glu Cys	
456 461 466 471	
atg gaa tgc ctt gaa aag ccc atg gcc ccc cag aac gac aag aat gag	1492
Met Glu Cys Leu Glu Lys Pro Met Ala Pro Gln Asn Asp Lys Asn Glu	
472 477 482 487	
aac atg ttt ggg ttg tgg aag cct atg gta ttc ttg gct att gca gct	1540
Asn Met Phe Gly Leu Trp Lys Pro Met Val Phe Leu Ala Ile Ala Ala	
488 493 498 503	
gtg gct ctg tat gtg tta ccc aac atg cga cag cag gag tca gag ttc	1588
Val Ala Leu Tyr Val Leu Pro Asn Met Arg Gln Gln Glu Ser Glu Phe	

504

509

514

519

tgc ctc atg gag tga tggcagacct tggccagcgc gagggcagat cccagtggc 1643
 Cys Leu Met Glu *
 520

caccaccctc agctttgggc aggacacact gtgccagaac cctccccata tgttccatgt 1703

gtccccatct cctcagcctc agtcacccag gctgaaaagg cttgtgggga gcggctgact 1763

tocatctcct gccttgtgta agaacctgag ttccttgtaa ttaaatatca actgaattac 1823

aaaaaaaaaa aa 1835

<210> 201

<211> 4029

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (316)..(1842)

<400> 201

gacggcaagt gccaaagctaa aattaaccct ccactaaagg gaataagctt gcgccgacca 60

tcgactcgcc aacgagagaa ggtcctgggg cacggacacc gacgggttgc gactgtgacg 120

tgaggtgttc tcgcgcgcgc tagcgcgcgt ctccgggtgc cgctgacggg cgtgcgcgct 180

tgtgcgaggc cggaggtggg ggccgaacca gccaaagggtg cgggggccgc agagccggac 240

gaagacggag ggcggagccg gcttcgggac tgccggagact acacaccgag cgagcgccctg 300

ggccccgaagg gagcg atg ctg tgg ttc cag ggc gcc att ccg gcc gcc atc 351

Met Leu Trp Phe Gln Gly Ala Ile Pro Ala Ala Ile
 1 5 10

gcg acg gcc aaa agg agc ggc gcg gtc ttc gtg gtg ttc gtg gca ggt 399

Ala Thr Ala Lys Arg Ser Gly Ala Val Phe Val Val Phe Val Ala Gly
 13 18 23 28

gat gat gaa cag tct aca cag atg gct gca agt tgg gaa gat gat aaa 447

Asp Asp Glu Gln Ser Thr Gln Met Ala Ala Ser Trp Glu Asp Asp Lys
 29 34 39 44

gtt aca gaa gca tct tca aac agt ttt gtt gct att aaa atc gat acc 495

Val Thr Glu Ala Ser Ser Asn Ser Phe Val Ala Ile Lys Ile Asp Thr
 45 50 55 60

aaa agt gaa gcc tgc cta cag ttt tca caa atc tat cct gta gtg tgt 543

Lys Ser Glu Ala Cys Leu Gln Phe Ser Gln Ile Tyr Pro Val Val Cys
 61 66 71 76

gtt cca tcc agt ttc ttt att gga gac agt gga att ccc ttg gaa gta	591
Val Pro Ser Ser Phe Phe Ile Gly Asp Ser Gly Ile Pro Leu Glu Val	
77 82 87 92	
ata gca gga agt gtt tct gca gat gag ctt gtt aca aga att cac aag	639
Ile Ala Gly Ser Val Ser Ala Asp Glu Leu Val Thr Arg Ile His Lys	
93 98 103 108	
gtc cga cag atg cat ttg cta aaa agt gaa aca tca gta gca aat ggc	687
Val Arg Gln Met His Leu Leu Lys Ser Glu Thr Ser Val Ala Asn Gly	
109 114 119 124	
agt cag tca gaa agt tca gtg tct act cca tct gcg tca ttt gaa cct	735
Ser Gln Ser Glu Ser Ser Val Ser Thr Pro Ser Ala Ser Phe Glu Pro	
125 130 135 140	
aac aac act tgt gaa aac tct cag tcc aga aat gca gag ctt tgt gag	783
Asn Asn Thr Cys Glu Asn Ser Gln Ser Arg Asn Ala Glu Leu Cys Glu	
141 146 151 156	
ata cca ccc act tct gat aca aag tca gat act gca aca gga gga gaa	831
Ile Pro Pro Thr Ser Asp Thr Lys Ser Asp Thr Ala Thr Gly Gly Glu	
157 162 167 172	
agt gca ggc cat gcc act tcc tct cag gag cct agt gga tgc tca gat	879
Ser Ala Gly His Ala Thr Ser Ser Gln Glu Pro Ser Gly Cys Ser Asp	
173 178 183 188	
cag aga cct gca gag gac ctc aac atc cga gtg gaa aga cta aca aaa	927
Gln Arg Pro Ala Glu Asp Leu Asn Ile Arg Val Glu Arg Leu Thr Lys	
189 194 199 204	
aaa ctt gaa gaa agg aga gaa gag aaa aga aaa gag gaa gaa cag aga	975
Lys Leu Glu Glu Arg Arg Glu Glu Lys Arg Lys Glu Glu Glu Gln Arg	
205 210 215 220	
gaa att aag aag gaa att gag agg aga aaa act gga aaa gaa atg ttg	1023
Glu Ile Lys Lys Glu Ile Glu Arg Arg Lys Thr Gly Lys Glu Met Leu	
221 226 231 236	
gat tat aaa aga aaa caa gaa gaa gaa tta aca aaa aga atg ctg gag	1071
Asp Tyr Lys Arg Lys Gln Glu Glu Glu Leu Thr Lys Arg Met Leu Glu	
237 242 247 252	
gaa aga aac aga gag aaa gca gaa gat agg gca gct cga gaa cgt ata	1119
Glu Arg Asn Arg Glu Lys Ala Glu Asp Arg Ala Ala Arg Glu Arg Ile	
253 258 263 268	
aaa cag cag att gca ttg gac cgt gca gag aga gct gct cgt ttt gca	1167
Lys Gln Gln Ile Ala Leu Asp Arg Ala Glu Arg Ala Ala Arg Phe Ala	
269 274 279 284	
aag aca aag gaa gaa gta gag gct gcc aaa gct gct gcc ttg cta gca	1215
Lys Thr Lys Glu Glu Val Glu Ala Ala Lys Ala Ala Ala Leu Leu Ala	
285 290 295 300	
aaa cag gca gaa atg gaa gtc aag agg gaa tct tat gca aga gaa aga	1263

Lys	Gln	Ala	Glu	Met	Glu	Val	Lys	Arg	Glu	Ser	Tyr	Ala	Arg	Glu	Arg		
301					306					311					316		
agc	act	gtt	gca	aga	att	caa	ttc	cgt	ctt	cct	gat	ggg	tct	tcc	ttt	1311	
Ser	Thr	Val	Ala	Arg	Ile	Gln	Phe	Arg	Leu	Pro	Asp	Gly	Ser	Ser	Phe		
317					322					327					332		
aca	aat	cag	ttc	cct	tct	gat	gct	cct	cta	gaa	gag	gca	agg	cag	ttt	1359	
Thr	Asn	Gln	Phe	Pro	Ser	Asp	Ala	Pro	Leu	Glu	Glu	Ala	Arg	Gln	Phe		
333					338					343					348		
gct	gca	cag	act	gtt	ggc	aac	act	tac	ggg	aat	ttt	tcg	tta	gca	acc	1407	
Ala	Ala	Gln	Thr	Val	Gly	Asn	Thr	Tyr	Gly	Asn	Phe	Ser	Leu	Ala	Thr		
349					354					359					364		
atg	ttt	ccc	agg	agg	gaa	ttt	acc	aaa	gaa	gat	tat	aaa	aag	aag	tta	1455	
Met	Phe	Pro	Arg	Arg	Glu	Phe	Thr	Lys	Glu	Asp	Tyr	Lys	Lys	Lys	Leu		
365					370					375					380		
ctg	gat	ttg	gaa	ctt	gcc	cca	agc	gct	tcg	gtg	gta	ctg	ttg	cca	gca	1503	
Leu	Asp	Leu	Glu	Leu	Ala	Pro	Ser	Ala	Ser	Val	Val	Leu	Leu	Pro	Ala		
381					386					391					396		
gga	aga	cca	act	gca	tcc	att	gta	cac	tct	tcc	agc	gga	gac	att	tgg	1551	
Gly	Arg	Pro	Thr	Ala	Ser	Ile	Val	His	Ser	Ser	Ser	Gly	Asp	Ile	Trp		
397					402					407					412		
acc	ttg	ttg	gga	aca	gtg	ctt	tat	cca	ttc	ctt	gcc	atc	tgg	aga	tta	1599	
Thr	Leu	Leu	Gly	Thr	Val	Leu	Tyr	Pro	Phe	Leu	Ala	Ile	Trp	Arg	Leu		
413					418					423					428		
att	agc	aat	ttc	ttg	ttt	agt	aat	ccg	cct	ccc	aca	cag	act	tca	gtg	1647	
Ile	Ser	Asn	Phe	Leu	Phe	Ser	Asn	Pro	Pro	Pro	Thr	Gln	Thr	Ser	Val		
429					434					439					444		
aga	gta	aca	tcg	tca	gaa	ccc	cca	aac	cct	gca	tca	tct	agc	aaa	tca	1695	
Arg	Val	Thr	Ser	Ser	Glu	Pro	Pro	Asn	Pro	Ala	Ser	Ser	Ser	Lys	Ser		
445					450					455					460		
gaa	aaa	agg	gaa	cca	gtg	aga	aaa	aga	gtg	ctg	gaa	aaa	cgt	gga	gac	1743	
Glu	Lys	Arg	Glu	Pro	Val	Arg	Lys	Arg	Val	Leu	Glu	Lys	Arg	Gly	Asp		
461					466					471					476		
gac	ttt	aaa	aag	gag	ggg	aaa	att	tat	aga	tta	agg	act	caa	gat	gat	1791	
Asp	Phe	Lys	Lys	Glu	Gly	Lys	Ile	Tyr	Arg	Leu	Arg	Thr	Gln	Asp	Asp		
477					482					487					492		
ggg	gaa	gat	gaa	aac	aac	act	tgg	aat	gga	aat	tcc	act	caa	cag	atg	1839	
Gly	Glu	Asp	Glu	Asn	Asn	Thr	Trp	Asn	Gly	Asn	Ser	Thr	Gln	Gln	Met		
493					498					503					508		
tag	tgtg	acaagtataa	tatgtgcaat	aatcattggt	tctcttatga	tttaattcaa										1896	
*																	
509																	
ctaaaattct	actggagaag	tgggactgct	ttatatatttc	caactgggtct	ataaaatgct											1956	

tctttattcc	tgcttagtgg	gtgtgggttg	aaggtgttta	actcagaaaa	gaaaagacag	2016
gaaataactc	tctgctaggt	ccttgcttat	atggcaacca	ctgctagaac	cctaaaagaa	2076
ccaaaaatct	gccacagcct	gcctccatca	gcttcttatt	tagtatttca	tatgcccatt	2136
agccctatgc	ttcagatgac	acgttttggt	tagagctact	ttgctccaag	actcttaagc	2196
ccaaagtaac	tggtatgtca	ctgagtaact	tgactcgggtg	tcagagcatt	ttactagcc	2256
actcagatga	gaatttatgt	ttactttctc	tttttactca	tcagctgcaa	gcaaaatctt	2316
gtagttttta	atcttaaaca	ctgaataaaa	aaactttccc	ctaaattgga	atgatcttag	2376
ttttgctttg	agttttgtta	tctagcatct	ttttgttgca	cagggctcta	ttgaggtcct	2436
atgtctctga	tttttttttt	ccccagtatt	gccctggagc	tgtctctgga	aagtagctgg	2496
cgaggttacc	ttactatca	ctgaagaaag	aaattttctg	acacactgat	ggcatgtgac	2556
ttgtctccta	agtcagtgag	gcataccttt	gtttgcataa	agtatacggg	ttgttaaggc	2616
ctttgttctt	gtgagatgca	aaacagctgc	tagtctgcaa	cctagttttc	cctctcacct	2676
ttactgacg	ttttgtcctc	aataattaca	caaggaccta	gagtacctat	aggacaaaaa	2736
gtatagaata	aaaatatgcc	tttagtcatt	tggtttttct	taaaaagttg	agattcttaa	2796
tctgacttac	atgttacttt	atccgtatgt	ctttgttagt	ggagaccgct	aaactaatga	2856
tgtttgaaaa	cagttcctct	gttttagatt	ggaagatagc	actctagagt	ggacatacgg	2916
aaagactgtg	actttatttt	gtaatgggag	gaagaaatth	tctcagagca	aactttctat	2976
tttttacctg	tgaaataaca	gtgacttttt	aaaatggtga	cagtgttggc	aaggaaacag	3036
caacacaggc	tgcgctgttg	gtaggagtga	aaaccagtat	aattcttctg	aaaaacattt	3096
atcagaaact	taaaatattt	cataccgttt	gatccagtag	cttcttctaa	atcataaatg	3156
cagacaatgt	ttaggtaaag	acatactcat	taagtgttat	ttattttact	caagaactgg	3216
aaaccaacta	aatgccttct	atagaagtaa	tttttgatga	ggagaaatgg	tacaatacta	3276
attaacaact	tggtttaaca	tgtttactga	gcatactgta	agtgttgggg	gaaaaagcag	3336
caggatccag	agctataggt	acagtgtgat	ctcagctttg	caaacacatt	ttctacatag	3396
atagtactag	gtattaatag	atatgtaaag	aaagaaatca	caccattaat	aatggtaaga	3456
ttggtttatg	tgattttagt	ggtatttttg	gcaccttat	atatgttttc	caaactttca	3516
gcagtgatat	tatttccata	acttaaaaag	tgagtttgaa	aaagaaaatc	tccagcaagc	3576
atctcattta	aataaagggt	tgatcatctt	aaaaatacag	caatatgtga	cttttttaaaa	3636
aagctgtcaa	ataggtgtga	ccctactaat	aattattaga	aatacattta	aaaacatcga	3696

gtacctcaag tcagtttgcc ttgaaaaata tcaaataata ctcttagaga aatgtacata 3756
aaagaatgct tcgtaatttt ggagtaggag gttccctcct caattttgta tttttaaaaa 3816
gtacatggta aaaaaaaaaa ttcacaacag tatataaggc tgtaaaatga gaattctgcc 3876
ccctcacctc ttaccccgag actattctcc agaggtaatc tattaacaat ttcttatgta 3936
attttcaaga aatttgtatg cgtatataag caaatatgta atctttatct tttaaataaa 3996
tgggatcata ttatatattc taaaaaaaaa aaa 4029

<210> 202
<211> 914
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (182)..(568)

<400> 202
cctgctctgt agagccggcg gcaaccgggt agcttggcca ggttgtagg aaccgcagcg 60
cccgcaggac cgggcccgtg agcctgcagc cgcgccgcgc cgtgacctgc gaccctagac 120
cccgaactccc tttggctcag cccgcgcgcc ccaggccccg cccgggcccgc ggcacggggag 180
g atg agc ggc ggg cgc gga agg agg agc cgc ctc agc cgc agc tgg 226
Met Ser Gly Gly Arg Gly Arg Arg Ser Arg Leu Ser Arg Ser Trp
1 5 10
cca acg ggg ccc tca aag tct ccg tct gga gta agg tgc tgc gga cga 274
Pro Thr Gly Pro Ser Lys Ser Pro Ser Gly Val Arg Cys Cys Gly Arg
16 21 26 31
cgc gcc tgg gag gat aag gat gaa ttt tta gat gtg atc tac tgg ttc 322
Arg Ala Trp Glu Asp Lys Asp Glu Phe Leu Asp Val Ile Tyr Trp Phe
32 37 42 47
cga cag atc att gct gtg gtc ctg ggt gtc att tgg gga gtt ttg cca 370
Arg Gln Ile Ile Ala Val Val Leu Gly Val Ile Trp Gly Val Leu Pro
48 53 58 63
tta cga ggg ttc ttg gga ata gca gga ttc tgc ctg atc aat gca gga 418
Leu Arg Gly Phe Leu Gly Ile Ala Gly Phe Cys Leu Ile Asn Ala Gly
64 69 74 79
gtc ctg tac ctc tac ttc agc aat tac cta cag att gat gag gaa gaa 466
Val Leu Tyr Leu Tyr Phe Ser Asn Tyr Leu Gln Ile Asp Glu Glu Glu
80 85 90 95
tat ggt ggc acg tgg gag ctc acg aag gaa ggg ttt atg acc tct ttt 514

Tyr Gly Gly Thr Trp Glu Leu Thr Lys Glu Gly Phe Met Thr Ser Phe
 96 101 106 111
 gcc ttg ttc atg gtc att tgg atc atc ttt tac act gcc atc cat tat 562
 Ala Leu Phe Met Val Ile Trp Ile Ile Phe Tyr Thr Ala Ile His Tyr
 112 117 122 127
 gac tga tgggtgtacag ctcccaagtg ctccctatcc agtccaaagg accctcttga 618
 Asp *
 128
 ttacagcaca ggaacttgat cgttggggaa cccagcccc ttggaacttg gaagaccctg 678
 gtttcttgga ccgcgaatca gtgtgttggg catcagtgtt ttctgcaagg gttgtgacct 738
 gaaactttttt aaaaaccccc cccctttggg gaagcatttt tgaatttatc catccccaac 798
 cattttttttt tggataccat caagtaacag ctattatttg ccaagtggag ctgtcattta 858
 atttgatgcc cctctggatt cagatgaaac attaaattgt tttctctgat tttcaa 914

 <210> 203
 <211> 1131
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (93)..(1082)

 <400> 203
 tttgaacgcc ttgaggtacc ggtccggaat tcccgggtcg acccacgcgt ccggaaagct 60
 tggttacaac ccgggacacc cggagcttca gg atg gtt cgt act aag aca tgg 113
 Met Val Arg Thr Lys Thr Trp
 1 5
 acc ctg aag aag cac ttt gtt ggc tat cct act aat agt gac ttt gag 161
 Thr Leu Lys Lys His Phe Val Gly Tyr Pro Thr Asn Ser Asp Phe Glu
 8 13 18 23
 ttg aag aca gct gag ctc cca ccc tta aaa aat gga gag gtc ctg ctt 209
 Leu Lys Thr Ala Glu Leu Pro Pro Leu Lys Asn Gly Glu Val Leu Leu
 24 29 34 39
 gaa gct ttg ttc ctc acc gtg gat ccc tac atg aga gtg gca gcc aaa 257
 Glu Ala Leu Phe Leu Thr Val Asp Pro Tyr Met Arg Val Ala Ala Lys
 40 45 50 55
 aga ttg aag gaa ggt gat aca atg atg ggg cag caa gtg gcc aaa gtt 305
 Arg Leu Lys Glu Gly Asp Thr Met Met Gly Gln Gln Val Ala Lys Val
 56 61 66 71
 gtg gaa agt aaa aat gta gcc cta cca aaa gga act att gta ctg gct 353

Val	Glu	Ser	Lys	Asn	Val	Ala	Leu	Pro	Lys	Gly	Thr	Ile	Val	Leu	Ala		
72					77					82					87		
tct	cca	ggc	tgg	aca	acg	cac	tcc	att	tct	gat	ggg	aaa	gat	ctg	gaa	401	
Ser	Pro	Gly	Trp	Thr	Thr	His	Ser	Ile	Ser	Asp	Gly	Lys	Asp	Leu	Glu		
88					93					98					103		
aag	ctg	ctg	aca	gag	tgg	cca	gac	aca	ata	cca	ctg	tct	ttg	gct	ctg	449	
Lys	Leu	Leu	Thr	Glu	Trp	Pro	Asp	Thr	Ile	Pro	Leu	Ser	Leu	Ala	Leu		
104					109					114					119		
ggg	aca	gtt	ggc	atg	cca	ggc	ctg	act	gcc	tac	ttt	ggc	cta	ctt	gaa	497	
Gly	Thr	Val	Gly	Met	Pro	Gly	Leu	Thr	Ala	Tyr	Phe	Gly	Leu	Leu	Glu		
120					125					130					135		
atc	tgt	ggt	gtg	aag	ggt	gga	gaa	aca	gtg	atg	gtt	aat	gca	gca	gct	545	
Ile	Cys	Gly	Val	Lys	Gly	Gly	Glu	Thr	Val	Met	Val	Asn	Ala	Ala	Ala		
136					141					146					151		
gga	gct	gtg	ggc	tca	gtc	gtg	ggg	cag	att	gca	aag	ctc	aag	ggc	tgc	593	
Gly	Ala	Val	Gly	Ser	Val	Val	Gly	Gln	Ile	Ala	Lys	Leu	Lys	Gly	Cys		
152					157					162					167		
aaa	gtt	gtt	gga	gca	gta	ggg	tct	gat	gaa	aag	gtt	gcc	tac	ctt	caa	641	
Lys	Val	Val	Gly	Ala	Val	Gly	Ser	Asp	Glu	Lys	Val	Ala	Tyr	Leu	Gln		
168					173					178					183		
aag	ctt	gga	ttt	gat	gtc	gtc	ttt	aac	tac	aag	acg	gta	gag	tct	ttg	689	
Lys	Leu	Gly	Phe	Asp	Val	Val	Phe	Asn	Tyr	Lys	Thr	Val	Glu	Ser	Leu		
184					189					194					199		
gaa	gaa	acc	ttg	aag	aaa	gcg	tct	cct	gat	ggt	tat	gat	tgt	tat	ttt	737	
Glu	Glu	Thr	Leu	Lys	Lys	Ala	Ser	Pro	Asp	Gly	Tyr	Asp	Cys	Tyr	Phe		
200					205					210					215		
gat	aat	gta	ggt	gga	gag	ttt	tca	aac	act	gtt	atc	ggc	cag	atg	aag	785	
Asp	Asn	Val	Gly	Gly	Glu	Phe	Ser	Asn	Thr	Val	Ile	Gly	Gln	Met	Lys		
216					221					226					231		
aaa	ttt	gga	agg	att	gcc	ata	tgt	gga	gcc	atc	tct	aca	tat	aac	aga	833	
Lys	Phe	Gly	Arg	Ile	Ala	Ile	Cys	Gly	Ala	Ile	Ser	Thr	Tyr	Asn	Arg		
232					237					242					247		
acc	ggc	cca	ctt	ccc	cca	ggc	cca	ccc	cca	gag	att	gtt	atc	tat	cag	881	
Thr	Gly	Pro	Leu	Pro	Pro	Gly	Pro	Pro	Pro	Glu	Ile	Val	Ile	Tyr	Gln		
248					253					258					263		
gag	ctt	cgc	atg	gaa	gct	ttt	gtc	gtc	tac	cgc	tgg	caa	gga	gat	gcc	929	
Glu	Leu	Arg	Met	Glu	Ala	Phe	Val	Val	Tyr	Arg	Trp	Gln	Gly	Asp	Ala		
264					269					274					279		
cgc	caa	aaa	gct	ctg	aag	gac	ttg	ctg	aaa	tgg	gtc	tta	gag	ggt	aaa	977	
Arg	Gln	Lys	Ala	Leu	Lys	Asp	Leu	Leu	Lys	Trp	Val	Leu	Glu	Gly	Lys		
280					285					290					295		
atc	cag	tac	aag	gaa	tat	atc	att	gaa	gga	ttt	gaa	aac	atg	cca	gct	1025	
Ile	Gln	Tyr	Lys	Glu	Tyr	Ile	Ile	Glu	Gly	Phe	Glu	Asn	Met	Pro	Ala		

296	301	306	311	
gca ttt atg gga atg ctg aaa gga gat aat ttg ggg aag aca ata gtg				1073
Ala Phe Met Gly Met Leu Lys Gly Asp Asn Leu Gly Lys Thr Ile Val				
312	317	322	327	
aaa gca tga aaaagag gacacatgga atctggaggc catttagatg attagttaat				1129
Lys Ala *				
328				
tg				1131

<210> 204
 <211> 1854
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (142)..(1758)

<400> 204	
tcatccaggc ttcgcccagt cagtctccgg cagcttctcg cggcttcgca agccccttcc	60
cgtgatgccc cgcgcctggc tgtcgcgggt gccgggcaac gcgctgtcca tgtcgcgggc	120
ctcgcctggga ctccctggga g atg agg ccg cga ggt ctc ccg ccg ctc ctg	171
Met Arg Pro Arg Gly Leu Pro Pro Leu Leu	
1 5	
gtg gtg ctc ctg ggc tgc tgg gcc tcc gtg agc gcc cag acc gat gcc	219
Val Val Leu Leu Gly Cys Trp Ala Ser Val Ser Ala Gln Thr Asp Ala	
11 16 21 26	
acc ccg gcg gtg acg aca gag ggc ctc aac tcc acc gag gca gcc ctg	267
Thr Pro Ala Val Thr Thr Glu Gly Leu Asn Ser Thr Glu Ala Ala Leu	
27 32 37 42	
gcc acc ttc gga act ttc ccg tcg acc agg ccc ccc ggg act ccc agg	315
Ala Thr Phe Gly Thr Phe Pro Ser Thr Arg Pro Pro Gly Thr Pro Arg	
43 48 53 58	
gct cca ggg ccc tcc tcc ggc ccc agg cct acc cca gtc acg gac gtt	363
Ala Pro Gly Pro Ser Ser Gly Pro Arg Pro Thr Pro Val Thr Asp Val	
59 64 69 74	
gct gtt ctc tgt gtc tgt gac tta tcc cca gca cag tgt gac atc aac	411
Ala Val Leu Cys Val Cys Asp Leu Ser Pro Ala Gln Cys Asp Ile Asn	
75 80 85 90	
tgc tgc tgt gat ccc gac tgc agc tcc gtg gat ttc agt gtc ttt tct	459
Cys Cys Cys Asp Pro Asp Cys Ser Ser Val Asp Phe Ser Val Phe Ser	
91 96 101 106	

gcc tgc tca gtt cca gtt gtc acg ggc gac agc cag ttt tgt agt caa	507
Ala Cys Ser Val Pro Val Val Thr Gly Asp Ser Gln Phe Cys Ser Gln	
107 112 117 122	
aaa gca gtc atc tat tca ttg aat ttt aca gca aac cca cct caa aga	555
Lys Ala Val Ile Tyr Ser Leu Asn Phe Thr Ala Asn Pro Pro Gln Arg	
123 128 133 138	
gta ttt gaa ctt gtt gac cag att aat cca tct att ttc tgc att cat	603
Val Phe Glu Leu Val Asp Gln Ile Asn Pro Ser Ile Phe Cys Ile His	
139 144 149 154	
att aca aac tat aaa cct gca tta tcc ttt att aat cca gaa gta cct	651
Ile Thr Asn Tyr Lys Pro Ala Leu Ser Phe Ile Asn Pro Glu Val Pro	
155 160 165 170	
gat gaa aac aat ttt gat aca ttg atg aaa aca tct gat ggt ttt aca	699
Asp Glu Asn Asn Phe Asp Thr Leu Met Lys Thr Ser Asp Gly Phe Thr	
171 176 181 186	
ttg aat gct gaa tca tat gtt tcc ttc aca acc aaa ctg gat att cct	747
Leu Asn Ala Glu Ser Tyr Val Ser Phe Thr Thr Lys Leu Asp Ile Pro	
187 192 197 202	
act gct gct aaa tat gag tat ggg gtt cct ctg cag act tca gat tcg	795
Thr Ala Ala Lys Tyr Glu Tyr Gly Val Pro Leu Gln Thr Ser Asp Ser	
203 208 213 218	
ttt ctg aga ttt cct tcg tcc ctg aca tca tct ctg tgc act gat aat	843
Phe Leu Arg Phe Pro Ser Ser Leu Thr Ser Ser Leu Cys Thr Asp Asn	
219 224 229 234	
aac cct gca gcg ttt ctg gtg aac cag gct gtt aag tgc acc aga aaa	891
Asn Pro Ala Ala Phe Leu Val Asn Gln Ala Val Lys Cys Thr Arg Lys	
235 240 245 250	
ata aat tta gaa cag tgt gaa gaa att gaa gcc ctc agc atg gct ttt	939
Ile Asn Leu Glu Gln Cys Glu Glu Ile Glu Ala Leu Ser Met Ala Phe	
251 256 261 266	
tac agc agc ccg gaa att ctg agg gta cct gat tca aga aaa aag gtc	987
Tyr Ser Ser Pro Glu Ile Leu Arg Val Pro Asp Ser Arg Lys Lys Val	
267 272 277 282	
cct atc act gtt cag tcc atc gtc att cag tct cta aat aaa acg ctc	1035
Pro Ile Thr Val Gln Ser Ile Val Ile Gln Ser Leu Asn Lys Thr Leu	
283 288 293 298	
acc cga cgg gag gac act gat gtg ctg cag ccg act ctc gtc aac gct	1083
Thr Arg Arg Glu Asp Thr Asp Val Leu Gln Pro Thr Leu Val Asn Ala	
299 304 309 314	
gga cac ttt agc ctt tgc gtg aat gtt gtt ctt gag gta aag tac agc	1131
Gly His Phe Ser Leu Cys Val Asn Val Val Leu Glu Val Lys Tyr Ser	
315 320 325 330	
ctc aca tac aca gat gca ggt gaa gtc acc aaa gct gat ctc tca ttc	1179

Leu Thr Tyr Thr Asp	Ala Gly Glu Val Thr	Lys Ala Asp Leu Ser Phe	
331	336	341	346
gtt ctg ggg aca gtt agc agc gta gtg gtc	cca ctg cag caa aag ttt	1227	
Val Leu Gly Thr Val Ser Ser Val Val Val	Pro Leu Gln Gln Lys Phe		
347	352 357	362	
gaa att cat ttt ctt cag gaa aat acc cag	cca gtc cct ctc agt gga	1275	
Glu Ile His Phe Leu Gln Glu Asn Thr Gln	Pro Val Pro Leu Ser Gly		
363	368 373	378	
aac cct ggt tat gtc gtg ggg ctc cca tta gct gct gga ttc cag cct	1323		
Asn Pro Gly Tyr Val Val Gly Leu Pro Leu Ala Ala Gly Phe Gln Pro			
379	384 389	394	
cat aag ggt gga gct ctc ccg tgt cag ctc gta gca cag aag gtg aag	1371		
His Lys Gly Gly Ala Leu Pro Cys Gln Leu Val Ala Gln Lys Val Lys			
395	400 405	410	
agc ctg ctg tgg ggc cag ggc ttc cca gat tac gtg gcc cct ttt gga	1419		
Ser Leu Leu Trp Gly Gln Gly Phe Pro Asp Tyr Val Ala Pro Phe Gly			
411	416 421	426	
aat tcc cag gcc cag gac atg ctg gac tgg gtg ccc atc cac ttc atc	1467		
Asn Ser Gln Ala Gln Asp Met Leu Asp Trp Val Pro Ile His Phe Ile			
427	432 437	442	
acc cag tca ttc aac agg aag gat tcc tgc cag ctc cca ggg gct ttg	1515		
Thr Gln Ser Phe Asn Arg Lys Asp Ser Cys Gln Leu Pro Gly Ala Leu			
443	448 453	458	
gtt ata gaa gtg aag tgg act aaa tac gga tcc ctg ctg aat cca cag	1563		
Val Ile Glu Val Lys Trp Thr Lys Tyr Gly Ser Leu Leu Asn Pro Gln			
459	464 469	474	
gcc aaa ata gtc aat gta act gca aat cta att tca tcc tcc ttt cct	1611		
Ala Lys Ile Val Asn Val Thr Ala Asn Leu Ile Ser Ser Ser Phe Pro			
475	480 485	490	
gag gcc aac tca gga aat gaa agg acg att ctt att tcc act gcg gtt	1659		
Glu Ala Asn Ser Gly Asn Glu Arg Thr Ile Leu Ile Ser Thr Ala Val			
491	496 501	506	
act ttt gtg gat gtg tct gca cct gca gag gca ggc ttc aga gct cca	1707		
Thr Phe Val Asp Val Ser Ala Pro Ala Glu Ala Gly Phe Arg Ala Pro			
507	512 517	522	
cca gcc atc aat gcc agg ctg ccc ttt aac ttc ttc ttc ccg ttt gtt	1755		
Pro Ala Ile Asn Ala Arg Leu Pro Phe Asn Phe Phe Phe Pro Phe Val			
523	528 533	538	
tga caat gctcagatgc atcagttcct taatatacac gtgaaatttg aaaactgtac	1812		
* 539			
attcggtgag attaaatttt atatacaact aaaaaaaaaa aa	1854		

<210> 205
 <211> 2785
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (402)..(2282)

<400> 205

caaggtgcgg	cggttagtgt	actcattcga	aggagaatac	ccc ⁵ caattca	ctagacgagc	60
ccctaattgg	gggtgcggtg	ccgggcgcgc	tctttctctc	ccctttccac	cagcaactgcc	120
ctcagttctg	cttctagcca	cgccctttcg	cgttcacgtc	cagcgccctg	gcgggattga	180
tttgaggacg	actggactgc	cattgcgcct	g ⁵ gcagggag	cccaaggcaa	gagccgctag	240
gctgccctgc	ccgaagggtc	caactgtcag	tgagcctgcg	caggaggcca	ataggctgcc	300
aatactcctt	ggactccccg	ccagggccct	gctgtcagtg	cgctgcgcg	cggtccggc	360
gccgaggttc	ttgactgctg	tgccggacgc	caggtgtagc	c	atg cag cga gcc	413
					Met Gln Arg Ala	
					1	
gat tcc gag cag ccc tcc aag cgt ccc cgt tgc	gat gac agc ccg aga	461				
Asp Ser Glu Gln Pro Ser Lys Arg Pro Arg Cys Asp Asp Ser Pro Arg						
5 10 15 20						
acc ccc tca aac acc cct tcc gca gag gca gac tgg tcc ccg ggc ctg	509					
Thr Pro Ser Asn Thr Pro Ser Ala Glu Ala Asp Trp Ser Pro Gly Leu						
21 26 31 36						
gaa ctc cat ccc gac tac aag aca tgg ggt ccg gag cag gtg tgc tcc	557					
Glu Leu His Pro Asp Tyr Lys Thr Trp Gly Pro Glu Gln Val Cys Ser						
37 42 47 52						
ttc ctc agg cgc ggt ggc ttt gaa gag ccg gtg ctg ctg aag aac atc	605					
Phe Leu Arg Arg Gly Gly Phe Glu Glu Pro Val Leu Leu Lys Asn Ile						
53 58 63 68						
cga gaa aat gaa atc aca ggc gca tta ctg cct tgt ctt gat gag tct	653					
Arg Glu Asn Glu Ile Thr Gly Ala Leu Leu Pro Cys Leu Asp Glu Ser						
69 74 79 84						
cgt ttt gaa aat ctt gga gta agt tcc ttg ggg gag agg aag aag ctg	701					
Arg Phe Glu Asn Leu Gly Val Ser Ser Leu Gly Glu Arg Lys Lys Leu						
85 90 95 100						
ctt agt tat atc cag cga ttg gtt caa atc cac gtt gat aca atg aag	749					
Leu Ser Tyr Ile Gln Arg Leu Val Gln Ile His Val Asp Thr Met Lys						
101 106 111 116						

gta att aat gat cct atc cat ggc cac att gag ctc cac cct ctc ctc	797
Val Ile Asn Asp Pro Ile His Gly His Ile Glu Leu His Pro Leu Leu	
117 122 127 132	
gtc cga atc att gat aca cct caa ttt caa cgt ctt cga tac atc aaa	845
Val Arg Ile Ile Asp Thr Pro Gln Phe Gln Arg Leu Arg Tyr Ile Lys	
133 138 143 148	
cag ctg gga ggt ggt tac tat gtt ttt cca gga gct tca cac aat cga	893
Gln Leu Gly Gly Gly Tyr Tyr Val Phe Pro Gly Ala Ser His Asn Arg	
149 154 159 164	
ttt gag cat agt cta ggg gtg ggg tat cta gca gga tgt cta gtt cac	941
Phe Glu His Ser Leu Gly Val Gly Tyr Leu Ala Gly Cys Leu Val His	
165 170 175 180	
gca ctg ggt gaa aaa caa cca gag ctg cag ata agt gaa cga gat gtt	989
Ala Leu Gly Glu Lys Gln Pro Glu Leu Gln Ile Ser Glu Arg Asp Val	
181 186 191 196	
ctc tgt gtt cag att gct gga ctt tgt cat gat ctc ggt cat ggg cca	1037
Leu Cys Val Gln Ile Ala Gly Leu Cys His Asp Leu Gly His Gly Pro	
197 202 207 212	
ttt tct cac atg ttt gat gga cga ttt att cca ctt gct cgc ccg gag	1085
Phe Ser His Met Phe Asp Gly Arg Phe Ile Pro Leu Ala Arg Pro Glu	
213 218 223 228	
gtg aaa tgg acg cat gaa caa ggc tca gtt atg atg ttt gag cac ctt	1133
Val Lys Trp Thr His Glu Gln Gly Ser Val Met Met Phe Glu His Leu	
229 234 239 244	
att aat tct aat gga att aag cct gtc atg gaa caa tat ggt ctc atc	1181
Ile Asn Ser Asn Gly Ile Lys Pro Val Met Glu Gln Tyr Gly Leu Ile	
245 250 255 260	
cct gaa gaa gat att tgc ttt ata aag gaa caa att gta gga cca ctt	1229
Pro Glu Glu Asp Ile Cys Phe Ile Lys Glu Gln Ile Val Gly Pro Leu	
261 266 271 276	
gaa tca cct gtc gaa gat tca ttg tgg cca tat aaa ggg cgt cct gaa	1277
Glu Ser Pro Val Glu Asp Ser Leu Trp Pro Tyr Lys Gly Arg Pro Glu	
277 282 287 292	
aac aaa agc ttc ctt tat gag ata gta tct aat aaa aga aat ggc att	1325
Asn Lys Ser Phe Leu Tyr Glu Ile Val Ser Asn Lys Arg Asn Gly Ile	
293 298 303 308	
gat gtg gac aaa tgg gat tat ttt gcc agg gac tgc cat cat ctt gga	1373
Asp Val Asp Lys Trp Asp Tyr Phe Ala Arg Asp Cys His His Leu Gly	
309 314 319 324	
atc caa aat aat ttt gat tac aag cgc ttt att aag ttt gcc cgt gtc	1421
Ile Gln Asn Asn Phe Asp Tyr Lys Arg Phe Ile Lys Phe Ala Arg Val	
325 330 335 340	
tgt gaa gta gac aat gag ttg cgt att tgt gct aga gat aag gaa gtt	1469

Cys	Glu	Val	Asp	Asn	Glu	Leu	Arg	Ile	Cys	Ala	Arg	Asp	Lys	Glu	Val		
341					346					351					356		
gga	aat	ctg	tat	gac	atg	ttc	cac	act	cg	aac	tct	tta	cac	cgt	aga	1517	
Gly	Asn	Leu	Tyr	Asp	Met	Phe	His	Thr	Arg	Asn	Ser	Leu	His	Arg	Arg		
357					362					367					372		
gct	tat	caa	cac	aaa	gtt	ggc	aac	att	att	gat	aca	atg	att	aca	gat	1565	
Ala	Tyr	Gln	His	Lys	Val	Gly	Asn	Ile	Ile	Asp	Thr	Met	Ile	Thr	Asp		
373					378					383					388		
gct	ttc	ctc	aaa	gca	gat	gac	tac	ata	gag	att	aca	ggt	gct	gga	gga	1613	
Ala	Phe	Leu	Lys	Ala	Asp	Asp	Tyr	Ile	Glu	Ile	Thr	Gly	Ala	Gly	Gly		
389					394					399					404		
aaa	aag	tat	cg	att	tct	aca	gca	att	gac	gac	atg	gaa	gcc	tat	act	1661	
Lys	Lys	Tyr	Arg	Ile	Ser	Thr	Ala	Ile	Asp	Asp	Met	Glu	Ala	Tyr	Thr		
405					410					415					420		
aag	ctg	aca	gat	aac	att	ttt	ctg	gag	att	tta	tac	tct	act	gat	ccc	1709	
Lys	Leu	Thr	Asp	Asn	Ile	Phe	Leu	Glu	Ile	Leu	Tyr	Ser	Thr	Asp	Pro		
421					426					431					436		
aaa	ttg	aaa	gac	gca	cga	gag	att	tta	aaa	caa	att	gaa	tac	cgt	aat	1757	
Lys	Leu	Lys	Asp	Ala	Arg	Glu	Ile	Leu	Lys	Gln	Ile	Glu	Tyr	Arg	Asn		
437					442					447					452		
cta	ttc	aag	tat	gtg	ggt	gag	acg	cag	cca	aca	gga	caa	ata	aag	att	1805	
Leu	Phe	Lys	Tyr	Val	Gly	Glu	Thr	Gln	Pro	Thr	Gly	Gln	Ile	Lys	Ile		
453					458					463					468		
aaa	agg	gag	gac	tat	gaa	tct	ctt	cca	aaa	gag	gtt	gcc	agt	gct	aaa	1853	
Lys	Arg	Glu	Asp	Tyr	Glu	Ser	Leu	Pro	Lys	Glu	Val	Ala	Ser	Ala	Lys		
469					474					479					484		
ccc	aaa	gta	ttg	cta	gac	gtg	aaa	ctg	aag	gct	gaa	gat	ttt	ata	gtg	1901	
Pro	Lys	Val	Leu	Leu	Asp	Val	Lys	Leu	Lys	Ala	Glu	Asp	Phe	Ile	Val		
485					490					495					500		
gat	gtt	atc	aac	atg	gat	tat	gga	atg	caa	gaa	aag	aat	cca	att	gat	1949	
Asp	Val	Ile	Asn	Met	Asp	Tyr	Gly	Met	Gln	Glu	Lys	Asn	Pro	Ile	Asp		
501					506					511					516		
cat	gtt	agc	ttc	tat	tgt	aag	act	gcc	ccc	aac	aga	gca	atc	agg	att	1997	
His	Val	Ser	Phe	Tyr	Cys	Lys	Thr	Ala	Pro	Asn	Arg	Ala	Ile	Arg	Ile		
517					522					527					532		
act	aaa	aac	cag	gtt	tca	caa	ctt	ctg	cca	gag	aaa	ttt	gca	gag	cag	2045	
Thr	Lys	Asn	Gln	Val	Ser	Gln	Leu	Leu	Pro	Glu	Lys	Phe	Ala	Glu	Gln		
533					538					543					548		
ctg	att	cga	gta	tat	tgt	aag	aag	gtg	gac	aga	aag	agt	ttg	tat	gcc	2093	
Leu	Ile	Arg	Val	Tyr	Cys	Lys	Lys	Val	Asp	Arg	Lys	Ser	Leu	Tyr	Ala		
549					554					559					564		
gca	aga	caa	tat	ttt	gtt	cag	tgg	tgt	gca	gac	aga	aat	ttc	acc	aag	2141	
Ala	Arg	Gln	Tyr	Phe	Val	Gln	Trp	Cys	Ala	Asp	Arg	Asn	Phe	Thr	Lys		

565	570	575	580	
ccg cag gat ggc gat gtt ata gcc cca ctc ata aca cct caa aaa aag				2189
Pro Gln Asp Gly Asp Val Ile Ala Pro Leu Ile Thr Pro Gln Lys Lys				
581	586	591	596	
gaa tgg aac gac agt act tca gtc caa aat cca act cgc ctc cga gaa				2237
Glu Trp Asn Asp Ser Thr Ser Val Gln Asn Pro Thr Arg Leu Arg Glu				
597	602	607	612	
gca tcc aaa agc aga gtc cag ctt ttt aaa gat gac cca atg tga atg				2285
Ala Ser Lys Ser Arg Val Gln Leu Phe Lys Asp Asp Pro Met *				
613	618	623		
tctgtagtca gttgtttaca aactccctct cctgcacaat tcatttagag gcttcaatca				2345
tagaattctg caaattaatg acaactcatg ctttaatttt gtattttgaa tgtacacgca				2405
tgctgaagct aagtaacttt taatcaaaga aataagatgg tattaggcaa atcttactat				2465
actatgaaaa gcattacctt gcctatTTTT aatattatta aagcctttct ccttcagtag				2525
tctatTTTTct tagaataaca actcttttat ctattctgaa ctctatTTTT tttctTTTT				2585
aagagacaag gttttgctct gttgcccagc ttggactcga actttcctgg gctcgagcga				2645
ccctcctgcc tcagcccccc aagtagctgg gactaaagtc atgtgccacc acaccagct				2705
tactctgaac ttttatgaca gatgattggt ttttgTTTT aatgtagaaa tgagacaagg				2765
gtacaaaattg gaactagaaa				2785

<210> 206
 <211> 2310
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (750)..(1427)

<220>
 <221> misc_feature
 <222> (1)..(2310)
 <223> n = a,t,c or g

<400> 206	
ctgacatcat aataaagtct acattttaca acgcaaacga acaaaaatgt cctgctcagt	60
gctgccccga gagcagaggt tattccagga ttcttgctcg cctctgtaaa gggatatccgt	120
tctgcagacc tttctgccgg tcacactgac ggcatattgc agagcctgcc agggactcac	180
aggggatgac aggggattta tcaggtgggt ttttactgca ctgtcattac tgggggcgaa	240

tccactttaa tacattcatg cctcctgagc ctgtgggaat tcaagaggaa cagaaccaga	300
aataattgaa ccataactgc cctttggcat cttgcctctt ctgggaggct taatttttta	360
caaatatgtg gctctgcttt tcaaatttta gtttgatgat tttctcttct tcntttttca	420
ggttttcccc ccacgacctg accgtgtcgc tatagtgcg ggaggacag atggcattgg	480
ctattctaca gcgaagcatc tggcgagact tggcatgcat gttatcatag ctggaaataa	540
tgacagcaaa gccaaacaag ttgtaagcaa aataaaagaa gaaaccttga acgacaaaga	600
gacgtgagtc ttgctgtgtt gcccgggctg gctttgcctc tggaactcaa gcgatcctcc	660
cacctcagcc tctcgaggag ctgggactac aggcgtgcac catcatttcc tcctaaaatt	720
tggaattttt atactgtgac ttggcttcc atg act tcc atc cgg cag ttt gtg	773
Met Thr Ser Ile Arg Gln Phe Val	
1 5	
cag aag ttc aag atg aag aag att cct ctc cat gtc ctg atc aac aat	821
Gln Lys Phe Lys Met Lys Lys Ile Pro Leu His Val Leu Ile Asn Asn	
9 14 19 24	
gct ggg gtg atg atg gtc cct cag agg aaa acc aga gat gga ttc gaa	869
Ala Gly Val Met Met Val Pro Gln Arg Lys Thr Arg Asp Gly Phe Glu	
25 30 35 40	
gaa cat ttc ggc ctg aac tac cta ggg cac ttc ctg ctg acc aac ctt	917
Glu His Phe Gly Leu Asn Tyr Leu Gly His Phe Leu Leu Thr Asn Leu	
41 46 51 56	
ctc ttg gat acg ctg aaa gag tct ggg tcc cct ggc cac agt gcg agg	965
Leu Leu Asp Thr Leu Lys Glu Ser Gly Ser Pro Gly His Ser Ala Arg	
57 62 67 72	
gtg gtc acc gtc tcc tct gcc acc cat tac gtc gct gag ctg aac atg	1013
Val Val Thr Val Ser Ser Ala Thr His Tyr Val Ala Glu Leu Asn Met	
73 78 83 88	
gat gac ctt cag agc agt gcc tgc tac tca ccc cac gca gcc tac gcc	1061
Asp Asp Leu Gln Ser Ser Ala Cys Tyr Ser Pro His Ala Ala Tyr Ala	
89 94 99 104	
cag agc aag ctg gcc ctt gtc ctg ttc acc tac cac ctc cag cgg ctg	1109
Gln Ser Lys Leu Ala Leu Val Leu Phe Thr Tyr His Leu Gln Arg Leu	
105 110 115 120	
ctg gcg gct gag gga agc cac gtg acc gcc aac gtg gtg gac ccc ggg	1157
Leu Ala Ala Glu Gly Ser His Val Thr Ala Asn Val Val Asp Pro Gly	
121 126 131 136	
gtg gtc aac acg gac gtc tac aag cac gtg ttc tgg gcc acc cgt ctg	1205
Val Val Asn Thr Asp Val Tyr Lys His Val Phe Trp Ala Thr Arg Leu	
137 142 147 152	

gcg aag aag ctt ctc ggc tgg ttg ctt ttc aag acc ccc gat gaa gga	1253
Ala Lys Lys Leu Leu Gly Trp Leu Leu Phe Lys Thr Pro Asp Glu Gly	
153 158 163 168	
gcg tgg act tcc atc tac gca gca gtc acc cca gag ctg gaa gga gtt	1301
Ala Trp Thr Ser Ile Tyr Ala Ala Val Thr Pro Glu Leu Glu Gly Val	
169 174 179 184	
ggt ggc cat tac cta tac aac aag aaa gag acc aag tcc ctc cac gtc	1349
Gly Gly His Tyr Leu Tyr Asn Lys Lys Glu Thr Lys Ser Leu His Val	
185 190 195 200	
acc tac aac cag aaa ctg cag cag cag ctg tgg tct aag agt tgt gag	1397
Thr Tyr Asn Gln Lys Leu Gln Gln Gln Leu Trp Ser Lys Ser Cys Glu	
201 206 211 216	
atg act ggg gtc ctt gat gtg acc ctg tga t atcctgtctc aggatagctg	1448
Met Thr Gly Val Leu Asp Val Thr Leu *	
217 222	
ctgcccccaag aaacacattg cacctgccaa tagcttgtgg gtctgtgaag actgcggtgt	1508
ttgagtttct cacaccacc tgcccacagg gctctgtcct ctagttttga gacagctgcc	1568
tcaacctctg cagaacttca agaagccaaa taaacatttt ggaggataat caccccaagt	1628
ggtcttcaac cataaacttt gtgattccaa agtgcccagt tgtcacaggt gccataaata	1688
attacatttt ccaacataaa tgtgccattt tccttgccgc gttaatacaa ctgagtacaa	1748
aagttccaag agagatgctc tcttttcagg ggctgcaatg tcctctctga gacctagtgg	1808
tggatgaggt ctctgtttg attttgttcc tgcactcact cattttttcca gagaccagc	1868
tgtgattcac aggtgtcaga catggggagg tgtgagcctt gcttgctaca gcctgtagga	1928
tgagtttgac gtggccagca gcaccatctg gtcaacctca ttccagaatg gcacagtcac	1988
aagtgaagca tgccactgtc aaatccgaga atgtaaaccg ctgaacagct atggatcaaa	2048
tggtagccct caaaagatat gtatcatgccc taaccctcag aacctataaa tattacttta	2108
tttggaaaag aatctttgca gatagaatta agaattttga gatgggtcat tatggatcat	2168
cccagtgaac ctaatgccat tcacgagggt tcttatncag aggacaggta gaggggagat	2228
ttggagtaca gaaggacaag atattncgtg tggatggtgg cagacagaga ngggagttaga	2288
tggccaccac aggccaggca tg	2310

<210> 207

<211> 1341

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> (210)..(1145)

<400> 207

gcacgagggc gcgcttaggc aggcgggtggc gcggtctggag tgccgcgggg agggctgtgc	60
cggttgcttt ctgcagccgc atctcggcca gctctcctcg ccgtccccgg ggcgctgtgc	120
gtctccagtc cgggaccgaa gccgcctgcc gtagcgggcg gccagatccg cgtcccgctt	180
cagcggccgg aggacatgcg ggagagaga atg agc cag agg gac acg ctg gtg	233
Met Ser Gln Arg Asp Thr Leu Val	
1 5	
cat ctg ttt gcc gga gga tgt ggt ggt aca gtg gga gct att ctg aca	281
His Leu Phe Ala Gly Gly Cys Gly Gly Thr Val Gly Ala Ile Leu Thr	
9 14 19 24	
tgt cca ctg gaa gtt gta aaa aca cga ctg cag tca tct tct gtg acg	329
Cys Pro Leu Glu Val Val Lys Thr Arg Leu Gln Ser Ser Ser Val Thr	
25 30 35 40	
ctt tat att tct gaa gtt cag ctg aac acc atg gct gga gcc agt gtc	377
Leu Tyr Ile Ser Glu Val Gln Leu Asn Thr Met Ala Gly Ala Ser Val	
41 46 51 56	
aac cga gta gtg tct ccc gga cct ctt cat tgc cta aag gtg atc ttg	425
Asn Arg Val Val Ser Pro Gly Pro Leu His Cys Leu Lys Val Ile Leu	
57 62 67 72	
gaa aaa gaa ggg cct cgt tcc ttg ttt aga gga cta ggc ccc aat tta	473
Glu Lys Glu Gly Pro Arg Ser Leu Phe Arg Gly Leu Gly Pro Asn Leu	
73 78 83 88	
gtg ggg gta gcc cct tcc aga gca ata tac ttt gct gct tat tca aac	521
Val Gly Val Ala Pro Ser Arg Ala Ile Tyr Phe Ala Ala Tyr Ser Asn	
89 94 99 104	
tgc aag gaa aag ttg aat gat gta ttt gat cct gat tct acc caa gta	569
Cys Lys Glu Lys Leu Asn Asp Val Phe Asp Pro Asp Ser Thr Gln Val	
105 110 115 120	
cat atg att tca gct gca atg gca ggt ttt act gca atc aca gca acc	617
His Met Ile Ser Ala Ala Met Ala Gly Phe Thr Ala Ile Thr Ala Thr	
121 126 131 136	
aac ccc att tgg ctt ata aag act cgg tta cag ctt gat gca agg aac	665
Asn Pro Ile Trp Leu Ile Lys Thr Arg Leu Gln Leu Asp Ala Arg Asn	
137 142 147 152	
cgc ggg gaa agg cga atg ggt gct ttt gaa tgt gtt cgt aaa gtg tat	713
Arg Gly Glu Arg Arg Met Gly Ala Phe Glu Cys Val Arg Lys Val Tyr	
153 158 163 168	
cag aca gat gga cta aaa gga ttt tat agg ggc atg tct gct tca tat	761

Gln Thr Asp Gly Leu Lys Gly Phe Tyr Arg Gly Met Ser Ala Ser Tyr	
169	174 179 184
gct ggt ata tca gag act gtt atc cat ttt gtt att tat gaa agt ata	809
Ala Gly Ile Ser Glu Thr Val Ile His Phe Val Ile Tyr Glu Ser Ile	
185	190 195 200
aaa caa aaa cta ctg gaa tat aag act gct tct aca atg gaa aat gat	857
Lys Gln Lys Leu Leu Glu Tyr Lys Thr Ala Ser Thr Met Glu Asn Asp	
201	206 211 216
gaa gag tct gtg aaa gaa gca tca gat ttt gtg gga atg atg cta gct	905
Glu Glu Ser Val Lys Glu Ala Ser Asp Phe Val Gly Met Met Leu Ala	
217	222 227 232
gct gcc acc tca aaa act tgt gcc aca act ata gca tat cca cat gaa	953
Ala Ala Thr Ser Lys Thr Cys Ala Thr Thr Ile Ala Tyr Pro His Glu	
233	238 243 248
gtt gta aga aca aga cta cgt gaa gag gga aca aaa tac aga tct ttt	1001
Val Val Arg Thr Arg Leu Arg Glu Glu Gly Thr Lys Tyr Arg Ser Phe	
249	254 259 264
ttt cag act cta tct ttg ctt gtt caa gaa gaa ggt tat ggg tct ctt	1049
Phe Gln Thr Leu Ser Leu Leu Val Gln Glu Glu Gly Tyr Gly Ser Leu	
265	270 275 280
tat cgt ggt ctg aca act cat cta gtg aga cag att cca aac aca gcc	1097
Tyr Arg Gly Leu Thr Thr His Leu Val Arg Gln Ile Pro Asn Thr Ala	
281	286 291 296
att atg atg gcc acc tat gaa ttg gtg gtt tac cta ctc aat gga tag	1145
Ile Met Met Ala Thr Tyr Glu Leu Val Val Tyr Leu Leu Asn Gly *	
297	302 307 312
cagcagcagg actgctgtac tgcaaaaaaa gaagacaaaa agattacagt ggaccatggg	1205
atacagaagc cagcatggca gacagaagaa aaatagtttg ggaacatgta actattctaa	1265
gtggaagttt tgtttagga attatagtaa tcacaccaca ttacttggcc tttcggtaat	1325
gtgaaaaaaa aaaaaa	1341

<210> 208

<211> 1262

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (210)..(1067)

<400> 208

gcacgagggc gcgcttaggc aggcggtggc gcggctggag tgccgcgggg agggctgtgc 60

cggttgcttt ctgcagccgc atctcggcca gctctctctg ccgtccccgg ggcgctgtgc	120
gtctccagtc cgggaccgaa gccgcctgcc gtagcgggcg gccagatccg cgtcccgct	180
cagcggccgg aggacatgcg ggagagaga atg agc cag agg gac acg ctg gtg	233
Met Ser Gln Arg Asp Thr Leu Val	
1 5	
cat ctg ttt gcc gga gga tgt ggt ggt aca gtg gga gct att ctg aca	281
His Leu Phe Ala Gly Gly Cys Gly Gly Thr Val Gly Ala Ile Leu Thr	
9 14 19 24	
tgt cca ctg gaa gtt gta aaa aca cga ctg cag tca tct tct gtg acg	329
Cys Pro Leu Glu Val Val Lys Thr Arg Leu Gln Ser Ser Ser Val Thr	
25 30 35 40	
ctt tat att tct gaa gtt cag ctg aac acc atg gct gga gcc agt gtc	377
Leu Tyr Ile Ser Glu Val Gln Leu Asn Thr Met Ala Gly Ala Ser Val	
41 46 51 56	
aac cga gta gtg tct ccc gga cct ctt cat tgc cta aaa gca ata tac	425
Asn Arg Val Val Ser Pro Gly Pro Leu His Cys Leu Lys Ala Ile Tyr	
57 62 67 72	
ttt gct gct tat tca aac tgc aag gaa aag ttg aat gat gta ttt gat	473
Phe Ala Ala Tyr Ser Asn Cys Lys Glu Lys Leu Asn Asp Val Phe Asp	
73 78 83 88	
cct gat tct acc caa gta cat atg att tca gct gca atg gca ggt ttt	521
Pro Asp Ser Thr Gln Val His Met Ile Ser Ala Ala Met Ala Gly Phe	
89 94 99 104	
act gca atc aca gca acc aac ccc att tgg ctt ata aag act cgg tta	569
Thr Ala Ile Thr Ala Thr Asn Pro Ile Trp Leu Ile Lys Thr Arg Leu	
105 110 115 120	
cag ctt gat gca agg aac cgc ggg gaa agg cga atg ggt gct ttt gaa	617
Gln Leu Asp Ala Arg Asn Arg Gly Glu Arg Arg Met Gly Ala Phe Glu	
121 126 131 136	
tgt gtt cgt aaa gtg tat cag aca gat gga cta aaa gga ttt tat agg	665
Cys Val Arg Lys Val Tyr Gln Thr Asp Gly Leu Lys Gly Phe Tyr Arg	
137 142 147 152	
ggc atg tct gct tca tat gct ggt ata tca gag act gtt atc cat ttt	713
Gly Met Ser Ala Ser Tyr Ala Gly Ile Ser Glu Thr Val Ile His Phe	
153 158 163 168	
gtt att tat gaa agt ata aaa caa aaa cta ctg gaa tat aag act gct	761
Val Ile Tyr Glu Ser Ile Lys Gln Lys Leu Leu Glu Tyr Lys Thr Ala	
169 174 179 184	
tct aca atg gaa aat gat gaa gag tct gtg aaa gaa gca tca gat ttt	809
Ser Thr Met Glu Asn Asp Glu Glu Ser Val Lys Glu Ala Ser Asp Phe	
185 190 195 200	

gtg gga atg atg cta gct gct gcc acc tca aaa act tgt gcc aca act 857
Val Gly Met Met Leu Ala Ala Ala Thr Ser Lys Thr Cys Ala Thr Thr
201 206 211 216

ata gca tat cca cat gaa gtt gta aga aca aga cta cgt gaa gag gga 905
Ile Ala Tyr Pro His Glu Val Val Arg Thr Arg Leu Arg Glu Glu Gly
217 222 227 232

aca aaa tac aga tct ttt ttt cag act cta tct ttg ctt gtt caa gaa 953
Thr Lys Tyr Arg Ser Phe Phe Gln Thr Leu Ser Leu Leu Val Gln Glu
233 238 243 248

gaa ggt tat ggg tct ctt tat cgt ggt ctg aca act cat cta gtg aga 1001
Glu Gly Tyr Gly Ser Leu Tyr Arg Gly Leu Thr Thr His Leu Val Arg
249 254 259 264

cag att cca aac aca gcc att atg atg gcc acc tat gaa ttg gtg gtt 1049
Gln Ile Pro Asn Thr Ala Ile Met Met Ala Thr Tyr Glu Leu Val Val
265 270 275 280

tac cta ctc aat gga tag cagcac gaggactgct gtactgcaaa aaaagaagac 1103
Tyr Leu Leu Asn Gly *
281 286

caaaagatta cagtggacca tgggatacag aagccagcat ggcagacaga agaaaaatag 1163

tttggaaca tgtaactatt ctaagtggaa gttttgttgt aggaattata gtaatcacac 1223

cacattactt ggcccttcgg taatgtgaaa aaaaaaaaaa 1262

<210> 209
<211> 2038
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (102) .. (1364)

<400> 209
gcacaggctg agatgtggtt ctgcgcgtgt gcggacggct gtctgttaac tccgcggtca 60
gttcccggaac tgggtggctgg tctgcagggt tgacctgcgc a atg cag agg ctg 113
Met Gln Arg Leu
1

cag gta gtg ctg ggc cac ctg agg ggt ccg gcc gat tcc ggc tgg atg 161
Gln Val Val Leu Gly His Leu Arg Gly Pro Ala Asp Ser Gly Trp Met
5 10 15 20

ccg cag gcc gcg cct tgc ctg agc ggt gcc ccg cag gcc tcg gcc gcg 209
Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln Ala Ser Ala Ala
21 26 31 36

gat	gtg	gtg	gtg	gtg	cac	ggg	cgg	cgc	acg	gcc	atc	tgc	cgg	gcg	ggc	257
Asp	Val	Val	Val	Val	His	Gly	Arg	Arg	Thr	Ala	Ile	Cys	Arg	Ala	Gly	
37					42					47					52	
/																
cgc	ggc	ggc	ttc	aag	gac	acc	acc	ccc	gac	gag	ctt	ctc	tcg	gca	gtc	305
Arg	Gly	Gly	Phe	Lys	Asp	Thr	Thr	Pro	Asp	Glu	Leu	Leu	Ser	Ala	Val	
53					58					63					68	
atg	acc	gcg	gtt	ctc	aag	gac	gtg	aat	ctg	agg	ccg	gaa	cag	ctg	ggg	353
Met	Thr	Ala	Val	Leu	Lys	Asp	Val	Asn	Leu	Arg	Pro	Glu	Gln	Leu	Gly	
69					74					79					84	
gac	atc	tgt	gtc	gga	aat	gtg	ctg	cag	cct	ggg	gcc	ggg	gca	atc	atg	401
Asp	Ile	Cys	Val	Gly	Asn	Val	Leu	Gln	Pro	Gly	Ala	Gly	Ala	Ile	Met	
85					90					95					100	
gcc	cga	atc	gcc	cag	ttt	ctg	agt	gac	atc	ccg	gag	act	gtg	cct	ttg	449
Ala	Arg	Ile	Ala	Gln	Phe	Leu	Ser	Asp	Ile	Pro	Glu	Thr	Val	Pro	Leu	
101					106					111					116	
tcc	act	gtc	aat	aga	cag	tgt	tcg	tcg	ggg	cta	cag	gca	gtg	gcc	agc	497
Ser	Thr	Val	Asn	Arg	Gln	Cys	Ser	Ser	Gly	Leu	Gln	Ala	Val	Ala	Ser	
117					122					127					132	
ata	gca	ggt	ggc	atc	aga	aat	ggg	tct	tat	gac	att	ggc	atg	gcc	tgt	545
Ile	Ala	Gly	Gly	Ile	Arg	Asn	Gly	Ser	Tyr	Asp	Ile	Gly	Met	Ala	Cys	
133					138					143					148	
ggg	gtg	gag	tcc	atg	tcc	ctg	gct	gac	aga	ggg	aac	cct	gga	aat	att	593
Gly	Val	Glu	Ser	Met	Ser	Leu	Ala	Asp	Arg	Gly	Asn	Pro	Gly	Asn	Ile	
149					154					159					164	
act	tcg	cgc	ttg	atg	gag	aag	gag	aag	gcc	aga	gat	tgc	ctg	att	cct	641
Thr	Ser	Arg	Leu	Met	Glu	Lys	Glu	Lys	Ala	Arg	Asp	Cys	Leu	Ile	Pro	
165					170					175					180	
atg	ggg	ata	acc	tct	gag	aat	gtg	gct	gag	cgg	ttt	ggc	att	tca	cgg	689
Met	Gly	Ile	Thr	Ser	Glu	Asn	Val	Ala	Glu	Arg	Phe	Gly	Ile	Ser	Arg	
181					186					191					196	
gag	aag	cag	gat	acc	ttt	gcc	ctg	gct	tcc	cag	cag	aag	gca	gca	aga	737
Glu	Lys	Gln	Asp	Thr	Phe	Ala	Leu	Ala	Ser	Gln	Gln	Lys	Ala	Ala	Arg	
197					202					207					212	
gcc	cag	agc	aag	ggc	tgt	ttc	caa	gct	gag	att	gtg	cct	gtg	acc	acc	785
Ala	Gln	Ser	Lys	Gly	Cys	Phe	Gln	Ala	Glu	Ile	Val	Pro	Val	Thr	Thr	
213					218					223					228	
acg	gtc	cat	gat	gac	aag	ggc	acc	aag	agg	agc	atc	act	gtg	acc	cag	833
Thr	Val	His	Asp	Asp	Lys	Gly	Thr	Lys	Arg	Ser	Ile	Thr	Val	Thr	Gln	
229					234					239					244	
gat	gag	ggt	atc	cgc	ccc	agc	acc	acc	atg	gag	ggc	ctg	gcc	aaa	ctg	881
Asp	Glu	Gly	Ile	Arg	Pro	Ser	Thr	Thr	Met	Glu	Gly	Leu	Ala	Lys	Leu	
245					250					255					260	
aag	cct	gcc	ttc	aag	aaa	gat	ggt	tct	acc	aca	gct	gga	aac	tct	agc	929

Lys	Pro	Ala	Phe	Lys	Lys	Asp	Gly	Ser	Thr	Thr	Ala	Gly	Asn	Ser	Ser	
261					266					271					276	
cag	gtg	agt	gat	ggg	gca	gct	gcc	atc/ctg	ctg	gcc	cgg	agg	tcc	aag		977
Gln	Val	Ser	Asp	Gly	Ala	Ala	Ala	Ile	Leu	Leu	Ala	Arg	Arg	Ser	Lys	
277					282					287					292	
gca	gaa	gag	ttg	ggc	ctt	ccc	atc	ctt	ggg	gtc	ctg	agg	tct	tat	gca	1025
Ala	Glu	Glu	Leu	Gly	Leu	Pro	Ile	Leu	Gly	Val	Leu	Arg	Ser	Tyr	Ala	
293					298					303					308	
gtg	gtt	ggg	gtc	cca	cct	gac	atc	atg	ggc	att	gga	cct	gcc	tat	gcc	1073
Val	Val	Gly	Val	Pro	Pro	Asp	Ile	Met	Gly	Ile	Gly	Pro	Ala	Tyr	Ala	
309					314					319					324	
atc	cca	gta	gct	ttg	caa	aaa	gca	ggg	ctg	aca	gtg	agt	gac	gtg	gac	1121
Ile	Pro	Val	Ala	Leu	Gln	Lys	Ala	Gly	Leu	Thr	Val	Ser	Asp	Val	Asp	
325					330					335					340	
atc	ttc	gag	atc	aat	gag	gcc	ttt	gca	agc	cag	gct	gcc	tac	tgt	gtg	1169
Ile	Phe	Glu	Ile	Asn	Glu	Ala	Phe	Ala	Ser	Gln	Ala	Ala	Tyr	Cys	Val	
341					346					351					356	
gag	aag	cta	cga	ctc	ccc	cct	gag	aag	gtg	aac	ccc	ctg	ggg	ggt	gca	1217
Glu	Lys	Leu	Arg	Leu	Pro	Pro	Glu	Lys	Val	Asn	Pro	Leu	Gly	Gly	Ala	
357					362					367					372	
gtg	gcc	tta	ggg	cac	cca	ctg	ggc	tgc	act	ggg	gca	cga	cag	gtc	atc	1265
Val	Ala	Leu	Gly	His	Pro	Leu	Gly	Cys	Thr	Gly	Ala	Arg	Gln	Val	Ile	
373					378					383					388	
acg	ctg	cca	tcc	tgc	tgg	ccc	gga	gtc	caa	ggc	aga	aga	gtt	ggg	cct	1313
Thr	Leu	Pro	Ser	Cys	Trp	Pro	Gly	Val	Gln	Gly	Arg	Arg	Val	Gly	Pro	
389					394					399					404	
tcc	cat	cct	tgg	ggt	cct	gag	gtc	tta	tgc	agt	ggt	tgg	ggt	ccc	acc	1361
Ser	His	Pro	Trp	Gly	Pro	Glu	Val	Leu	Cys	Ser	Gly	Trp	Gly	Pro	Thr	
405					410					415					420	
tga	catc	atgggcattg	gacctgccta	tgccatccca	gtagctttgc	aaaaagcagg										1418
*																
421																
gctgacagtg	agtgacgtgg	acatcttcga	gatcaatgag	gcctttgcaa	gccaggctgc											1478
ctactgtgtg	gagaagctac	gactcccccc	tgagaaggtg	aaccccttg	gggggtgcagt											1538
ggccttaggg	caccactgg	gctgcactgg	ggcacgacag	gtcatcacgc	tgctcaatga											1598
gctgaagcgc	cgtgggaaga	gggcatacgg	agtggtgtcc	atgtgcatcg	ggactggaat											1658
gggagccgct	gccgtctttg	aataccctgg	gaactgagtg	aggtcccagg	ctggaggcgc											1718
tacgcagaca	gtcctgtctgc	tctagcagca	aggcagtaac	accacaaaag	caaaaccaca											1778
tgggaaaact	cagcactggt	ggtggtggca	gtggacagat	caaggcactt	caactcattt											1838

ggaaaatgtg aacactgatg acatgggtata ggagtgggtg ggggtgttgag ccacccatca 1898
 gaccctcttt agctgtgcaa gataaaagca gcctgggtca cccaggccac aaggccatgg 1958
 ttaattctta aggcaaggca aatccatgga tgagaagtgc aatgggcata gtaaaagtgc 2018
 atgaatttaa aaaaaaaaaa 2038

<210> 210
 <211> 2022
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (133)..(1548)

<400> 210
 tagtgccaat tggttcgttg tcataactat ctattcgatg atgaagatac cccaccaaac 60
 ccaaaaaaag agatctctcg aggatccgaa ttcgcggccg cgtcgacca aaaggcaaaa 120
 acaaagggagc tg atg gca aag aag gta gct gtg att gga gct ggg gtc 168
 Met Ala Lys Lys Val Ala Val Ile Gly Ala Gly Val
 1 5 10
 agt ggc cta att tct ctg aag tgc tgt gtg gat gag gga ctt gag ccc 216
 Ser Gly Leu Ile Ser Leu Lys Cys Cys Val Asp Glu Gly Leu Glu Pro
 13 18 23 28
 act tgc ttt gag aga act gaa gat att gga gga gtg tgg agg ttc aaa 264
 Thr Cys Phe Glu Arg Thr Glu Asp Ile Gly Gly Val Trp Arg Phe Lys
 29 34 39 44
 gag aat gtg gaa gat ggc cga gca agt atc tat caa tct gtc gtt acc 312
 Glu Asn Val Glu Asp Gly Arg Ala Ser Ile Tyr Gln Ser Val Val Thr
 45 50 55 60
 aac acc agc aaa gaa atg tcc tgt ttc agt gac ttt cca atg oct gaa 360
 Asn Thr Ser Lys Glu Met Ser Cys Phe Ser Asp Phe Pro Met Pro Glu
 61 66 71 76
 gat ttt cca aac ttc ctg cat aat tct aaa ctt ctg gaa tat ttc agg 408
 Asp Phe Pro Asn Phe Leu His Asn Ser Lys Leu Leu Glu Tyr Phe Arg
 77 82 87 92
 att ttt gct aaa aaa ttt gat ctg cta aaa tat att cag ttc cag aca 456
 Ile Phe Ala Lys Lys Phe Asp Leu Leu Lys Tyr Ile Gln Phe Gln Thr
 93 98 103 108
 act gtc ctt agt gtg aga aaa tgt cca gat ttc tca tcc tct ggc caa 504
 Thr Val Leu Ser Val Arg Lys Cys Pro Asp Phe Ser Ser Ser Gly Gln
 109 114 119 124

tgg aag gtt gtc act cag agc aac ggc aag gag cag agt gct gtc ttt	552
Trp Lys Val Val Thr Gln Ser Asn Gly Lys Glu Gln Ser Ala Val Phe	
125 130 135 140	
gac gca gtt atg gtt tgc agt ggc cac cac att cta cct cat atc cca	600
Asp Ala Val Met Val Cys Ser Gly His His Ile Leu Pro His Ile Pro	
141 146 151 156	
ctg aag tca ttt cca ggt atg gag agg ttc aaa ggc caa tat ttc cat	648
Leu Lys Ser Phe Pro Gly Met Glu Arg Phe Lys Gly Gln Tyr Phe His	
157 162 167 172	
agc cgc caa tac aag cat cca gat gga ttt gag gga aaa cgc atc ctg	696
Ser Arg Gln Tyr Lys His Pro Asp Gly Phe Glu Gly Lys Arg Ile Leu	
173 178 183 188	
gtg att gga atg gga aac tca ggc tca gat att gct gtt gag ctg agt	744
Val Ile Gly Met Gly Asn Ser Gly Ser Asp Ile Ala Val Glu Leu Ser	
189 194 199 204	
aag aat gct gct cag gtt ttt atc agc acc agg cat ggc acc tgg gtc	792
Lys Asn Ala Ala Gln Val Phe Ile Ser Thr Arg His Gly Thr Trp Val	
205 210 215 220	
atg agc cgt atc tct gaa gat ggc tat cct tgg gac tca gtg ttc cac	840
Met Ser Arg Ile Ser Glu Asp Gly Tyr Pro Trp Asp Ser Val Phe His	
221 226 231 236	
acc cgg ttt cgt tct atg ctc cgc aat gta ctg cca cga aca gct gta	888
Thr Arg Phe Arg Ser Met Leu Arg Asn Val Leu Pro Arg Thr Ala Val	
237 242 247 252	
aaa tgg atg ata gaa caa cag atg aat cgg tgg ttc aac cat gaa aat	936
Lys Trp Met Ile Glu Gln Gln Met Asn Arg Trp Phe Asn His Glu Asn	
253 258 263 268	
tat ggc ctt gag cct caa aac aaa tac att atg aag gaa cct gta cta	984
Tyr Gly Leu Glu Pro Gln Asn Lys Tyr Ile Met Lys Glu Pro Val Leu	
269 274 279 284	
aat gat gat gtc cca agt cgt cta ctc tgt gga gcc atc aag gtg aaa	1032
Asn Asp Asp Val Pro Ser Arg Leu Leu Cys Gly Ala Ile Lys Val Lys	
285 290 295 300	
tct aca gtg aaa gag ctc aca gaa act tct gcc atc ttt gag gat gga	1080
Ser Thr Val Lys Glu Leu Thr Glu Thr Ser Ala Ile Phe Glu Asp Gly	
301 306 311 316	
aca gtg gag gag aac att gat gtc atc att ttt gca aca gga tat agt	1128
Thr Val Glu Glu Asn Ile Asp Val Ile Ile Phe Ala Thr Gly Tyr Ser	
317 322 327 332	
ttc tct ttt ccc ttc ctt gaa gat tca ctc gtt aaa gta gag aat aat	1176
Phe Ser Phe Pro Phe Leu Glu Asp Ser Leu Val Lys Val Glu Asn Asn	
333 338 343 348	
atg gtc tca ctg tat aaa tac ata ttc ccc gct cac ctg gac aag tca	1224

Met Val Ser Leu Tyr Lys Tyr Ile Phe Pro Ala His Leu Asp Lys Ser	
349 354 359 364	
acc ctc gcg tgc att ggt ctc atc cag ccc cta ggt tcc att ttc cca	1272
Thr Leu Ala Cys Ile Gly Leu Ile Gln Pro Leu Gly Ser Ile Phe Pro	
365 370 375 380	
act gct gaa ctt caa gct cgt tgg gtg aca aga gtt ttc aaa ggc ttg	1320
Thr Ala Glu Leu Gln Ala Arg Trp Val Thr Arg Val Phe Lys Gly Leu	
381 386 391 396	
tgt agc ctg ccc tca gag aga act atg atg atg gac att atc aaa agg	1368
Cys Ser Leu Pro Ser Glu Arg Thr Met Met Met Asp Ile Ile Lys Arg	
397 402 407 412	
aat gaa aaa aga att gac ctg ttt gga gaa agc cag agc cag acg ttg	1416
Asn Glu Lys Arg Ile Asp Leu Phe Gly Glu Ser Gln Ser Gln Thr Leu	
413 418 423 428	
cag acc aat tat gtt gac tac ttg gac gag ctc gcc tta gag ata ggt	1464
Gln Thr Asn Tyr Val Asp Tyr Leu Asp Glu Leu Ala Leu Glu Ile Gly	
429 434 439 444	
gcg aag cca gat ttc tgc tct ctc ttg ttc aaa gat cct aaa ctg gct	1512
Ala Lys Pro Asp Phe Cys Ser Leu Leu Phe Lys Asp Pro Lys Leu Ala	
445 450 455 460	
gtg aga ctc tat ttc gga ccc tgc aac tcc tat tag tatc gcctgggttg	1562
Val Arg Leu Tyr Phe Gly Pro Cys Asn Ser Tyr *	
461 466 471	
gcctggggcaa tgggaaggag ccagaaatgc catcttcacc cagaaacaaa gaatactgaa	1622
gccactcaag actcggggccc tgaaggattc atctaatttc tcagtttctt ttctgttgaa	1682
aatcctgggc cttcttgctg ttgttggtggc ctttttttgc caacttcaat ggtcctagtc	1742
agcataatgc tttgggcttt attatcttgt cagtcactac ctccctaaaga aaaaaaaaaa	1802
ggctaaaaaa aaaaacatta cattcatggt ctaattataa attttaaagt taggtactac	1862
aggcaggggg gaaattgtaa agaattagca aaattaggct tatgtacaaa accaaaattt	1922
ggccatgaaa ttttgccttt ccatgcttcc ctcaagttcac caaagttacc aaaatgtaaa	1982
ataaaaataaa actggctcag gtaagtaggg ctgccaaacc	2022

<210> 211

<211> 2843

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

[illegible]

gtgctggctt	gatgtaccta	tctattcgat	gatgaagata	ccccacaaa	cccaaaaaaa	60
gagatctctc	gaggatccga	attcgcggcc	gcgtcgacca	aggtcctcca	gcgttctctag	120
agcggagaag	aaagcgctcc	gaagagctag	agctgacact	cggcgatgag	ctaagacgct	180
gtttcagagc	gtttgggtcc	tctgaggccc	cttgaccagg	agtgctctctg	aagatacagt	240
ccaaagaaag	ttctccaaaa	caaggagagc	agtctgaagc	tgggg	atg gca aca	294
					Met Ala Thr	

gca ttg gtg agt gcc cat tcc ctg gct ccc ctg aat ctg aag aag gag 342
Ala Leu Val Ser Ala His Ser Leu Ala Pro Leu Asn Leu Lys Lys Glu
4 9 14 19

ggg ctt cgg gta gtg agg gag gat cac tac tct act tgg gaa cag gga 390
Gly Leu Arg Val Val Arg Glu Asp His Tyr Ser Thr Trp Glu Gln Gly
20 25 30 35

ttc aag ctg caa gga aac agt aaa ggc ctt gga cag gag cca ttg tgc 438
Phe Lys Leu Gln Gly Asn Ser Lys Gly Leu Gly Gln Glu Pro Leu Cys
36 41 46 51

aaa caa ttc agg cag ttg cgt tat gaa gag acc aca gga cct cga gaa 486
Lys Gln Phe Arg Gln Leu Arg Tyr Glu Glu Thr Thr Gly Pro Arg Glu
52 57 62 67

gca cta agt cgg ctc cgg gag ctc tgt caa cag tgg cta cag ccc gag 534
Ala Leu Ser Arg Leu Arg Glu Leu Cys Gln Gln Trp Leu Gln Pro Glu
68 73 78 83

acc cat acc aag gag cag atc ctg gag ctg ctg gtg ctg gag cag ttt 582
Thr His Thr Lys Glu Gln Ile Leu Glu Leu Leu Val Leu Glu Gln Phe
84 89 94 99

ctg atc atc ctg cct aag gag ctc cag gcc cgg gtg cag gag cat cac 630
Leu Ile Ile Leu Pro Lys Glu Leu Gln Ala Arg Val Gln Glu His His
100 105 110 115

cca gag agc agg gag gac gtg gtt gtt gtt ctg gag gat ttg cag ctg 678
Pro Glu Ser Arg Glu Asp Val Val Val Val Leu Glu Asp Leu Gln Leu
116 121 126 131

gat ctt gga gaa aca gga caa cag gtg gac cca gac cag cca aag aaa 726
Asp Leu Gly Glu Thr Gly Gln Gln Val Asp Pro Asp Gln Pro Lys Lys
132 137 142 147

caa aaa ata ctt gtg gag gag atg gcc cct ctg aaa gga gta cag gaa 774
Gln Lys Ile Leu Val Glu Glu Met Ala Pro Leu Lys Gly Val Gln Glu
148 153 158 163

cag cag gtt cgg cat gag tgt gaa gtt aca aag cct gag aaa gag aag 822
Gln Gln Val Arg His Glu Cys Glu Val Thr Lys Pro Glu Lys Glu Lys

164	169	174	179	
ggt gag gag aca agg att gag aat ggg aag ctt att gta gta aca gac				870
Gly Glu Glu Thr Arg Ile Glu Asn Gly Lys Leu Ile Val Val Thr Asp				
180	185	190	195	
tct tgt gga aga gta gag tca tct ggg aaa ata tct gaa ccc atg gag				918
Ser Cys Gly Arg Val Glu Ser Ser Gly Lys Ile Ser Glu Pro Met Glu				
196	201	206	211	
gct cat aat gag ggc tct aac ttg gaa agg cat cag gcc aag ccc aaa				966
Ala His Asn Glu Gly Ser Asn Leu Glu Arg His Gln Ala Lys Pro Lys				
212	217	222	227	
gag aag att gag tat aaa tgc tca gaa cgt gag cag aga ttc atc cag				1014
Glu Lys Ile Glu Tyr Lys Cys Ser Glu Arg Glu Gln Arg Phe Ile Gln				
228	233	238	243	
cac ttg gac ctg att gaa cat gcg agt aca cac acg gga aag aaa tcc				1062
His Leu Asp Leu Ile Glu His Ala Ser Thr His Thr Gly Lys Lys Ser				
244	249	254	259	
tgc gag tct gat gtg tgt cag agt tcc agt ctt aca gga cat aag aaa				1110
Cys Glu Ser Asp Val Cys Gln Ser Ser Ser Leu Thr Gly His Lys Lys				
260	265	270	275	
gtc ctc tct aga gag aaa ggt cat cag tgt cat gag tgt ggg aaa gcc				1158
Val Leu Ser Arg Glu Lys Gly His Gln Cys His Glu Cys Gly Lys Ala				
276	281	286	291	
ttt cag agg agt tca cac ctc gtc aga cat cag aaa atc cat ctt ggt				1206
Phe Gln Arg Ser Ser His Leu Val Arg His Gln Lys Ile His Leu Gly				
292	297	302	307	
gag aag cct tat cag tgc aat gag tgt ggc aaa gtc ttt agc cag aat				1254
Glu Lys Pro Tyr Gln Cys Asn Glu Cys Gly Lys Val Phe Ser Gln Asn				
308	313	318	323	
gca ggc ctt ttg gaa cat ctc aga att cat act gga gag aaa cct tat				1302
Ala Gly Leu Leu Glu His Leu Arg Ile His Thr Gly Glu Lys Pro Tyr				
324	329	334	339	
cta tgt atc cat tgt gga aaa aat ttt agg cgc agc tct cac ctt aat				1350
Leu Cys Ile His Cys Gly Lys Asn Phe Arg Ser Ser His Leu Asn				
340	345	350	355	
cga cat cag aga att cac agt cag gag gag ccc tgt gag tgc aag gag				1398
Arg His Gln Arg Ile His Ser Gln Glu Glu Pro Cys Glu Cys Lys Glu				
356	361	366	371	
tgt gga aaa acc ttt agt cag gcc tta ctc ctc acc cac cat cag aga				1446
Cys Gly Lys Thr Phe Ser Gln Ala Leu Leu Leu Thr His His Gln Arg				
372	377	382	387	
atc cat agt cac tcc aaa agc cat caa tgt aac gag tgt gga aaa gct				1494
Ile His Ser His Ser Lys Ser His Gln Cys Asn Glu Cys Gly Lys Ala				
388	393	398	403	

ttc agt ttg acc tca gac ctt att cga cac cac aga att cat act gga	1542
Phe Ser Leu Thr Ser Asp Leu Ile Arg His His Arg Ile His Thr Gly	
404 409 414 419	
gaa aaa cct ttc aag tgt aac ata tgc cag aaa gcc ttc cga cta aac	1590
Glu Lys Pro Phe Lys Cys Asn Ile Cys Gln Lys Ala Phe Arg Leu Asn	
420 425 430 435	
tca cac ctt gct cag cat gta aga atc cac aat gaa gaa aaa ccc tat	1638
Ser His Leu Ala Gln His Val Arg Ile His Asn Glu Glu Lys Pro Tyr	
436 441 446 451	
cag tgt agt gaa tgt gga gaa gcc ttc agg caa agg tca ggt ctt ttt	1686
Gln Cys Ser Glu Cys Gly Glu Ala Phe Arg Gln Arg Ser Gly Leu Phe	
452 457 462 467	
caa cat cag aga tat cac cac aaa gac aaa ctg gct tga tgaggtgttc	1735
Gln His Gln Arg Tyr His His Lys Asp Lys Leu Ala *	
468 473 478	
tctccttgta gaacatcaga gaaggcacat tgactagcaa acagcacttt aggaaaagtc	1795
accgtagccc actgtggcat cagaaaattc ttgggggctg agttggaggc tccctgcctc	1855
tattctctct cctttgcttt ccttgaagtc agctttggac cacaataatt tcaactgtaga	1915
tgatatgcta ggatcaaagt taaacagcat tcttcaactgc aggacatctc agagcatgta	1975
acataactgc atgattatat actctaagca atagagagct tcatgactga gtaagagttt	2035
tgaagtcagc agtgaatcaa gtgcccacag atttgcaggc ttaagcagaa caaggggaaga	2095
ttgatatttt tggatatgct atagcagctt tctcctatga aataaaaactg atgatgtttg	2155
gaagtatact actctcaaag gtgtctttta agtacagggtt aatgggtgaac attttcccc	2215
agtggttca cctcattcct cccactggcc ttaccocctc cttccccagt ggaagcattt	2275
tcaaaagcaa agataatttt cgctggtgaa cttcagaact tgccttcagg gttagcttca	2335
tgtaatttta ccatttccca tccccattcc ccaccacatt atgtcaagat tcaagttata	2395
aattaacggtt ttacttagac tttgaaagag atttcatgag taatttgaat gaaccttgct	2455
gaattaatct gaatagcaac tgtctgactt gataactoca gtgccagtat agtggctgct	2515
gcatagacac tattcagtaa atgtctgatg aaagaaattg gactttttcc ctttaatact	2575
gatgatgcaa ttttgaaatg ttgcttgctt tggaatactt cggaagttaa acaataaagt	2635
cagcttggag aggagatcat gatctttata ctgtgaatag cagaatgtca cagatgaaga	2695
atattaaaat taggggcgtc cactccaaaa catatcacca gagtgacaac ttcagccctc	2755
agcctctgca atccatatat atcctgggtct tgggagtcca tagaatactg tttccttcta	2815

ataaaggttt caaacaaaaa aaaaaaat

2843

<210> 212
<211> 3134
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (110)..(2812)

<400> 212

gccccgtcc atatgaggca atggagaccc tgcagtaccg gtccggaatt cccgggtcga 60
cccacgcgtc cgccggttcc ggttgcacatca gcgagggatt cacggcgaa atg aga 115
Met Arg
1

ctg ttc gtg agt gat ggc gtc ccg ggt tgc ttg ccg gtg ctg gcc gcc 163
Leu Phe Val Ser Asp Gly Val Pro Gly Cys Leu Pro Val Leu Ala Ala
3 8 13 18

gcc ggg aga gcc cgg ggc aga gca gag gtg ctc atc agc act gta ggc 211
Ala Gly Arg Ala Arg Gly Arg Ala Glu Val Leu Ile Ser Thr Val Gly
19 24 29 34

ccg gaa gat tgt gtg gtc ccg ttc ctg acc cgg cct aag gtc cct gtc 259
Pro Glu Asp Cys Val Val Pro Phe Leu Thr Arg Pro Lys Val Pro Val
35 40 45 50

ttg cag ctg gat agc ggc aac tac ctc ttc tcc act agt gca atc tgc 307
Leu Gln Leu Asp Ser Gly Asn Tyr Leu Phe Ser Thr Ser Ala Ile Cys
51 56 61 66

cga tat ttt ttt ttg tta tct ggc tgg gag caa gat gac ctc act aac 355
Arg Tyr Phe Phe Leu Leu Ser Gly Trp Glu Gln Asp Asp Leu Thr Asn
67 72 77 82

cag tgg ctg gaa tgg gaa gcg aca gag ctg cag cca gct ttg tct gct 403
Gln Trp Leu Glu Trp Glu Ala Thr Glu Leu Gln Pro Ala Leu Ser Ala
83 88 93 98

gcc ctg tac tat tta gtg gtc caa ggc aag aag ggg gaa gat gtt ctt 451
Ala Leu Tyr Tyr Leu Val Val Gln Gly Lys Lys Gly Glu Asp Val Leu
99 104 109 114

ggt tca gtg cgg aga gcc ctg act cac att gac cac agc ttg agt cgt 499
Gly Ser Val Arg Arg Ala Leu Thr His Ile Asp His Ser Leu Ser Arg
115 120 125 130

cag aac tgt cct ttc ctg gct ggg gag aca gaa tct cta gcc gac att 547
Gln Asn Cys Pro Phe Leu Ala Gly Glu Thr Glu Ser Leu Ala Asp Ile
131 136 141 146

gtt ttg tgg gga gcc cta tac cca tta ctg caa gat ccc gcc tac ctc	595
Val Leu Trp Gly Ala Leu Tyr Pro Leu Leu Gln Asp Pro Ala Tyr Leu	
147 152 157 162	
cct gag gag ctg agt gcc ctg cac agc tgg ttc cag aca ctg agt acc	643
Pro Glu Glu Leu Ser Ala Leu His Ser Trp Phe Gln Thr Leu Ser Thr	
163 168 173 178	
cag gaa cca tgt cag cga gct gca gag act gta ctg aaa cag caa ggt	691
Gln Glu Pro Cys Gln Arg Ala Ala Glu Thr Val Leu Lys Gln Gln Gly	
179 184 189 194	
gtc ctg gct ctc cgg cct tac ctc caa aag cag ccc cag ccc agc ccc	739
Val Leu Ala Leu Arg Pro Tyr Leu Gln Lys Gln Pro Gln Pro Ser Pro	
195 200 205 210	
gct gag gga agg gct gtc acc aat gag cct gag gag gag gag ctg gct	787
Ala Glu Gly Arg Ala Val Thr Asn Glu Pro Glu Glu Glu Glu Leu Ala	
211 216 221 226	
acc cta tct gag gag gag att gct atg gct gtt act gct tgg gag aag	835
Thr Leu Ser Glu Glu Glu Ile Ala Met Ala Val Thr Ala Trp Glu Lys	
227 232 237 242	
ggc cta gaa agt ttg ccc ccg ctg cgg ccc cag cag aat cca gtg ttg	883
Gly Leu Glu Ser Leu Pro Pro Leu Arg Pro Gln Gln Asn Pro Val Leu	
243 248 253 258	
cct gtg gct gga gaa agg aat gtg ctc atc acc agt gcc ctc cct tac	931
Pro Val Ala Gly Glu Arg Asn Val Leu Ile Thr Ser Ala Leu Pro Tyr	
259 264 269 274	
gtc aac aat gtc ccc cac ctt ggg aac atc att ggt tgt gtg ctc agt	979
Val Asn Asn Val Pro His Leu Gly Asn Ile Ile Gly Cys Val Leu Ser	
275 280 285 290	
gcc gat gtc ttt gcc agg tac tct cgc ctc cgc cag tgg aac acc ctc	1027
Ala Asp Val Phe Ala Arg Tyr Ser Arg Leu Arg Gln Trp Asn Thr Leu	
291 296 301 306	
tat ctg tgt ggg aca gat gag tat ggt aca gca aca gag acc aag gct	1075
Tyr Leu Cys Gly Thr Asp Glu Tyr Gly Thr Ala Thr Glu Thr Lys Ala	
307 312 317 322	
ctg gag gag gga cta acc ccc cag gag atc tgc gac aag tac cac atc	1123
Leu Glu Glu Gly Leu Thr Pro Gln Glu Ile Cys Asp Lys Tyr His Ile	
323 328 333 338	
atc cat gct gac atc tac cgc tgg ttt aac att tcg ttt gat att ttt	1171
Ile His Ala Asp Ile Tyr Arg Trp Phe Asn Ile Ser Phe Asp Ile Phe	
339 344 349 354	
ggt cgc acc acc act cca cag cag acc aaa atc acc cag gac att ttc	1219
Gly Arg Thr Thr Thr Pro Gln Gln Thr Lys Ile Thr Gln Asp Ile Phe	
355 360 365 370	
cag cag ttg ctg aaa cga ggt ttt gtg ctg caa gat act gtg gag caa	1267

Gln	Gln	Leu	Leu	Lys	Arg	Gly	Phe	Val	Leu	Gln	Asp	Thr	Val	Glu	Gln		
371					376					381					386		
ctg	cga	tgt	gag	cac	tgt	gct	cgc	ttc	ctg	gct	gac	cgc	ttc	gtg	gag	1315	
Leu	Arg	Cys	Glu	His	Cys	Ala	Arg	Phe	Leu	Ala	Asp	Arg	Phe	Val	Glu		
387					392					397					402		
ggc	gtg	tgt	ccc	ttc	tgt	ggc	tat	gag	gag	gct	cgg	ggg	gac	cag	tgt	1363	
Gly	Val	Cys	Pro	Phe	Cys	Gly	Tyr	Glu	Glu	Ala	Arg	Gly	Asp	Gln	Cys		
403					408					413					418		
gac	aag	tgt	ggc	aag	ctc	atc	aat	gct	gtc	gag	ctt	aag	aag	cct	cag	1411	
Asp	Lys	Cys	Gly	Lys	Leu	Ile	Asn	Ala	Val	Glu	Leu	Lys	Lys	Pro	Gln		
419					424					429					434		
tgt	aaa	gtc	tgc	cga	tca	tgc	cct	gtg	gtg	cag	tcg	agc	cag	cac	ctg	1459	
Cys	Lys	Val	Cys	Arg	Ser	Cys	Pro	Val	Val	Gln	Ser	Ser	Gln	His	Leu		
435					440					445					450		
ttt	ctg	gac	ctg	cct	aag	ctg	gag	aag	cga	ctg	gag	gag	tgg	ttg	ggg	1507	
Phe	Leu	Asp	Leu	Pro	Lys	Leu	Glu	Lys	Arg	Leu	Glu	Glu	Trp	Leu	Gly		
451					456					461					466		
agg	aca	ttg	cct	ggc	agt	gac	tgg	aca	ccc	aat	gcc	cag	ttt	atc	acc	1555	
Arg	Thr	Leu	Pro	Gly	Ser	Asp	Trp	Thr	Pro	Asn	Ala	Gln	Phe	Ile	Thr		
467					472					477					482		
cgt	tct	tgg	ctt	cgg	gat	ggc	ctc	aag	cca	cgc	tgc	ata	acc	cga	gac	1603	
Arg	Ser	Trp	Leu	Arg	Asp	Gly	Leu	Lys	Pro	Arg	Cys	Ile	Thr	Arg	Asp		
483					488					493					498		
ctc	aaa	tgg	gga	acc	cct	gta	ccc	tta	gaa	ggg	ttt	gaa	gac	aag	gta	1651	
Leu	Lys	Trp	Gly	Thr	Pro	Val	Pro	Leu	Glu	Gly	Phe	Glu	Asp	Lys	Val		
499					504					509					514		
ttc	tat	gtc	tgg	ttt	gat	gcc	act	att	ggc	tat	ctg	tcc	atc	aca	gcc	1699	
Phe	Tyr	Val	Trp	Phe	Asp	Ala	Thr	Ile	Gly	Tyr	Leu	Ser	Ile	Thr	Ala		
515					520					525					530		
aac	tac	aca	gac	cag	tgg	gag	aga	tgg	tgg	aag	aac	cca	gag	caa	gtg	1747	
Asn	Tyr	Thr	Asp	Gln	Trp	Glu	Arg	Trp	Trp	Lys	Asn	Pro	Glu	Gln	Val		
531					536					541					546		
gac	ctg	tat	cag	ttc	atg	gcc	aaa	gac	aat	gtt	cct	ttc	cat	agc	tta	1795	
Asp	Leu	Tyr	Gln	Phe	Met	Ala	Lys	Asp	Asn	Val	Pro	Phe	His	Ser	Leu		
547					552					557					562		
gtc	ttt	cct	tgc	tca	gcc	cta	gga	gct	gag	gat	aac	tat	acc	ttg	gtc	1843	
Val	Phe	Pro	Cys	Ser	Ala	Leu	Gly	Ala	Glu	Asp	Asn	Tyr	Thr	Leu	Val		
563					568					573					578		
agc	cac	ctc	att	gct	aca	gag	tac	ctg	aac	tat	gag	gat	ggg	aaa	ttc	1891	
Ser	His	Leu	Ile	Ala	Thr	Glu	Tyr	Leu	Asn	Tyr	Glu	Asp	Gly	Lys	Phe		
579					584					589					594		
tct	aag	agc	cgc	ggg	gtg	gga	gtg	ttt	ggg	gac	atg	gcc	cag	gac	acg	1939	
Ser	Lys	Ser	Arg	Gly	Val	Gly	Val	Phe	Gly	Asp	Met	Ala	Gln	Asp	Thr		

595	600	605	610	
ggg atc cct gct gac atc tgg cgc ttc tat ctg ctg tac att cgg cct				1987
Gly Ile Pro Ala Asp Ile Trp Arg Phe Tyr Leu Leu Tyr Ile Arg Pro				
611	616	621	626	
gag ggc cag gac agt gct ttc tcc tgg acg gac ctg ctg ctg aag aat				2035
Glu Gly Gln Asp Ser Ala Phe Ser Trp Thr Asp Leu Leu Leu Lys Asn				
627	632	637	642	
aat tct gag ctg ctt aac aac ctg ggc aac ttc atc aac aga gct ggg				2083
Asn Ser Glu Leu Leu Asn Asn Leu Gly Asn Phe Ile Asn Arg Ala Gly				
643	648	653	658	
atg ttt gtg tct aag ttc ttt ggg ggc tat gtg cct gag atg gtg ctc				2131
Met Phe Val Ser Lys Phe Phe Gly Gly Tyr Val Pro Glu Met Val Leu				
659	664	669	674	
acc cct gat gat cag cgc ctg ctg gcc cat gtc acc ctg gag ctc cag				2179
Thr Pro Asp Asp Gln Arg Leu Leu Ala His Val Thr Leu Glu Leu Gln				
675	680	685	690	
cac tat cac cag cta ctt gag aag gtt cgg atc cgg gat gcc ttg cgc				2227
His Tyr His Gln Leu Leu Glu Lys Val Arg Ile Arg Asp Ala Leu Arg				
691	696	701	706	
agt atc ctc acc ata tct cga cat ggc aac caa tat att cag gtg aat				2275
Ser Ile Leu Thr Ile Ser Arg His Gly Asn Gln Tyr Ile Gln Val Asn				
707	712	717	722	
gag ccc tgg aag cgg att aaa ggc agt gag gct gac agg caa cgg gca				2323
Glu Pro Trp Lys Arg Ile Lys Gly Ser Glu Ala Asp Arg Gln Arg Ala				
723	728	733	738	
gga aca gtg act ggc ttg gca gtg aat ata gct gcc ttg ctc tct gtc				2371
Gly Thr Val Thr Gly Leu Ala Val Asn Ile Ala Ala Leu Leu Ser Val				
739	744	749	754	
atg ctt cag cct tac atg ccc acg gtt agt gcc aca atc cag gcc cag				2419
Met Leu Gln Pro Tyr Met Pro Thr Val Ser Ala Thr Ile Gln Ala Gln				
755	760	765	770	
ctg cag ctc cca cct cca gcc tgc agt atc ctg ctg aca aac ttc ctg				2467
Leu Gln Leu Pro Pro Pro Ala Cys Ser Ile Leu Leu Thr Asn Phe Leu				
771	776	781	786	
tgt acc tta cca gca gga cac cag att ggc aca gtc agt ccc ttg ttc				2515
Cys Thr Leu Pro Ala Gly His Gln Ile Gly Thr Val Ser Pro Leu Phe				
787	792	797	802	
caa aaa ttg gaa aat gac cag att gaa agt tta agg cag cgc ttt gga				2563
Gln Lys Leu Glu Asn Asp Gln Ile Glu Ser Leu Arg Gln Arg Phe Gly				
803	808	813	818	
ggg ggc cag gca aaa acg tcc ctg aag cca gca gtt gta gag act gtt				2611
Gly Gly Gln Ala Lys Thr Ser Leu Lys Pro Ala Val Val Glu Thr Val				
819	824	829	834	

cgc gaa gat tgt gtg gtc ccg ttc ctg acc cgg cct aag gtc cct gtc	259
Pro Glu Asp Cys Val Val Pro Phe Leu Thr Arg Pro Lys Val Pro Val	
35 40 45 50	
ttg cag ctg gat agc ggc aac tac ctc ttc tcc act agt gca atc tgc	307
Leu Gln Leu Asp Ser Gly Asn Tyr Leu Phe Ser Thr Ser Ala Ile Cys	
51 56 61 66	
cga tat ttt ttt ttg tta tct ggc tgg gag caa gat gac ctc act aac	355
Arg Tyr Phe Phe Leu Leu Ser Gly Trp Glu Gln Asp Asp Leu Thr Asn	
67 72 77 82	
cag tgg ctg gaa tgg gaa gcg aca gag ctg cag cca gct ttg tct gct	403
Gln Trp Leu Glu Trp Glu Ala Thr Glu Leu Gln Pro Ala Leu Ser Ala	
83 88 93 98	
gcc ctg tac tat tta gtg gtc caa ggc aag aag ggg gaa gat gtt ctt	451
Ala Leu Tyr Tyr Leu Val Val Gln Gly Lys Lys Gly Glu Asp Val Leu	
99 104 109 114	
ggc tca gtg cgg aga gcc ctg act cac att gac cac agc ttg agt cgt	499
Gly Ser Val Arg Arg Ala Leu Thr His Ile Asp His Ser Leu Ser Arg	
115 120 125 130	
cag aac tgt cct ttc ctg gct ggg gag gag ctg agt gcc ctg cac agc	547
Gln Asn Cys Pro Phe Leu Ala Gly Glu Glu Leu Ser Ala Leu His Ser	
131 136 141 146	
tgg ttc cag aca ctg agt acc cag gaa cca tgt cag cga gct gca gag	595
Trp Phe Gln Thr Leu Ser Thr Gln Glu Pro Cys Gln Arg Ala Ala Glu	
147 152 157 162	
act gta ctg aaa cag caa ggt gtc ctg gct ctc cgg cct tac ctc caa	643
Thr Val Leu Lys Gln Gln Gly Val Leu Ala Leu Arg Pro Tyr Leu Gln	
163 168 173 178	
aag cag ccc cag ccc agc ccc gct gag gga agg gct gtc acc aat gag	691
Lys Gln Pro Gln Pro Ser Pro Ala Glu Gly Arg Ala Val Thr Asn Glu	
179 184 189 194	
cct gag gag gag gag ctg gct acc cta tct gag gag gag att gct atg	739
Pro Glu Glu Glu Glu Leu Ala Thr Leu Ser Glu Glu Glu Ile Ala Met	
195 200 205 210	
gct gtt act gct tgg gag aag ggc cta gaa agt ttg ccc ccg ctg cgg	787
Ala Val Thr Ala Trp Glu Lys Gly Leu Glu Ser Leu Pro Pro Leu Arg	
211 216 221 226	
ccc cag cag aat cca gtg ttg cct gtg gct gga gaa agg aat gtg ctc	835
Pro Gln Gln Asn Pro Val Leu Pro Val Ala Gly Glu Arg Asn Val Leu	
227 232 237 242	
atc acc agt gcc ctc cct tac gtc aac aat gtc ccc cac ctt ggg aac	883
Ile Thr Ser Ala Leu Pro Tyr Val Asn Asn Val Pro His Leu Gly Asn	
243 248 253 258	

atc att ggt tgt gtg ctc agt gcc gat gtc ttt gcc agg tac tct cgc	931
Ile Ile Gly Cys Val Leu Ser Ala Asp Val Phe Ala Arg Tyr Ser Arg	
259 264 269 274	
ctc cgc cag tgg aac acc ctc tat ctg tgt ggg aca gat gag tat ggt	979
Leu Arg Gln Trp Asn Thr Leu Tyr Leu Cys Gly Thr Asp Glu Tyr Gly	
275 280 285 290	
aca gca aca gag acc aag gct ctg gag gag gga cta acc ccc cag gag	1027
Thr Ala Thr Glu Thr Lys Ala Leu Glu Glu Gly Leu Thr Pro Gln Glu	
291 296 301 306	
atc tgc gac aag tac cac atc atc cat gct gac atc tac cgc tgg ttt	1075
Ile Cys Asp Lys Tyr His Ile Ile His Ala Asp Ile Tyr Arg Trp Phe	
307 312 317 322	
aac att tcg ttt gat att ttt ggt cgc acc acc act cca cag cag acc	1123
Asn Ile Ser Phe Asp Ile Phe Gly Arg Thr Thr Thr Pro Gln Gln Thr	
323 328 333 338	
aaa atc acc cag gac att ttc cag cag ttg ctg aaa cga ggt ttt gtg	1171
Lys Ile Thr Gln Asp Ile Phe Gln Gln Leu Leu Lys Arg Gly Phe Val	
339 344 349 354	
ctg caa gat act gtg gag caa ctg cga tgt gag cac tgt gct cgc ttc	1219
Leu Gln Asp Thr Val Glu Gln Leu Arg Cys Glu His Cys Ala Arg Phe	
355 360 365 370	
ctg gct gac cgc ttc gtg gag ggc gtg tgt ccc ttc tgt ggc tat gag	1267
Leu Ala Asp Arg Phe Val Glu Gly Val Cys Pro Phe Cys Gly Tyr Glu	
371 376 381 386	
gag gct cgg ggt gac cag tgt gac aag tgt ggc aag ctc atc aat gct	1315
Glu Ala Arg Gly Asp Gln Cys Asp Lys Cys Gly Lys Leu Ile Asn Ala	
387 392 397 402	
gtc gag ctt aag aag cct cag tgt aaa gtc tgc cga tca tgc cct gtg	1363
Val Glu Leu Lys Lys Pro Gln Cys Lys Val Cys Arg Ser Cys Pro Val	
403 408 413 418	
gtg cag tcg agc cag cac ctg ttt ctg gac ctg cct aag ctg gag aag	1411
Val Gln Ser Ser Gln His Leu Phe Leu Asp Leu Pro Lys Leu Glu Lys	
419 424 429 434	
cga ctg gag gag tgg ttg ggg agg aca ttg cct ggc agt gac tgg aca	1459
Arg Leu Glu Glu Trp Leu Gly Arg Thr Leu Pro Gly Ser Asp Trp Thr	
435 440 445 450	
ccc aat gcc cag ttt atc acc cgt tct tgg ctt cgg gat ggc ctc aag	1507
Pro Asn Ala Gln Phe Ile Thr Arg Ser Trp Leu Arg Asp Gly Leu Lys	
451 456 461 466	
cca cgc tgc ata acc cga gac ctc aaa tgg gga acc cct gta ccc tta	1555
Pro Arg Cys Ile Thr Arg Asp Leu Lys Trp Gly Thr Pro Val Pro Leu	
467 472 477 482	
gaa ggt ttt gaa gac aag gta ttc tat gtc tgg ttt gat gcc act att	1603

Glu Gly Phe Glu Asp Lys Val Phe Tyr Val Trp Phe Asp Ala Thr Ile	
483 488 493 498	
ggc tat ctg tcc atc aca gcc aac tac aca gac cag tgg gag aga tgg	1651
Gly Tyr Leu Ser Ile Thr Ala Asn Tyr Thr Asp Gln Trp Glu Arg Trp	
499 504 509 514	
tgg aag aac cca gag caa gtg gac ctg tat cag ttc atg gcc aaa gac	1699
Trp Lys Asn Pro Glu Gln Val Asp Leu Tyr Gln Phe Met Ala Lys Asp	
515 520 525 530	
aat gtt cct ttc cat agc tta gtc ttt cct tgc tca gcc cta gga gct	1747
Asn Val Pro Phe His Ser Leu Val Phe Pro Cys Ser Ala Leu Gly Ala	
531 536 541 546	
gag gat aac tat acc ttg gtc agc cac ctc att gct aca gag tac ctg	1795
Glu Asp Asn Tyr Thr Leu Val Ser His Leu Ile Ala Thr Glu Tyr Leu	
547 552 557 562	
aac tat gag gat ggg aaa ttc tct aag agc cgc ggt gtg gga gtg ttt	1843
Asn Tyr Glu Asp Gly Lys Phe Ser Lys Ser Arg Gly Val Gly Val Phe	
563 568 573 578	
ggg gac atg gcc cag gac acg ggg atc cct gct gac atc tgg cgc ttc	1891
Gly Asp Met Ala Gln Asp Thr Gly Ile Pro Ala Asp Ile Trp Arg Phe	
579 584 589 594	
tat ctg ctg tac att cgg cct gag ggc cag gac agt gct ttc tcc tgg	1939
Tyr Leu Leu Tyr Ile Arg Pro Glu Gly Gln Asp Ser Ala Phe Ser Trp	
595 600 605 610	
acg gac ctg ctg ctg aag aat aat tct gag ctg ctt aac aac ctg ggc	1987
Thr Asp Leu Leu Leu Lys Asn Asn Ser Glu Leu Leu Asn Asn Leu Gly	
611 616 621 626	
aac ttc atc aac aga gct ggg atg ttt gtg tct aag ttc ttt ggg ggc	2035
Asn Phe Ile Asn Arg Ala Gly Met Phe Val Ser Lys Phe Phe Gly Gly	
627 632 637 642	
tat gtg cct gag atg gtg ctc acc cct gat gat cag cgc ctg ctg gcc	2083
Tyr Val Pro Glu Met Val Leu Thr Pro Asp Asp Gln Arg Leu Leu Ala	
643 648 653 658	
cat gtc acc ctg gag ctc cag cac tat cac cag cta ctt gag aag gtt	2131
His Val Thr Leu Glu Leu Gln His Tyr His Gln Leu Leu Glu Lys Val	
659 664 669 674	
cgg atc cgg gat gcc ttg cgc agt atc ctc acc ata tct cga cat ggc	2179
Arg Ile Arg Asp Ala Leu Arg Ser Ile Leu Thr Ile Ser Arg His Gly	
675 680 685 690	
aac caa tat att cag gtg aat gag ccc tgg aag cgg att aaa ggc agt	2227
Asn Gln Tyr Ile Gln Val Asn Glu Pro Trp Lys Arg Ile Lys Gly Ser	
691 696 701 706	
gag gct gac agg caa cgg gca gga aca gtg act ggc ttg gca gtg aat	2275
Glu Ala Asp Arg Gln Arg Ala Gly Thr Val Thr Gly Leu Ala Val Asn	

707	712	717	722	
ata gct gcc ttg ctc tct gtc atg ctt cag cct tac atg ccc acg gtt				2323
Ile Ala Ala Leu Leu Ser Val Met Leu Gln Pro Tyr Met Pro Thr Val				
723	728	733	738	
agt gcc aca atc cag gcc cag ctg cag ctc cca cct cca gcc tgc agt				2371
Ser Ala Thr Ile Gln Ala Gln Leu Gln Leu Pro Pro Pro Ala Cys Ser				
739	744	749	754	
atc ctg ctg aca aac ttc ctg tgt acc tta cca gca gga cac cag att				2419
Ile Leu Leu Thr Asn Phe Leu Cys Thr Leu Pro Ala Gly His Gln Ile				
755	760	765	770	
ggc aca gtc agt ccc ttg ttc caa aaa ttg gaa aat gac cag att gaa				2467
Gly Thr Val Ser Pro Leu Phe Gln Lys Leu Glu Asn Asp Gln Ile Glu				
771	776	781	786	
agt tta agg cag cgc ttt gga ggg ggc cag gca aaa acg tcc ctg aag				2515
Ser Leu Arg Gln Arg Phe Gly Gly Gly Gln Ala Lys Thr Ser Leu Lys				
787	792	797	802	
cca gca gtt gta gag act gtt aca aca gcc aag cca cag cag ata caa				2563
Pro Ala Val Val Glu Thr Val Thr Thr Ala Lys Pro Gln Gln Ile Gln				
803	808	813	818	
gcg ctg atg gat gaa gtg aca aaa caa gga aac att gtc cga gaa ctg				2611
Ala Leu Met Asp Glu Val Thr Lys Gln Gly Asn Ile Val Arg Glu Leu				
819	824	829	834	
aaa gca caa aag gca gac aag aac gag gtt gct gcg gag gtg gcg aaa				2659
Lys Ala Gln Lys Ala Asp Lys Asn Glu Val Ala Ala Glu Val Ala Lys				
835	840	845	850	
ctc ttg gat cta aag aaa cag ttg gct gta gct gag ggg aaa ccc cct				2707
Leu Leu Asp Leu Lys Lys Gln Leu Ala Val Ala Glu Gly Lys Pro Pro				
851	856	861	866	
gaa gcc cct aaa ggc aag aag aaa aag taa a agaccttggc tcatagaaag				2758
Glu Ala Pro Lys Gly Lys Lys Lys Lys *				
867	872			
tcactttaat agatagggac agtaataaat aaatgtacaa tctctatata caagctgaga				2818
cctttccttt tgtctactcc aagccttccc cctgcgtatg tgggattgag ggtcacatca				2878
ttggcactag tgagagggtg gtcagtagcc acttctggga aaggtgggta gtgtggccca				2938
agtgggggac tgatgctccc aagtcgacgc ggccggatat ttaatagtag tagtcgaccc				2998
gggaattccg gaccggtacc tgcaaggcgt accagcttcc cccaatagtg aattcgtatt				3058
a				3059

<210> 214
 <211> 3068
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (110)..(2746)

<400> 214

```

gccccgtcc atatgaggca atggagaccc tgcagtaccg gtccggaatt cccgggtcga      60

cccacgcgtc cgccggttcc ggttgcattca gcgagggatt cacggcgaa      atg aga      115
                                   Met Arg
                                   1

ctg ttc gtg agt gat ggc gtc ccg ggt tgc ttg ccg gtg ctg gcc gcc      163
Leu Phe Val Ser Asp Gly Val Pro Gly Cys Leu Pro Val Leu Ala Ala
  3                               8                               13                               18

gcc ggg aga gcc cgg ggc aga gca gag gtg ctc atc agc act gta ggc      211
Ala Gly Arg Ala Arg Gly Arg Ala Glu Val Leu Ile Ser Thr Val Gly
  19                               24                               29                               34

ccg gaa gat tgt gtg gtc ccg ttc ctg acc cgg cct aag gtc cct gtc      259
Pro Glu Asp Cys Val Val Pro Phe Leu Thr Arg Pro Lys Val Pro Val
  35                               40                               45                               50

ttg cag ctg gat agc ggc aac tac ctc ttc tcc act agt gca atc tgc      307
Leu Gln Leu Asp Ser Gly Asn Tyr Leu Phe Ser Thr Ser Ala Ile Cys
  51                               56                               61                               66

cga tat ttt ttt ttg tta tct ggc tgg gag caa gat gac ctc act aac      355
Arg Tyr Phe Phe Leu Leu Ser Gly Trp Glu Gln Asp Asp Leu Thr Asn
  67                               72                               77                               82

cag tgg ctg gaa tgg gaa gcg aca gag ctg cag cca gct ttg tct gct      403
Gln Trp Leu Glu Trp Glu Ala Thr Glu Leu Gln Pro Ala Leu Ser Ala
  83                               88                               93                               98

gcc ctg tac tat tta gtg gtc caa ggc aag aag ggg gaa gat gtt ctt      451
Ala Leu Tyr Tyr Leu Val Val Gln Gly Lys Lys Gly Glu Asp Val Leu
  99                               104                               109                               114

ggt tca gtg cgg aga gcc ctg act cac att gac cac agc ttg agt cgt      499
Gly Ser Val Arg Arg Ala Leu Thr His Ile Asp His Ser Leu Ser Arg
  115                               120                               125                               130

cag aac tgt cct ttc ctg gct ggg gag aca gaa tct cta gcc gac att      547
Gln Asn Cys Pro Phe Leu Ala Gly Glu Thr Glu Ser Leu Ala Asp Ile
  131                               136                               141                               146

gtt ttg tgg gga gcc cta tac cca tta ctg caa gat ccc gcc tac ctc      595
Val Leu Trp Gly Ala Leu Tyr Pro Leu Leu Gln Asp Pro Ala Tyr Leu
  147                               152                               157                               162

cct gag gag ctg agt gcc ctg cac agc tgg ttc cag aca ctg agt acc      643

```

Pro Glu Glu Leu Ser Ala Leu His Ser Trp Phe Gln Thr Leu Ser Thr	
163 168 173 178	
cag gaa cca tgt cag cga gct gca gag act gta ctg aaa cag caa ggt	691
Gln Glu Pro Cys Gln Arg Ala Ala Glu Thr Val Leu Lys Gln Gln Gly	
179 184 189 194	
gtc ctg gct ctc cgg cct tac ctc caa aag cag ccc cag ccc agc ccc	739
Val Leu Ala Leu Arg Pro Tyr Leu Gln Lys Gln Pro Gln Pro Ser Pro	
195 200 205 210	
gct gag gga agg gct gtc acc aat gag cct gag gag gag gag ctg gct	787
Ala Glu Gly Arg Ala Val Thr Asn Glu Pro Glu Glu Glu Glu Leu Ala	
211 216 221 226	
acc cta tct gag gag gag att gct atg gct gtt act gct tgg gag aag	835
Thr Leu Ser Glu Glu Glu Ile Ala Met Ala Val Thr Ala Trp Glu Lys	
227 232 237 242	
ggc cta gaa agt ttg ccc ccg ctg cgg ccc cag cag aat cca gtg ttg	883
Gly Leu Glu Ser Leu Pro Pro Leu Arg Pro Gln Gln Asn Pro Val Leu	
243 248 253 258	
cct gtg gct gga gaa agg aat gtg ctc atc acc agt gcc ctc cct tac	931
Pro Val Ala Gly Glu Arg Asn Val Leu Ile Thr Ser Ala Leu Pro Tyr	
259 264 269 274	
gtc aac aat gtc ccc cac ctt ggg aac atc att ggt tgt gtg ctc agt	979
Val Asn Asn Val Pro His Leu Gly Asn Ile Ile Gly Cys Val Leu Ser	
275 280 285 290	
gcc gat gtc ttt gcc agg tac tct cgc ctc cgc cag tgg aac acc ctc	1027
Ala Asp Val Phe Ala Arg Tyr Ser Arg Leu Arg Gln Trp Asn Thr Leu	
291 296 301 306	
tat ctg tgt ggg aca gat gag tat ggt aca gca aca gag acc aag gct	1075
Tyr Leu Cys Gly Thr Asp Glu Tyr Gly Thr Ala Thr Glu Thr Lys Ala	
307 312 317 322	
ctg gag gag gga cta acc ccc cag gag atc tgc gac aag tac cac atc	1123
Leu Glu Glu Gly Leu Thr Pro Gln Glu Ile Cys Asp Lys Tyr His Ile	
323 328 333 338	
atc cat gct gac atc tac cgc tgg ttt aac att tcg ttt gat att ttt	1171
Ile His Ala Asp Ile Tyr Arg Trp Phe Asn Ile Ser Phe Asp Ile Phe	
339 344 349 354	
ggt cgc acc acc act cca cag cag acc aaa atc acc cag gac att ttc	1219
Gly Arg Thr Thr Thr Pro Gln Gln Thr Lys Ile Thr Gln Asp Ile Phe	
355 360 365 370	
cag cag ttg ctg aaa cga ggt ttt gtg ctg caa gat act gtg gag caa	1267
Gln Gln Leu Leu Lys Arg Gly Phe Val Leu Gln Asp Thr Val Glu Gln	
371 376 381 386	
ctg cga tgt gag cac tgt gct cgc ttc ctg gct gac cgc ttc gtg gag	1315
Leu Arg Cys Glu His Cys Ala Arg Phe Leu Ala Asp Arg Phe Val Glu	

387	392	397	402	
ggc gtg tgt ccc ttc	tgt ggc tat gag gag gct cgg ggt gac cag tgt			1363
Gly Val Cys Pro Phe	Cys Gly Tyr Glu Glu Ala Arg Gly Asp Gln Cys			
403	408	413	418	
gac aag tgt ggc aag	ctc atc aat gct gtc gag ctt aag aag cct cag			1411
Asp Lys Cys Gly Lys	Leu Ile Asn Ala Val Glu Leu Lys Lys Pro Gln			
419	424	429	434	
tgt aaa gtc tgc cga	tca tgc cct gtg gtg cag tgc agc cag cac ctg			1459
Cys Lys Val Cys Arg	Ser Cys Pro Val Val Gln Ser Ser Gln His Leu			
435	440	445	450	
ttt ctg gac ctg cct	aag ctg gag aag cga ctg gag gag tgg ttg ggg			1507
Phe Leu Asp Leu Pro	Lys Leu Glu Lys Arg Leu Glu Glu Trp Leu Gly			
451	456	461	466	
agg aca ttg cct ggc	agt gac tgg aca ccc aat gcc cag ttt atc acc			1555
Arg Thr Leu Pro Gly	Ser Asp Trp Thr Pro Asn Ala Gln Phe Ile Thr			
467	472	477	482	
cgt tct tgg ctt cgg	gat ggc ctc aag cca cgc tgc ata acc cga gac			1603
Arg Ser Trp Leu Arg	Asp Gly Leu Lys Pro Arg Cys Ile Thr Arg Asp			
483	488	493	498	
ctc aaa tgg gga acc	cct gta ccc tta gaa ggt ttt gaa gac aag gta			1651
Leu Lys Trp Gly Thr	Pro Val Pro Leu Glu Gly Phe Glu Asp Lys Val			
499	504	509	514	
ttc tat gtc tgg ttt	gat gcc act att ggc tat ctg tcc atc aca gcc			1699
Phe Tyr Val Trp Phe	Asp Ala Thr Ile Gly Tyr Leu Ser Ile Thr Ala			
515	520	525	530	
aac tac aca gac cag	tgg gag aga tgg tgg aag aac cca gag caa gcc			1747
Asn Tyr Thr Asp Gln	Trp Glu Arg Trp Trp Lys Asn Pro Glu Gln Ala			
531	536	541	546	
cta gga gct gag gat	aac tat acc ttg gtc agc cac ctc att gct aca			1795
Leu Gly Ala Glu Asp	Asn Tyr Thr Leu Val Ser His Leu Ile Ala Thr			
547	552	557	562	
gag tac ctg aac tat	gag gat ggg aaa ttc tct aag agc cgc ggt gtg			1843
Glu Tyr Leu Asn Tyr	Glu Asp Gly Lys Phe Ser Lys Ser Arg Gly Val			
563	568	573	578	
gga gtg ttt ggg gac	atg gcc cag gac acg ggg atc cct gct gac atc			1891
Gly Val Phe Gly Asp	Met Ala Gln Asp Thr Gly Ile Pro Ala Asp Ile			
579	584	589	594	
tgg cgc ttc tat ctg	ctg tac att cgg cct gag ggc cag gac agt gct			1939
Trp Arg Phe Tyr Leu	Leu Tyr Ile Arg Pro Glu Gly Gln Asp Ser Ala			
595	600	605	610	
ttc tcc tgg acg gac	ctg ctg ctg aag aat aat tct gag ctg ctt aac			1987
Phe Ser Trp Thr Asp	Leu Leu Leu Lys Asn Asn Ser Glu Leu Leu Asn			
611	616	621	626	

aac ctg ggc aac ttc atc aac aga gct ggg atg ttt gtg tct aag ttc	2035
Asn Leu Gly Asn Phe Ile Asn Arg Ala Gly Met Phe Val Ser Lys Phe	
627 632 637 642	
ttt ggg ggc tat gtg cct gag atg gtg ctc acc cct gat gat cag cgc	2083
Phe Gly Gly Tyr Val Pro Glu Met Val Leu Thr Pro Asp Asp Gln Arg	
643 648 653 658	
ctg ctg gcc cat gtc acc ctg gag ctc cag cac tat cac cag cta ctt	2131
Leu Leu Ala His Val Thr Leu Glu Leu Gln His Tyr His Gln Leu Leu	
659 664 669 674	
gag aag gtt cgg atc cgg gat gcc ttg cgc agt atc ctc acc ata tct	2179
Glu Lys Val Arg Ile Arg Asp Ala Leu Arg Ser Ile Leu Thr Ile Ser	
675 680 685 690	
cga cat ggc aac caa tat att cag gtg aat gag ccc tgg aag cgg att	2227
Arg His Gly Asn Gln Tyr Ile Gln Val Asn Glu Pro Trp Lys Arg Ile	
691 696 701 706	
aaa ggc agt gag gct gac agg caa cgg gca gga aca gtg act ggc ttg	2275
Lys Gly Ser Glu Ala Asp Arg Gln Arg Ala Gly Thr Val Thr Gly Leu	
707 712 717 722	
gca gtg aat ata gct gcc ttg ctc tct gtc atg ctt cag cct tac atg	2323
Ala Val Asn Ile Ala Ala Leu Leu Ser Val Met Leu Gln Pro Tyr Met	
723 728 733 738	
ccc acg gtt agt gcc aca atc cag gcc cag ctg cag ctc cca cct cca	2371
Pro Thr Val Ser Ala Thr Ile Gln Ala Gln Leu Gln Leu Pro Pro Pro	
739 744 749 754	
gcc tgc agt atc ctg ctg aca aac ttc ctg tgt acc tta cca gca gga	2419
Ala Cys Ser Ile Leu Leu Thr Asn Phe Leu Cys Thr Leu Pro Ala Gly	
755 760 765 770	
cac cag att ggc aca gtc agt ccc ttg ttc caa aaa ttg gaa aat gac	2467
His Gln Ile Gly Thr Val Ser Pro Leu Phe Gln Lys Leu Glu Asn Asp	
771 776 781 786	
cag att gaa agt tta agg cag cgc ttt gga ggg ggc cag gca aaa acg	2515
Gln Ile Glu Ser Leu Arg Gln Arg Phe Gly Gly Gly Gln Ala Lys Thr	
787 792 797 802	
tcc ctg aag cca gca gtt gta gag act gtt aca aca gcc aag cca cag	2563
Ser Leu Lys Pro Ala Val Val Glu Thr Val Thr Thr Ala Lys Pro Gln	
803 808 813 818	
cag ata caa gcg ctg atg gat gaa gtg aca aaa caa gga aac att gtc	2611
Gln Ile Gln Ala Leu Met Asp Glu Val Thr Lys Gln Gly Asn Ile Val	
819 824 829 834	
cga gaa ctg aaa gca caa aag gca gac aag aac gag gtt gct gcg gag	2659
Arg Glu Leu Lys Ala Gln Lys Ala Asp Lys Asn Glu Val Ala Ala Glu	
835 840 845 850	

67	72	77	82	
cag tgg ctg gaa tgg gaa gcg aca gag ctg cag cca gct ttg tct gct				403
Gln Trp Leu Glu Trp Glu Ala Thr Glu Leu Gln Pro Ala Leu Ser Ala				
83	88	93	98	
gcc ctg tac tat tta gtg gtc caa ggc aag aag ggg gaa gat gtt ctt				451
Ala Leu Tyr Tyr Leu Val Val Gln Gly Lys Lys Gly Glu Asp Val Leu				
99	104	109	114	
ggg tca gtg cgg aga gcc ctg act cac att gac cac agc ttg agt cgt				499
Gly Ser Val Arg Arg Ala Leu Thr His Ile Asp His Ser Leu Ser Arg				
115	120	125	130	
cag aac tgt cct ttc ctg gct ggg gag aca gaa tct cta gcc gac att				547
Gln Asn Cys Pro Phe Leu Ala Gly Glu Thr Glu Ser Leu Ala Asp Ile				
131	136	141	146	
gtt ttg tgg gga gcc cta tac cca tta ctg caa gat ccc gcc tac ctc				595
Val Leu Trp Gly Ala Leu Tyr Pro Leu Leu Gln Asp Pro Ala Tyr Leu				
147	152	157	162	
cct gag gag ctg agt gcc ctg cac agc tgg ttc cag aca ctg agt acc				643
Pro Glu Glu Leu Ser Ala Leu His Ser Trp Phe Gln Thr Leu Ser Thr				
163	168	173	178	
cag gaa cca tgt cag cga gct gca gag act gta ctg aaa cag caa ggt				691
Gln Glu Pro Cys Gln Arg Ala Ala Glu Thr Val Leu Lys Gln Gln Gly				
179	184	189	194	
gtc ctg gct ctc cgg cct tac ctc caa aag cag ccc cag ccc agc ccc				739
Val Leu Ala Leu Arg Pro Tyr Leu Gln Lys Gln Pro Gln Pro Ser Pro				
195	200	205	210	
gct gag gga agg gct gtc acc aat gag cct gag gag gag gag ctg gct				787
Ala Glu Gly Arg Ala Val Thr Asn Glu Pro Glu Glu Glu Glu Leu Ala				
211	216	221	226	
acc cta tct gag gag gag att gct atg gct gtt act gct tgg gag aag				835
Thr Leu Ser Glu Glu Glu Ile Ala Met Ala Val Thr Ala Trp Glu Lys				
227	232	237	242	
ggc cta gaa agt ttg ccc ccg ctg cgg ccc cag cag aat cca gtg ttg				883
Gly Leu Glu Ser Leu Pro Pro Leu Arg Pro Gln Gln Asn Pro Val Leu				
243	248	253	258	
cct gtg gct gga gaa agg aat gtg ctc atc acc agt gcc ctc cct tac				931
Pro Val Ala Gly Glu Arg Asn Val Leu Ile Thr Ser Ala Leu Pro Tyr				
259	264	269	274	
gtc aac aat gtc ccc cac ctt ggg aac atc att ggt tgt gtg ctc agt				979
Val Asn Asn Val Pro His Leu Gly Asn Ile Ile Gly Cys Val Leu Ser				
275	280	285	290	
gcc gat gtc ttt gcc agg tac tct cgc ctc cgc cag tgg aac acc ctc				1027
Ala Asp Val Phe Ala Arg Tyr Ser Arg Leu Arg Gln Trp Asn Thr Leu				
291	296	301	306	

tat ctg tgt ggg aca gat gag tat ggt aca gca aca gag acc aag gct	1075
Tyr Leu Cys Gly Thr Asp Glu Tyr Gly Thr Ala Thr Glu Thr Lys Ala	
307 312 317 322	
ctg gag gag gga cta acc ccc cag gag atc tgc gac aag tac cac atc	1123
Leu Glu Glu Gly Leu Thr Pro Gln Glu Ile Cys Asp Lys Tyr His Ile	
323 328 333 338	
atc cat gct gac atc tac cgc tgg ttt aac att tcg ttt gat att ttt	1171
Ile His Ala Asp Ile Tyr Arg Trp Phe Asn Ile Ser Phe Asp Ile Phe	
339 344 349 354	
ggt cgc acc acc act cca cag cag acc aaa atc acc cag gac att ttc	1219
Gly Arg Thr Thr Thr Pro Gln Gln Thr Lys Ile Thr Gln Asp Ile Phe	
355 360 365 370	
cag cag ttg ctg aaa cga ggt ttt gtg ctg caa gat act gtg gag caa	1267
Gln Gln Leu Leu Lys Arg Gly Phe Val Leu Gln Asp Thr Val Glu Gln	
371 376 381 386	
ctg cga tgt gag cac tgt gct cgc ttc ctg gct gac cgc ttc gtg gag	1315
Leu Arg Cys Glu His Cys Ala Arg Phe Leu Ala Asp Arg Phe Val Glu	
387 392 397 402	
ggc gtg tgt ccc ttc tgt ggc tat gag gag gct cgg ggt gac cag tgt	1363
Gly Val Cys Pro Phe Cys Gly Tyr Glu Glu Ala Arg Gly Asp Gln Cys	
403 408 413 418	
gac aag tgt ggc aag ctc atc aat gct gtc gag ctt aag aag cct cag	1411
Asp Lys Cys Gly Lys Leu Ile Asn Ala Val Glu Leu Lys Lys Pro Gln	
419 424 429 434	
tgt aaa gtc tgc cga tca tgc cct gtg gtg cag tcg agc cag cac ctg	1459
Cys Lys Val Cys Arg Ser Cys Pro Val Val Gln Ser Ser Gln His Leu	
435 440 445 450	
ttt ctg gac ctg cct aag ctg gag aag cga ctg gag gag tgg ttg ggg	1507
Phe Leu Asp Leu Pro Lys Leu Glu Lys Arg Leu Glu Glu Trp Leu Gly	
451 456 461 466	
agg aca ttg cct ggc agt gac tgg aca ccc aat gcc cag ttt atc acc	1555
Arg Thr Leu Pro Gly Ser Asp Trp Thr Pro Asn Ala Gln Phe Ile Thr	
467 472 477 482	
cgt tct tgg ctt cgg gat ggc ctc aag cca cgc tgc ata acc cga gac	1603
Arg Ser Trp Leu Arg Asp Gly Leu Lys Pro Arg Cys Ile Thr Arg Asp	
483 488 493 498	
ctc aaa tgg gga acc cct gta ccc tta gaa ggt ttt gaa gac aag gta	1651
Leu Lys Trp Gly Thr Pro Val Pro Leu Glu Gly Phe Glu Asp Lys Val	
499 504 509 514	
ttc tat gtc tgg ttt gat gcc act att ggc tat ctg tcc atc aca gcc	1699
Phe Tyr Val Trp Phe Asp Ala Thr Ile Gly Tyr Leu Ser Ile Thr Ala	
515 520 525 530	

aac tac aca gac cag tgg gag aga tgg tgg aag aac cca gag caa gtg	1747
Asn Tyr Thr Asp Gln Trp Glu Arg Trp Trp Lys Asn Pro Glu Gln Val	
531 536 541 546	
gac ctg tat cag ttc atg gcc aaa gac aat gtt cct ttc cat agc tta	1795
Asp Leu Tyr Gln Phe Met Ala Lys Asp Asn Val Pro Phe His Ser Leu	
547 552 557 562	
gtc ttt cct tgc tca gcc cta gga gct gag gat aac tat acc ttg gtc	1843
Val Phe Pro Cys Ser Ala Leu Gly Ala Glu Asp Asn Tyr Thr Leu Val	
563 568 573 578	
agc cac ctc att gct aca gag tac ctg aac tat gag gat ggg aaa ttc	1891
Ser His Leu Ile Ala Thr Glu Tyr Leu Asn Tyr Glu Asp Gly Lys Phe	
579 584 589 594	
tct aag agc cgc ggt gtg gga gtg ttt ggg gac atg gcc cag gac acg	1939
Ser Lys Ser Arg Gly Val Gly Val Phe Gly Asp Met Ala Gln Asp Thr	
595 600 605 610	
ggg atc cct gct gac atc tgg cgc ttc tat ctg ctg tac att cgg cct	1987
Gly Ile Pro Ala Asp Ile Trp Arg Phe Tyr Leu Leu Tyr Ile Arg Pro	
611 616 621 626	
gag ggc cag gac agt gct ttc tcc tgg acg gac ctg ctg ctg aag aat	2035
Glu Gly Gln Asp Ser Ala Phe Ser Trp Thr Asp Leu Leu Leu Lys Asn	
627 632 637 642	
aat tct gag ctg ctt aac aac ctg ggc aac ttc atc aac aga gct ggg	2083
Asn Ser Glu Leu Leu Asn Asn Leu Gly Asn Phe Ile Asn Arg Ala Gly	
643 648 653 658	
atg ttt gtg tct aag ttc ttt ggg ggc tat gtg cct gag atg gtg ctc	2131
Met Phe Val Ser Lys Phe Phe Gly Gly Tyr Val Pro Glu Met Val Leu	
659 664 669 674	
acc cct gat gat cag cgc ctg ctg gcc cat gtc acc ctg gag ctc cag	2179
Thr Pro Asp Asp Gln Arg Leu Leu Ala His Val Thr Leu Glu Leu Gln	
675 680 685 690	
cac tat cac cag cta ctt gag aag gtt cgg atc cgg gat gcc ttg cgc	2227
His Tyr His Gln Leu Leu Glu Lys Val Arg Ile Arg Asp Ala Leu Arg	
691 696 701 706	
agt atc ctc acc ata tct cga cat ggc aac caa tat att cag gtg aat	2275
Ser Ile Leu Thr Ile Ser Arg His Gly Asn Gln Tyr Ile Gln Val Asn	
707 712 717 722	
gag ccc tgg aag cgg att aaa ggc agt gag gct gac agg caa cgg gca	2323
Glu Pro Trp Lys Arg Ile Lys Gly Ser Glu Ala Asp Arg Gln Arg Ala	
723 728 733 738	
gga aca gtg act ggc ttg gca gtg aat ata gct gcc ttg ctc tct gtc	2371
Gly Thr Val Thr Gly Leu Ala Val Asn Ile Ala Ala Leu Leu Ser Val	
739 744 749 754	
atg ctt cag cct tac atg ccc acg gtt agt gcc aca atc cag gcc cag	2419

Met Leu Gln Pro Tyr Met Pro Thr Val Ser Ala Thr Ile Gln Ala Gln	
755 760 765 770	
ctg cag ctc cca cct cca gcc tgc agt atc ctg ctg aca aac ttc ctg	2467
Leu Gln Leu Pro Pro Pro Ala Cys Ser Ile Leu Leu Thr Asn Phe Leu	
771 776 781 786	
tgt acc tta cca gca gga cac cag att ggc aca gtc agt ccc ttg ttc	2515
Cys Thr Leu Pro Ala Gly His Gln Ile Gly Thr Val Ser Pro Leu Phe	
787 792 797 802	
caa aaa ttg gaa aat gac cag att gaa agt tta agg cag cgc ttt gga	2563
Gln Lys Leu Glu Asn Asp Gln Ile Glu Ser Leu Arg Gln Arg Phe Gly	
803 808 813 818	
ggg ggc cag gca aaa acg tcc ctg aag cca gca gtt gta gag act gtt	2611
Gly Gly Gln Ala Lys Thr Ser Leu Lys Pro Ala Val Val Glu Thr Val	
819 824 829 834	
aca aca gcc aag cca cag cag ata caa gcg ctg atg gat gaa gtg aca	2659
Thr Thr Ala Lys Pro Gln Gln Ile Gln Ala Leu Met Asp Glu Val Thr	
835 840 845 850	
aaa caa gga aac ctc ttg gat cta aag aaa cag ttg gct gta gct gag	2707
Lys Gln Gly Asn Leu Leu Asp Leu Lys Lys Gln Leu Ala Val Ala Glu	
851 856 861 866	
ggg aaa ccc cct gaa gcc cct aaa ggc aag aag aaa aag taa aagacct	2756
Gly Lys Pro Pro Glu Ala Pro Lys Gly Lys Lys Lys Lys *	
867 872 877	
tggctcatag aaagtcactt taatagatag ggacagtaat aaataaatgt acaatctcta	2816
tatacaagct gagacctttc cttttgtcta ctccaagcct tccccctgcg tatgtgggat	2876
tgagggtcac atcattggca ctagtgagag ggtagtcagt agccacttct gggaaagggtg	2936
ggtagtgtgg cccaagtggg ggactgatgc tccaagtgcg acgcggccgg atatttaata	2996
gtagtagtcg acccggaat tccggaccgg tacctgcaag gcgtaccagc tttccccaat	3056
agtgaattcg tatta	3071

<210> 216
 <211> 1302
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (427)..(1107)

<400> 216
 atttggccct cgaggccaag aattcggcac gataaggagg agagaccaa agggaggcct 60

gaactctcaa actccgaatc tgattttcac tctcccagga aggtctcgga aatcactgtg	120
gattgtcaat acaggagtcc atactgactg aatccctaatt tttggcctgt attcttctcc	180
ctctgtgaac catcttctta gaagtcactg aaccaagagt gccagaaaac catcccaaga	240
ctcacacaga gttgttcttc catagtggat gttttggcca ctggacatca gaaccacatt	300
ttgggtttga agaatcttct acatgctgag aaagtggaaac tccagagaca ctctgaaat	360
tgctctaagt caaaggagcc aaacggtgta cgagctccct ctctgccgtc ccctctgaga	420
gcagcc atg gcc ctg agt gat gtc gat gtg aaa aag cag att aag cac	468
Met Ala Leu Ser Asp Val Asp Val Lys Lys Gln Ile Lys His	
1 5 10	
atg atg gct ttc att gag cag gaa gcc aat gag aaa gca gag gaa atc	516
Met Met Ala Phe Ile Glu Gln Glu Ala Asn Glu Lys Ala Glu Glu Ile	
15 20 25 30	
gat gcc aag gct gag gaa gag ttt aac att gag aaa gga cgc ctc gtg	564
Asp Ala Lys Ala Glu Glu Glu Phe Asn Ile Glu Lys Gly Arg Leu Val	
31 36 41 46	
caa acc caa cga ctg aag att atg gag tat tat gag aaa aag gag aag	612
Gln Thr Gln Arg Leu Lys Ile Met Glu Tyr Tyr Glu Lys Lys Glu Lys	
47 52 57 62	
cag ata gag cag cag aag aaa atc ctg atg tcc acc atg agg aat cag	660
Gln Ile Glu Gln Gln Lys Lys Ile Leu Met Ser Thr Met Arg Asn Gln	
63 68 73 78	
gcg agg ctg aaa gtc ctg aga gcc cga aat gac ctc atc tca gat ttg	708
Ala Arg Leu Lys Val Leu Arg Ala Arg Asn Asp Leu Ile Ser Asp Leu	
79 84 89 94	
ctc agt gag gcg aag ctg aga ctc agc agg att gtg gag gac cca gag	756
Leu Ser Glu Ala Lys Leu Arg Leu Ser Arg Ile Val Glu Asp Pro Glu	
95 100 105 110	
gtc tac cag ggg ctg ctg gat aaa ctg gtg ctc cag ggt ctg ctc cga	804
Val Tyr Gln Gly Leu Leu Asp Lys Leu Val Leu Gln Gly Leu Leu Arg	
111 116 121 126	
ctg ctg gaa cct gtg atg att gta cgc tgc cgg cca caa gac ctc ctc	852
Leu Leu Glu Pro Val Met Ile Val Arg Cys Arg Pro Gln Asp Leu Leu	
127 132 137 142	
ctg gtg gag gct gct gta caa aaa gcc atc ccc gag tac atg aca att	900
Leu Val Glu Ala Ala Val Gln Lys Ala Ile Pro Glu Tyr Met Thr Ile	
143 148 153 158	
tcc cag aaa cat gtg gag gtc cag att gat aaa gag gca tac ctg gct	948
Ser Gln Lys His Val Glu Val Gln Ile Asp Lys Glu Ala Tyr Leu Ala	
159 164 169 174	

gtg aat gca gct gga ggt gtg gag gtc tac agt ggc aat cag aga ata 996
Val Asn Ala Ala Gly Gly Val Glu Val Tyr Ser Gly Asn Gln Arg Ile
175 180 185 190

aag gtt tca aat acc ttg gaa agc cga ctg gat ctc tca gcc aag caa 1044
Lys Val Ser Asn Thr Leu Glu Ser Arg Leu Asp Leu Ser Ala Lys Gln
191 196 201 206

aag atg cca gaa ata cga atg gcc ttg ttt ggt gct aac acc aac aga 1092
Lys Met Pro Glu Ile Arg Met Ala Leu Phe Gly Ala Asn Thr Asn Arg
207 212 217 222

aag ttc ttt ata taa gcctctggga agtgaagcta gtgttgaacc actaaaccat 1147
Lys Phe Phe Ile *
223

aaaagtttaa gttttttggg gaaaggaaac tagtagtggt tctctctctt tgatgctctg 1207

atactgttct gtttttcttc acgaaatacc ctttggatag ctaaagtgtt aactttgaaa 1267

taaagcccaa attaatgctc agaaaaaaaa aaaaa 1302

<210> 217
<211> 1512
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (150)..(1415)

<400> 217

gcacgaggcg ggctggggga ggggagcgtg gggccgacag ttttgggggt gaaaaggcaa 60

aaggcgggtg aaaggctgcc tcccgagact ctcttgctt ggaattctgc ccactctgcg 120

gagttagcag tcacgacctc cagcacagg atg tgg tac cac aga ttg tcc cac 173
Met Trp Tyr His Arg Leu Ser His
1 5

cta cac agc agg ctt cag gac ttg ctg aag gga gga gtc ata tat ccg 221
Leu His Ser Arg Leu Gln Asp Leu Leu Lys Gly Gly Val Ile Tyr Pro
9 14 19 24

gcc ctt cca cag ccc aac ttc aaa agc tta ctt cct tta gct gtc cat 269
Ala Leu Pro Gln Pro Asn Phe Lys Ser Leu Leu Pro Leu Ala Val His
25 30 35 40

tgg cac cat aca gcc tcc aag tct ctg act tgt gct tgg cag caa cat 317
Trp His His Thr Ala Ser Lys Ser Leu Thr Cys Ala Trp Gln Gln His
41 46 51 56

gaa gat cat ttt gag ctg aaa tat gct aat acc gtg atg cgc ttt gat 365
Glu Asp His Phe Glu Leu Lys Tyr Ala Asn Thr Val Met Arg Phe Asp

57	62	67	72	
tac gtc tgg ctt cga gac cac tgc cgc tca gca tgc tgc tac aac tct				413
Tyr Val Trp Leu Arg Asp His Cys Arg Ser Ala Ser Cys Tyr Asn Ser				
73	78	83	88	
aag act cac cag cgc agc ctg gat act gcc agt gtg gat tta tgt atc				461
Lys Thr His Gln Arg Ser Leu Asp Thr Ala Ser Val Asp Leu Cys Ile				
89	94	99	104	
aag cca aag acc att cgt ctg gat gag acc aca ctc ttt ttc act tgg				509
Lys Pro Lys Thr Ile Arg Leu Asp Glu Thr Thr Leu Phe Phe Thr Trp				
105	110	115	120	
cca gat ggt cat gtg act aaa tat gat ttg aat tgg ctg gtg aaa aac				557
Pro Asp Gly His Val Thr Lys Tyr Asp Leu Asn Trp Leu Val Lys Asn				
121	126	131	136	
agc tat gaa ggg cag aaa caa aaa gtc atc cag cct aga ata cta tgg				605
Ser Tyr Glu Gly Gln Lys Gln Lys Val Ile Gln Pro Arg Ile Leu Trp				
137	142	147	152	
aat gct gaa atc tac cag caa gcc caa gtt cca tgc gta gat tgc cag				653
Asn Ala Glu Ile Tyr Gln Gln Ala Gln Val Pro Ser Val Asp Cys Gln				
153	158	163	168	
agc ttc tta gaa acc aac gag gga ctg aag aag ttt ctg caa aac ttt				701
Ser Phe Leu Glu Thr Asn Glu Gly Leu Lys Lys Phe Leu Gln Asn Phe				
169	174	179	184	
ctg ctc tat gga att gca ttc gta gaa aat gtc cct ccc act caa gag				749
Leu Leu Tyr Gly Ile Ala Phe Val Glu Asn Val Pro Pro Thr Gln Glu				
185	190	195	200	
cac aca gag aag ttg gca gaa agg atc agc tta atc aga gaa acc att				797
His Thr Glu Lys Leu Ala Glu Arg Ile Ser Leu Ile Arg Glu Thr Ile				
201	206	211	216	
tat ggg agg atg tgg tat ttc act tca gac ttc tcc aga ggt gac act				845
Tyr Gly Arg Met Trp Tyr Phe Thr Ser Asp Phe Ser Arg Gly Asp Thr				
217	222	227	232	
gcg tac acc aag cta gct ctg gat cgg cac act gac act acc tat ttt				893
Ala Tyr Thr Lys Leu Ala Leu Asp Arg His Thr Asp Thr Thr Tyr Phe				
233	238	243	248	
caa gag ccc tgt ggc att caa gtg ttt cat tgt ctt aaa cat gaa gga				941
Gln Glu Pro Cys Gly Ile Gln Val Phe His Cys Leu Lys His Glu Gly				
249	254	259	264	
act ggt ggc agg aca ctg cta gta gat gga ttc tat gca gca gaa cag				989
Thr Gly Gly Arg Thr Leu Leu Val Asp Gly Phe Tyr Ala Ala Glu Gln				
265	270	275	280	
gta ctt caa aag gca cct gag gaa ttt gaa ctc ctc agt aaa gtg cca				1037
Val Leu Gln Lys Ala Pro Glu Glu Phe Glu Leu Leu Ser Lys Val Pro				
281	286	291	296	

ttg aag cat gaa tat att gaa gat gtt gga gaa tgt cac aac cac atg	1085
Leu Lys His Glu Tyr Ile Glu Asp Val Gly Glu Cys His Asn His Met	
297 302 307 312	
att ggg att ggg cca gtc tta aat atc tac cca tgg aat aaa gag ctg	1133
Ile Gly Ile Gly Pro Val Leu Asn Ile Tyr Pro Trp Asn Lys Glu Leu	
313 318 323 328	
tat ttg atc agg tac aac aac tat gac cgg gct gtc atc aat acc gtt	1181
Tyr Leu Ile Arg Tyr Asn Asn Tyr Asp Arg Ala Val Ile Asn Thr Val	
329 334 339 344	
cct tat gat gtc gtc cat cgc tgg tat aca gca cac cgg act cta acg	1229
Pro Tyr Asp Val Val His Arg Trp Tyr Thr Ala His Arg Thr Leu Thr	
345 350 355 360	
ata gag ttg agg aga cct gag aat gag ttt tgg gtc aaa cta aag cct	1277
Ile Glu Leu Arg Arg Pro Glu Asn Glu Phe Trp Val Lys Leu Lys Pro	
361 366 371 376	
ggc agg gtc cta ttt ata gac aac tgg cgt gtc cta cat ggc agg gaa	1325
Gly Arg Val Leu Phe Ile Asp Asn Trp Arg Val Leu His Gly Arg Glu	
377 382 387 392	
tgc ttc act ggc tac cgc caa ctg tgt ggc tgc tat tta aca aga gat	1373
Cys Phe Thr Gly Tyr Arg Gln Leu Cys Gly Cys Tyr Leu Thr Arg Asp	
393 398 403 408	
gat gta tta aac act gct cgc ctc ttg ggg ctt cag gct taa aattgac	1422
Asp Val Leu Asn Thr Ala Arg Leu Leu Gly Leu Gln Ala *	
409 414 419	
agcatctgga ttatgaatac acctggcacc ctggctacca gaatttcata tgggcagaat	1482
aatattgtgt caaactctaa aaaaaaaaaa	1512

<210> 218

<211> 2727

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (272)..(2353)

<400> 218

aattcggcac aggagacagg ttcattgtga cctcagtggc tcccgatttg ggtctccagt	60
gcttgggact cccaaagaac cagtagtaga agtctattct tgttcctatt gtacaaattc	120
gccaatattc aacagcgttc ttaaactgaa caagcatatc aaagagaatc ataaaaacat	180
tccottggcc ctgaattata tccacaatgg gaagaaatcc agggccttaa gcccctatc	240

tcctgtggcc atagagcaga catctcttaa g	atg atg cag gca gta gga ggt	292
	Met Met Gln Ala Val Gly Gly	
	1 5	
gca cct gca cgt ccc act gga gaa tat atc tgt aat caa tgt ggt gct	340	
Ala Pro Ala Arg Pro Thr Gly Glu Tyr Ile Cys Asn Gln Cys Gly Ala		
8 13 18 23		
aag tac aca tcc cta gac agc ttt cag act cac cta aaa act cat ctc	388	
Lys Tyr Thr Ser Leu Asp Ser Phe Gln Thr His Leu Lys Thr His Leu		
24 29 34 39		
gac act gtg ctt cca aaa ttg acc tgt cct cag tgc aac aag gaa ttc	436	
Asp Thr Val Leu Pro Lys Leu Thr Cys Pro Gln Cys Asn Lys Glu Phe		
40 45 50 55		
ccc aac caa gaa tcc ttg ctg aag cat gtt acc att cac ttt atg atc	484	
Pro Asn Gln Glu Ser Leu Leu Lys His Val Thr Ile His Phe Met Ile		
56 61 66 71		
act tca acg tat tac atc tgt gag agt tgt gac aag caa ttc aca tca	532	
Thr Ser Thr Tyr Tyr Ile Cys Glu Ser Cys Asp Lys Gln Phe Thr Ser		
72 77 82 87		
gtg gat gac ctt cag aaa cac ctg ctg gac atg cac acc ttt gtc ttc	580	
Val Asp Asp Leu Gln Lys His Leu Leu Asp Met His Thr Phe Val Phe		
88 93 98 103		
ttt cgc tgc acc ctc tgc cag gaa gtt ttt gac tca aaa gtc tcc att	628	
Phe Arg Cys Thr Leu Cys Gln Glu Val Phe Asp Ser Lys Val Ser Ile		
104 109 114 119		
cag ctc cac ttg gct gtg aag cac agt aac gaa aag aaa gtc tat agg	676	
Gln Leu His Leu Ala Val Lys His Ser Asn Glu Lys Lys Val Tyr Arg		
120 125 130 135		
tgc aca tct tgc aac tgg gac ttc cgc aac gaa act gac ttg cag ctc	724	
Cys Thr Ser Cys Asn Trp Asp Phe Arg Asn Glu Thr Asp Leu Gln Leu		
136 141 146 151		
cat gtg aaa cac aac cac ctg gaa aac caa ggg aaa gtg cat aag tgc	772	
His Val Lys His Asn His Leu Glu Asn Gln Gly Lys Val His Lys Cys		
152 157 162 167		
att ttc tgc ggt gag tcc ttt ggc acc gag gtg gag ctg caa tgc cac	820	
Ile Phe Cys Gly Glu Ser Phe Gly Thr Glu Val Glu Leu Gln Cys His		
168 173 178 183		
atc acc act cac agt aag aag tac aac tgc aag ttc tgt agc aaa gcc	868	
Ile Thr Thr His Ser Lys Lys Tyr Asn Cys Lys Phe Cys Ser Lys Ala		
184 189 194 199		
ttc cat gcg atc att ttg tta gaa aaa cac ttg cga gaa aaa cac tgt	916	
Phe His Ala Ile Ile Leu Leu Glu Lys His Leu Arg Glu Lys His Cys		
200 205 210 215		

gta ttc gaa acc aag aca ccc aac tgt gga aca aat gga gct tcc gag	964
Val Phe Glu Thr Lys Thr Pro Asn Cys Gly Thr Asn Gly Ala Ser Glu	
216 221 226 231	
caa gtg cag aaa gag gaa gtg gag ctg cag act ttg ctg acc aac agc	1012
Gln Val Gln Lys Glu Glu Val Glu Leu Gln Thr Leu Leu Thr Asn Ser	
232 237 242 247	
cag gag tcc cac aac agt cac gat ggg agc gaa gaa gac gtt gac acc	1060
Gln Glu Ser His Asn Ser His Asp Gly Ser Glu Glu Asp Val Asp Thr	
248 253 258 263	
tct gag cct atg tac ggc tgc gac att tgt ggg gca gcc tac act atg	1108
Ser Glu Pro Met Tyr Gly Cys Asp Ile Cys Gly Ala Ala Tyr Thr Met	
264 269 274 279	
gaa act ttg ctg cag aat cac cag ctc cga gac cac aac atc aga cct	1156
Glu Thr Leu Leu Gln Asn His Gln Leu Arg Asp His Asn Ile Arg Pro	
280 285 290 295	
gga gaa agt gcc atc gtg aaa aag aaa gct gag ctc att aaa ggg aat	1204
Gly Glu Ser Ala Ile Val Lys Lys Lys Ala Glu Leu Ile Lys Gly Asn	
296 301 306 311	
tac aag tgc aac gtg tgc tct cga acc ttc ttc tcc gaa aat ggc ctc	1252
Tyr Lys Cys Asn Val Cys Ser Arg Thr Phe Phe Ser Glu Asn Gly Leu	
312 317 322 327	
cgg gaa cat atg cag acc cac cta ggc cct gtc aaa cac tac atg tgc	1300
Arg Glu His Met Gln Thr His Leu Gly Pro Val Lys His Tyr Met Cys	
328 333 338 343	
cct att tgc gga gag cgg ttt ccc tcc ctt tta act ctt act gaa cac	1348
Pro Ile Cys Gly Glu Arg Phe Pro Ser Leu Leu Thr Leu Thr Glu His	
344 349 354 359	
aaa gtc acg cat agt aag agt ctt gat act gga aac tgc cgg att tgc	1396
Lys Val Thr His Ser Lys Ser Leu Asp Thr Gly Asn Cys Arg Ile Cys	
360 365 370 375	
aag atg cct ctc cag agt gaa gag gag ttt tta gag cat tgc caa atg	1444
Lys Met Pro Leu Gln Ser Glu Glu Glu Phe Leu Glu His Cys Gln Met	
376 381 386 391	
cac cct gac ttg agg aat tcc ctg aca ggc ttt cgc tgc gtg gtg tgc	1492
His Pro Asp Leu Arg Asn Ser Leu Thr Gly Phe Arg Cys Val Val Cys	
392 397 402 407	
atg cag aca gtg acc tcc acc ttg gaa ctc aaa atc cat ggg acg ttc	1540
Met Gln Thr Val Thr Ser Thr Leu Glu Leu Lys Ile His Gly Thr Phe	
408 413 418 423	
cac atg caa aag aca ggg aat ggg tct gca gtt cag acc aca ggg cgg	1588
His Met Gln Lys Thr Gly Asn Gly Ser Ala Val Gln Thr Thr Gly Arg	
424 429 434 439	
ggc cag cac gtc caa aaa ctg tat aag tgc gca tct tgc ctc aaa gaa	1636

Gly Gln His Val Gln Lys Leu Tyr Lys Cys Ala Ser Cys Leu Lys Glu	
440 445 450 455	
ttc cgt tcc aag caa gat ctg gtg aaa ctt gat atc aat ggc ctg cca	1684
Phe Arg Ser Lys Gln Asp Leu Val Lys Leu Asp Ile Asn Gly Leu Pro	
456 461 466 471	
tat ggt ctg tgt gcc ggc tgc gtg aat ctc agt aag agc gcc agc cca	1732
Tyr Gly Leu Cys Ala Gly Cys Val Asn Leu Ser Lys Ser Ala Ser Pro	
472 477 482 487	
ggc att aac gtc cct ccc ggc acg aat aga cca ggc ttg ggc cag aat	1780
Gly Ile Asn Val Pro Pro Gly Thr Asn Arg Pro Gly Leu Gly Gln Asn	
488 493 498 503	
gag aat ctg agt gcc att gag ggg aaa ggc aag gtg ggg gga ctg aag	1828
Glu Asn Leu Ser Ala Ile Glu Gly Lys Gly Lys Val Gly Gly Leu Lys	
504 509 514 519	
aca cgc tgc tct agc tgc aac gtt aag ttt gag tct gaa agt gaa ctc	1876
Thr Arg Cys Ser Ser Cys Asn Val Lys Phe Glu Ser Glu Ser Glu Leu	
520 525 530 535	
cag aac cac atc caa acc atc cac cga gag ctc gtg cca gac agc aac	1924
Gln Asn His Ile Gln Thr Ile His Arg Glu Leu Val Pro Asp Ser Asn	
536 541 546 551	
agc aca cag ttg aaa acg ccc caa gta tca cca atg ccc aga atc agt	1972
Ser Thr Gln Leu Lys Thr Pro Gln Val Ser Pro Met Pro Arg Ile Ser	
552 557 562 567	
ccc tcc cag tcg gat gag aag aag acc tat caa tgc atc aag tgt cag	2020
Pro Ser Gln Ser Asp Glu Lys Lys Thr Tyr Gln Cys Ile Lys Cys Gln	
568 573 578 583	
atg gtt ttc tac aat gaa tgg gat att cag gtt cat gtt gca aat cac	2068
Met Val Phe Tyr Asn Glu Trp Asp Ile Gln Val His Val Ala Asn His	
584 589 594 599	
atg att gat gaa gga ctg aac cat gaa tgc aaa ctc tgc agc cag acc	2116
Met Ile Asp Glu Gly Leu Asn His Glu Cys Lys Leu Cys Ser Gln Thr	
600 605 610 615	
ttt gac tct cct gcc aaa ctc cag tgc cac ctg ata gag cac agc ttc	2164
Phe Asp Ser Pro Ala Lys Leu Gln Cys His Leu Ile Glu His Ser Phe	
616 621 626 631	
gaa ggg atg gga ggc acc ttc aag tgt cca gtc tgc ttt aca gta ttt	2212
Glu Gly Met Gly Gly Thr Phe Lys Cys Pro Val Cys Phe Thr Val Phe	
632 637 642 647	
gtt caa gca aac aag ttg cag cag cat att ttc tct gcc cat gga caa	2260
Val Gln Ala Asn Lys Leu Gln Gln His Ile Phe Ser Ala His Gly Gln	
648 653 658 663	
gaa gac aag atc tat gac tgt aca caa tgt cca cag aag ttt ttc ttc	2308
Glu Asp Lys Ile Tyr Asp Cys Thr Gln Cys Pro Gln Lys Phe Phe Phe	

664	669	674	679	
caa aca gag ctg cag aat cat aca atg acc caa cac agc agt tag tgc				2356
Gln Thr Glu Leu Gln Asn His Thr Met Thr Gln His Ser Ser *				
680	685	690		
aagtacagtc totcaaggag aattgatttt gtggcacaaa aagggaacat gttttactct				2416
ttgcacgaaa ctttcattgt taatgtatat tattcagaaa cattgtattg taccataaaa				2476
cttgattat caaactgttg gatgttcattg tgtttgaact tttgcgcacc ggatagaccc				2536
cttgatatata aagtgttgca catgtattat gtcgtctgat actaaaatgg tcttataaag				2596
acaagtggac ttgggcccta ttcaggcaag attaaaaaaaa aaaaaaaagg gcggccgctc				2656
tagaggatcc aagcttacgt acgcgtgcat gcgacgtcat agctctctcc ctatagtgat				2716
cgtattataa g				2727

<210> 219
 <211> 550
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (6) .. (509)

<400> 219				
cagtc atg gcg cag gaa gag gaa gat gtt aga gat tac aat ttg act				47
Met Ala Gln Glu Glu Glu Asp Val Arg Asp Tyr Asn Leu Thr				
1 5 10				
gaa gaa cag aag gcg atc aag gcc aag tat ccg cca gtc aat agg aag				95
Glu Glu Gln Lys Ala Ile Lys Ala Lys Tyr Pro Pro Val Asn Arg Lys				
15 20 25 30				
tac gag tat ttg gat cat aca gca gat gtc cag tta cac gca tgg gga				143
Tyr Glu Tyr Leu Asp His Thr Ala Asp Val Gln Leu His Ala Trp Gly				
31 36 41 46				
gat act ctg gag gaa gca ttt gag caa tgt gca atg gcc atg ttt ggt				191
Asp Thr Leu Glu Glu Ala Phe Glu Gln Cys Ala Met Ala Met Phe Gly				
47 52 57 62				
tac atg aca gat act ggg aca gtg gag ccc ctc caa aca gta gaa gta				239
Tyr Met Thr Asp Thr Gly Thr Val Glu Pro Leu Gln Thr Val Glu Val				
63 68 73 78				
gaa acc caa gga gat gac tta cag tct ctt ctg ttt cac ttt ttg gat				287
Glu Thr Gln Gly Asp Asp Leu Gln Ser Leu Leu Phe His Phe Leu Asp				
79 84 89 94				

gaa tgg ctt tat aag ttc agt gct gat gaa ttc ttc ata ccc cgg gaa	335
Glu Trp Leu Tyr Lys Phe Ser Ala Asp Glu Phe Phe Ile Pro Arg Glu	
95 100 105 110	
gtg aaa gta ctt agc att gat caa aga aat ttc aaa tta cga tca att	383
Val Lys Val Leu Ser Ile Asp Gln Arg Asn Phe Lys Leu Arg Ser Ile	
111 116 121 126	
ggg tgg gga gaa gaa ttt tca ttg tcc aag cac cct cag gga aca gaa	431
Gly Trp Gly Glu Glu Phe Ser Leu Ser Lys His Pro Gln Gly Thr Glu	
127 132 137 142	
gtc aaa gca ata aca tat tca gca atg cag gtc tat aat gaa gag aac	479
Val Lys Ala Ile Thr Tyr Ser Ala Met Gln Val Tyr Asn Glu Glu Asn	
143 148 153 158	
ccg gaa gtt ttt gtg atc att gac att taa g acaccaaaaa ataaaagact	530
Pro Glu Val Phe Val Ile Ile Asp Ile *	
159 164	
cctacgaaga aaaaaaaaaa	550

<210> 220
 <211> 2742
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (842) .. (2014)

<400> 220	
acctccctcc gcggagcagc cagacagcga gggccccggc cgggggcagg ggggacgccc	60
cgtcgggggc accccccccg gctctgagcc gccgcggggg ccggcctcgg cccggagcgg	120
aggaaggagt cgccgaggag cagcctgagg cccagagtc tgagacgagc cgccgccgcc	180
cccgccactg cggggaggag ggggaggagg agcgggagga gggacgagct ggtcgggaga	240
agaggaaaaa aacttttgag acttttccgt tgccgctggg agccggaggc gcggggacct	300
cttggcgcga cgctgccccg cgaggaggca ggacttgggg accccagacc gcctcccttt	360
gccgcggggg acgettgtc cctccctgcc cctacacgg cgtccctcag gcgcccccat	420
tccggaccag cctcgggag tcgccgaccc ggccctccgc aaagactttt cccagacct	480
cgggcgcacc cctgcacgc cgccttcac cccggcctgt ctctgagcc cccgcgcac	540
ctagaccctt tctcctccag gagacggatc tctctccgac ctgccacaga tcccctattc	600
aagaccaccc accttctggt accagatcgc gcccatctag gttatttccg tgggatactg	660

agacaccccc ggtccaagcc tcccctccac cactgcgccc ttctccctga ggagcctcag 720
 ctttccctcg aggeccctect accttttgcc gggagacccc cagccctctgc aggggcgggg 780
 cctccccacc acaccagccc tggtcgcgct ctgggcagtg ccggggggcg ccgcctcccc 840
 c atg ccg ccc tcc ggg ctg cgg ctg ctg ccg ctg ctg cta ccg ctg 886
 Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu
 1 5 10
 ctg tgg cta ctg gtg ctg acg cct ggc cgg ccg gcc gcg gga cta tcc 934
 Leu Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser
 16 21 26 31
 acc tgc aag act atc gac atg gag ctg gtg aag cgg aag cgc atc gag 982
 Thr Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu
 32 37 42 47
 gcc atc cgc ggc cag atc ctg tcc aag ctg cgg ctc gcc agc ccc ccg 1030
 Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro
 48 53 58 63
 agc cag ggg gag gtg ccg ccc ggc ccg ctg ccc gag gcc gtg ctc gcc 1078
 Ser Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala
 64 69 74 79
 ctg tac aac agc acc cgc gac cgg gtg gcc ggg gag agt gca gaa ccg 1126
 Leu Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Glu Pro
 80 85 90 95
 gag ccc gag cct gag gcc gac tac tac gcc aag gag gtc acc cgc gtg 1174
 Glu Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val
 96 101 106 111
 cta atg gtg gaa acc cac aac gaa atc tat gac aag ttc aag cag agt 1222
 Leu Met Val Glu Thr His Asn Glu Ile Tyr Asp Lys Phe Lys Gln Ser
 112 117 122 127
 aca cac agc ata tat atg ttc ttc aac aca tca gag ctc cga gaa gcg 1270
 Thr His Ser Ile Tyr Met Phe Phe Asn Thr Ser Glu Leu Arg Glu Ala
 128 133 138 143
 gta cct gaa ccc gtg ttg ctc tcc cgg gca gag ctg cgt ctg ctg agg 1318
 Val Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg
 144 149 154 159
 ctc aag tta aaa gtg gag cag cac gtg gag ctg tac cag aaa tac agc 1366
 Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser
 160 165 170 175
 aac aat tcc tgg cga tac ctc agc aac cgg ctg ctg gca ccc agc gac 1414
 Asn Asn Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp
 176 181 186 191
 tcg cca gag tgg tta tct ttt gat gtc acc gga gtt gtg cgg cag tgg 1462
 Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp
 192 197 202 207

ttg agc cgt gga ggg gaa att gag ggc ttt cgc ctt agc gcc cac tgc	1510
Leu Ser Arg Gly Gly Ile Glu Gly Phe Arg Leu Ser Ala His Cys	
208 213 218 223	
tcc tgt gac agc agg gat aac aca ctg caa gtg gac atc aac ggg ttc	1558
Ser Cys Asp Ser Arg Asp Asn Thr Leu Gln Val Asp Ile Asn Gly Phe	
224 229 234 239	
act acc ggc cgc cga ggt gac ctg gcc acc att cat ggc atg aac cgg	1606
Thr Thr Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg	
240 245 250 255	
cct ttc ctg ctt ctc atg gcc acc ccg ctg gag agg gcc cag cat ctg	1654
Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu	
256 261 266 271	
caa agc tcc cgg cac cgc cga gcc ctg gac acc aac tat tgc ttc agc	1702
Gln Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser	
272 277 282 287	
tcc acg gag aag aac tgc tgc gtg cgg cag ctg tac att gac ttc cgc	1750
Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg	
288 293 298 303	
aag gac ctc ggc tgg aag tgg atc cac gag ccc aag ggc tac cat gcc	1798
Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala	
304 309 314 319	
aac ttc tgc ctc ggg ccc tgc ccc tac att tgg agc ctg gac acg cag	1846
Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln	
320 325 330 335	
tac agc aag gtc ctg gcc ctg tac aac cag cat aac ccg ggc gcc tgc	1894
Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser	
336 341 346 351	
gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag ccg ctg ccc atc gtg	1942
Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val	
352 357 362 367	
tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc aac atg atc	1990
Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile	
368 373 378 383	
gtg cgc tcc tgc aag tgc agc tga ggtcccgccc cgccccgccc cgccccggca	2044
Val Arg Ser Cys Lys Cys Ser *	
384 389	
ggccccggccc ccccccgccc cgcccccgct gccttgccca tgggggctgt atttaaggac	2104
accogtgccc caagcccacc tgggggccc ttaaagatgg agagaggact gcggatctct	2164
gtgtcattgg gcgcctgcct ggggtctcca tcctgacgt tccccactc ccactccctc	2224
tctctccctc tctgcctcct cctgcctgtc tgcactattc ctttgcccgg catcaaggca	2284

caggggacca gtggggaaca ctactgtagt tagatctatt tattgagcac cttgggcact 2344
gttgaagtgc cttacattaa tgaactcatt cagtcaccat agcaacactc tgagatgcag 2404
ggactctgat aacaccatt ttaaagggtga ggaaacaagc ccagagaggt taagggagga 2464
gttcctgccc accaggaacc tgcttttagtg ggggtagtg aagaagaaa taaaagatag 2524
tagttcaggc caggcggggt gctcacgcct gtaatcctag cacttttggg aggcagagat 2584
gggaggatta cttgaatcca ggcatttgag accagcctgg gtaacatagt gagaccctat 2644
ctctacaaaa cacttttaaa aaatgtacac ctgtgggtccc agctactctg gaggctaagg 2704
tgggaggatc acttgatcct gggagggtcaa ggctgcag 2742

<210> 221
<211> 1994
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (123)..(1463)

<400> 221
ccagtgcggt ggaattcgga attcgctcctt ttcattcttca gaactggaag cagaaagtta 60
atcagactaa gaaagcagaa tttgtacgca cagcagaaaa atttaaaaaat caagtaatta 120
ac atg gaa aaa gat aaa cac agt cat ttc tac aac caa aaa agt gac 167
Met Glu Lys Asp Lys His Ser His Phe Tyr Asn Gln Lys Ser Asp
1 5 10
ttc aga att gag cat agt atg cta gaa gaa ttg gaa aat aaa ttg att 215
Phe Arg Ile Glu His Ser Met Leu Glu Glu Leu Glu Asn Lys Leu Ile
16 21 26 31
cac agc agg aaa aca gaa aga gca aaa atc cag caa caa ttg gcc aaa 263
His Ser Arg Lys Thr Glu Arg Ala Lys Ile Gln Gln Gln Leu Ala Lys
32 37 42 47
ata cat aat aat gta aag aaa ctt cag cat caa tta aaa gat gtg aag 311
Ile His Asn Asn Val Lys Lys Leu Gln His Gln Leu Lys Asp Val Lys
48 53 58 63
cct aca cct gat ttt gtt gag aag ctc aga gaa atg atg gaa gaa att 359
Pro Thr Pro Asp Phe Val Glu Lys Leu Arg Glu Met Met Glu Glu Ile
64 69 74 79
gaa aat gca att aac act ttt aaa gaa gag cag agg ttg ata tat gaa 407
Glu Asn Ala Ile Asn Thr Phe Lys Glu Glu Gln Arg Leu Ile Tyr Glu
80 85 90 95

gag cta att aaa gaa gag aag aca act aat aat gag ttg agt gcc ata	455
Glu Leu Ile Lys Glu Glu Lys Thr Thr Asn Asn Glu Leu Ser Ala Ile	
96 101 106 111	
tca aga aaa att gac aca tgg gct ttg ggt aat tca gaa aca gag aaa	503
Ser Arg Lys Ile Asp Thr Trp Ala Leu Gly Asn Ser Glu Thr Glu Lys	
112 117 122 127	
gct ttc aga gca atc tca agc aaa gtt cct gta gac aaa gta aca cca	551
Ala Phe Arg Ala Ile Ser Ser Lys Val Pro Val Asp Lys Val Thr Pro	
128 133 138 143	
agt act ctt cca gaa gag gta cta gat ttt gaa aaa ttc ctt cag caa	599
Ser Thr Leu Pro Glu Glu Val Leu Asp Phe Glu Lys Phe Leu Gln Gln	
144 149 154 159	
aca gga ggg cga caa ggt gcc tgg gat gat tat gat cac cag aac ttt	647
Thr Gly Gly Arg Gln Gly Ala Trp Asp Asp Tyr Asp His Gln Asn Phe	
160 165 170 175	
gta aag gtg aga aac aaa cat aaa ggg aag cca aca ttt atg gaa gaa	695
Val Lys Val Arg Asn Lys His Lys Gly Lys Pro Thr Phe Met Glu Glu	
176 181 186 191	
gtt cta gaa cac ctt cct gga aaa aca caa gat gaa gtt caa cag cat	743
Val Leu Glu His Leu Pro Gly Lys Thr Gln Asp Glu Val Gln Gln His	
192 197 202 207	
gaa aaa tgg tat caa aag ttt ctg gct cta gaa gaa aga aaa gag	791
Glu Lys Trp Tyr Gln Lys Phe Leu Ala Leu Glu Glu Arg Lys Lys Glu	
208 213 218 223	
tca att cag att tgg aaa act aaa aag cag caa aaa agg gag gaa att	839
Ser Ile Gln Ile Trp Lys Thr Lys Lys Gln Gln Lys Arg Glu Glu Ile	
224 229 234 239	
ttc aag tta aag gaa aag gca gac aac aca cct gtg ctt ttt cat aat	887
Phe Lys Leu Lys Glu Lys Ala Asp Asn Thr Pro Val Leu Phe His Asn	
240 245 250 255	
aaa caa gag gat aat caa aag caa aaa gag gaa caa aga aag aaa cag	935
Lys Gln Glu Asp Asn Gln Lys Gln Lys Glu Glu Gln Arg Lys Lys Gln	
256 261 266 271	
aaa ttg gca gtt gaa gct tgg aag aaa cag aaa agt ata gaa atg tca	983
Lys Leu Ala Val Glu Ala Trp Lys Lys Gln Lys Ser Ile Glu Met Ser	
272 277 282 287	
atg aaa tgt gct tcc cag tta aaa gaa gaa gaa gag aaa gag aaa aaa	1031
Met Lys Cys Ala Ser Gln Leu Lys Glu Glu Glu Glu Lys Glu Lys Lys	
288 293 298 303	
cat cag aaa gaa cgc cag cgc cag ttt aag tta aaa tta cta cta gaa	1079
His Gln Lys Glu Arg Gln Arg Gln Phe Lys Leu Lys Leu Leu Leu Glu	
304 309 314 319	
agt tat acc cag cag aag aaa gaa cag gaa gaa ttt ttg agg ctt gaa	1127

Ser Tyr Thr Gln Gln Lys Lys Glu Gln Glu Glu Phe Leu Arg Leu Glu	
320 325 330 335	
aag gag ata agg gaa aag gca gaa aag gca gaa aaa agg aaa aat gct	1175
Lys Glu Ile Arg Glu Lys Ala Glu Lys Ala Glu Lys Arg Lys Asn Ala	
336 341 346 351	
gct gat gaa att tcc aga ttt caa gaa aga gat tta cat aaa ctt gaa	1223
Ala Asp Glu Ile Ser Arg Phe Gln Glu Arg Asp Leu His Lys Leu Glu	
352 357 362 367	
ctg aaa att cta gat aga cag gca aag gaa gat gaa aag tca caa aaa	1271
Leu Lys Ile Leu Asp Arg Gln Ala Lys Glu Asp Glu Lys Ser Gln Lys	
368 373 378 383	
caa aga aga ctg gca aaa tta aaa gaa aag gtt gaa aac aat gtt agt	1319
Gln Arg Arg Leu Ala Lys Leu Lys Glu Lys Val Glu Asn Asn Val Ser	
384 389 394 399	
aga gat ccc tct agg ctt tac aaa ccc acc aaa ggt tgg gaa gaa cga	1367
Arg Asp Pro Ser Arg Leu Tyr Lys Pro Thr Lys Gly Trp Glu Glu Arg	
400 405 410 415	
acc aaa aag ata gga cca aca ggc tct ggg cca ctt cta cat atc cca	1415
Thr Lys Lys Ile Gly Pro Thr Gly Ser Gly Pro Leu Leu His Ile Pro	
416 421 426 431	
cat agg gct att cca acc tgg aga caa gga ata cag aga aga gta tga	1463
His Arg Ala Ile Pro Thr Trp Arg Gln Gly Ile Gln Arg Arg Val *	
432 437 442 447	
gataatcaaaa ttgctactca gttgataaga atgttaacat actaagttat accagggaga	1523
gagtgactaa ccacattctt taaatatcaa tagcttagtc agattgatta ttgtgctata	1583
ttgtgaattg agaggtatta agtttcatga ggctttgtca ttagtattcc tgcttctacc	1643
aagaaggtat ttaatatatg tgttggccta ttattgatgt aaaagttatt taaataagtt	1703
aatgttagaa acattattca atttaaatac tgaaaacatt tcaaagagat tttgtttttg	1763
ttatagcata gcaaagtaaa ttggaacaat catacaatga catttttttaa accaaaat	1823
tgtaactttt ataacttgga gttaagttag cttgagtaac aaaaaggtaa agtggttttt	1883
gtttagagtt acgaaatggt agtacttttt ctatgtttta caaattggca gtttgtcagt	1943
tatgacattt ttgtgtaata aatattttgt atttgtttga aaaaaaaaa a	1994

<210> 222
 <211> 2363
 <212> DNA
 <213> Homo sapiens

<222> (317) .. (1582)

agatatctcc	ggcgccgccc	gccattttga	ctccagtgtc	tcgtttgacag	tcggcgcttt	60
aggggaaactg	tcttcctccg	caggcgcgag	gctgggtaca	gggtctattg	tctgtggttg	120
actccgtact	ttggtctgag	gccttcggga	gctttcccg	ggcagtttagc	agaagccgca	180
gcggccgccc	cgcgcgtct	cctctgtccc	tgggcccggg	agggaaccaac	ttggcgctcac	240
gcccctcagc	ggtcgccact	ctcttctctg	ttgttgggtc	cgcctcgtat	tcccgggaatc	300
agacggtgcc	ccatag	atg gcc agc ttt ccc ccg agg gtc aac gag aaa				349
		Met Ala Ser Phe Pro Pro Arg Val Asn Glu Lys				
		1	5			

gag atc gtg aga tca cgt act ata ggt gaa ctt tta gct cct gca gct 397
Glu Ile Val Arg Ser Arg Thr Ile Gly Glu Leu Leu Ala Pro Ala Ala
12 17 22 27

cct ttt gac aag aaa tgt ggt cgt gaa aat tgg act gtt gct ttt gct 445
Pro Phe Asp Lys Lys Cys Gly Arg Glu Asn Trp Thr Val Ala Phe Ala
28 33 38 43

cca gat ggt tca tac ttt gct tgg tca caa gga cat cgc aca gta aag 493
Pro Asp Gly Ser Tyr Phe Ala Trp Ser Gln Gly His Arg Thr Val Lys
44 49 54 59

ctt gtt ccg tgg tcc cag tgc ctt cag aac ttt ctc ttg cat ggc acc 541
Leu Val Pro Trp Ser Gln Cys Leu Gln Asn Phe Leu Leu His Gly Thr
60 65 70 75

aag aat gtt acc aat tca agc agt tta aga ttg cca aga caa aat agt 589
Lys Asn Val Thr Asn Ser Ser Ser Leu Arg Leu Pro Arg Gln Asn Ser
76 81 86 91

gat ggt ggt cag aaa aat aag cct cgt gaa cat att ata gac tgt gga 637
Asp Gly Gly Gln Lys Asn Lys Pro Arg Glu His Ile Ile Asp Cys Gly
92 97 102 107

gat ata gtc tgg agt ctt gct ttt ggg tca tca gtt cca gaa aaa cag 685
Asp Ile Val Trp Ser Leu Ala Phe Gly Ser Ser Val Pro Glu Lys Gln
108 113 118 123

agt cgc tgt gta aat ata gaa tgg cat cgc ttc aga ttt gga caa gat 733
Ser Arg Cys Val Asn Ile Glu Trp His Arg Phe Arg Phe Gly Gln Asp
124 129 134 139

cag cta ctt ctt gct aca ggg ttg aac aat ggg cgt atc aaa ata tgg 781
Gln Leu Leu Leu Ala Thr Gly Leu Asn Asn Gly Arg Ile Lys Ile Trp
140 145 150 155

gat gta tat aca gga aaa ctc ctc ctt aac ttg gta gat cat act gaa 829
Asp Val Tyr Thr Gly Lys Leu Leu Leu Asn Leu Val Asp His Thr Glu

156	161	166	171	
gtg gtc aga gat tta act ttt gct cca gat gga agc ttg atc ctg gtg				877
Val Val Arg Asp Leu Thr Phe Ala Pro Asp Gly Ser Leu Ile Leu Val				
172	177	182	187	
tca gct tca aga gac aaa act ctc aga gta tgg gac ctg aaa gat gat				925
Ser Ala Ser Arg Asp Lys Thr Leu Arg Val Trp Asp Leu Lys Asp Asp				
188	193	198	203	
gga aac atg atg aaa gta ttg agg ggg cat cag aat tgg gtg tac agc				973
Gly Asn Met Met Lys Val Leu Arg Gly His Gln Asn Trp Val Tyr Ser				
204	209	214	219	
tgt gca ttc tct cct gac tct tct atg ctg tgt tca gtc gga gcc agt				1021
Cys Ala Phe Ser Pro Asp Ser Ser Met Leu Cys Ser Val Gly Ala Ser				
220	225	230	235	
aaa gca gtt ttc ctt tgg aat atg gat aaa tac acc atg ata cgg aaa				1069
Lys Ala Val Phe Leu Trp Asn Met Asp Lys Tyr Thr Met Ile Arg Lys				
236	241	246	251	
cta gaa gga cat cac cat gat gtg gta gct tgt gac ttt tct cct gat				1117
Leu Glu Gly His His His Asp Val Val Ala Cys Asp Phe Ser Pro Asp				
252	257	262	267	
gga gca tta ctg gct act gca tct tat gat act cga gta tat atc tgg				1165
Gly Ala Leu Leu Ala Thr Ala Ser Tyr Asp Thr Arg Val Tyr Ile Trp				
268	273	278	283	
gat cca cat aat gga gac att ctg atg gaa ttt ggg cac ctg ttt ccc				1213
Asp Pro His Asn Gly Asp Ile Leu Met Glu Phe Gly His Leu Phe Pro				
284	289	294	299	
cca cct act cca ata ttt gct gga gga gca aat gac cgg tgg gta cga				1261
Pro Pro Thr Pro Ile Phe Ala Gly Gly Ala Asn Asp Arg Trp Val Arg				
300	305	310	315	
tct gta tct ttt agc cat gat gga ctg cat gtt gca agc ctt gct gat				1309
Ser Val Ser Phe Ser His Asp Gly Leu His Val Ala Ser Leu Ala Asp				
316	321	326	331	
gat aaa atg gtg agg ttc tgg aga att gat gag gat tat cca gtg caa				1357
Asp Lys Met Val Arg Phe Trp Arg Ile Asp Glu Asp Tyr Pro Val Gln				
332	337	342	347	
gtt gca cct ttg agc aat ggt ctt tgc tgt gcc ttc tct act gat ggc				1405
Val Ala Pro Leu Ser Asn Gly Leu Cys Cys Ala Phe Ser Thr Asp Gly				
348	353	358	363	
agt gtt tta gct gct ggg aca cat gac gga agt gtg tat ttt tgg gcc				1453
Ser Val Leu Ala Ala Gly Thr His Asp Gly Ser Val Tyr Phe Trp Ala				
364	369	374	379	
act cca cgg cag gtc cct agc ctg caa cat tta tgt cgc atg tca atc				1501
Thr Pro Arg Gln Val Pro Ser Leu Gln His Leu Cys Arg Met Ser Ile				
380	385	390	395	

Ala	Ser	Gly	Ala	Tyr	Asn	Pro	Tyr	Ile	Glu	Ile	Ile	Glu	Gln	Pro	Arg		
2					7					12					17		
cag	agg	gga	atg	cgt	ttt	aga	tac	aaa	tgt	gaa	ggg	cga	tca	gca	ggc	273	
Gln	Arg	Gly	Met	Arg	Phe	Arg	Tyr	Lys	Cys	Glu	Gly	Arg	Ser	Ala	Gly		
18					23					28					33		
agc	att	cca	ggg	gag	cac	agc	aca	gac	aac	aac	cga	aca	tac	cct	tct	321	
Ser	Ile	Pro	Gly	Glu	His	Ser	Thr	Asp	Asn	Asn	Arg	Thr	Tyr	Pro	Ser		
34					39					44					49		
atc	cag	att	atg	aac	tat	tat	gga	aaa	gga	aaa	gtg	aga	att	aca	tta	369	
Ile	Gln	Ile	Met	Asn	Tyr	Tyr	Gly	Lys	Gly	Lys	Val	Arg	Ile	Thr	Leu		
50					55					60					65		
gta	aca	aag	aat	gac	cca	tat	aaa	cct	cat	cct	cat	gat	tta	gtt	gga	417	
Val	Thr	Lys	Asn	Asp	Pro	Tyr	Lys	Pro	His	Pro	His	Asp	Leu	Val	Gly		
66					71					76					81		
aaa	gac	tgc	aga	gac	ggc	tac	tat	gaa	gca	gaa	ttt	gga	caa	gaa	cgc	465	
Lys	Asp	Cys	Arg	Asp	Gly	Tyr	Tyr	Glu	Ala	Glu	Phe	Gly	Gln	Glu	Arg		
82					87					92					97		
aga	cct	ttg	ttt	ttc	caa	aat	ttg	ggg	att	cga	tgt	gtg	aag	aaa	aaa	513	
Arg	Pro	Leu	Phe	Phe	Gln	Asn	Leu	Gly	Ile	Arg	Cys	Val	Lys	Lys	Lys		
98					103					108					113		
gaa	gta	aaa	gaa	gct	att	att	aca	aga	ata	aag	gca	gga	atc	aat	cca	561	
Glu	Val	Lys	Glu	Ala	Ile	Ile	Thr	Arg	Ile	Lys	Ala	Gly	Ile	Asn	Pro		
114					119					124					129		
ttc	aat	gtc	cct	gaa	aaa	cag	ctg	aat	gat	att	gaa	gat	tgt	gac	ctc	609	
Phe	Asn	Val	Pro	Glu	Lys	Gln	Leu	Asn	Asp	Ile	Glu	Asp	Cys	Asp	Leu		
130					135					140					145		
aat	gtg	gtg	aga	ctg	tgt	ttt	caa	gtt	ttt	ctc	cct	gat	gaa	cat	ggg	657	
Asn	Val	Val	Arg	Leu	Cys	Phe	Gln	Val	Phe	Leu	Pro	Asp	Glu	His	Gly		
146					151					156					161		
aat	ttg	acg	act	gct	ctt	cct	cct	gtt	gtc	tcg	aac	cca	att	tat	gac	705	
Asn	Leu	Thr	Thr	Ala	Leu	Pro	Pro	Val	Val	Ser	Asn	Pro	Ile	Tyr	Asp		
162					167					172					177		
aac	cgt	gct	cca	aat	act	gca	gaa	tta	agg	att	tgt	cgt	gta	aac	aag	753	
Asn	Arg	Ala	Pro	Asn	Thr	Ala	Glu	Leu	Arg	Ile	Cys	Arg	Val	Asn	Lys		
178					183					188					193		
aat	tgt	gga	agt	gtc	aga	gga	gga	gat	gaa	ata	ttt	cta	ctt	tgt	gac	801	
Asn	Cys	Gly	Ser	Val	Arg	Gly	Gly	Asp	Glu	Ile	Phe	Leu	Leu	Cys	Asp		
194					199					204					209		
aaa	gtt	cag	aaa	gat	gac	ata	gaa	gtt	cgt	ttt	gtg	ttg	aac	gat	tgg	849	
Lys	Val	Gln	Lys	Asp	Asp	Ile	Glu	Val	Arg	Phe	Val	Leu	Asn	Asp	Trp		
210					215					220					225		
gaa	gca	aaa	ggc	atc	ttt	tca	caa	gct	gat	gta	cac	cgt	caa	gta	gcc	897	
Glu	Ala	Lys	Gly	Ile	Phe	Ser	Gln	Ala	Asp	Val	His	Arg	Gln	Val	Ala		

226	231	236	241	
att gtt ttc aaa act cca cca tat tgc aaa gct atc aca gaa ccc gta				945
Ile Val Phe Lys Thr Pro Pro Tyr Cys Lys Ala Ile Thr Glu Pro Val				
242	247	252	257	
aca gta aaa atg cag ttg cgg aga cct tct gac cag gaa gtt agt gaa				993
Thr Val Lys Met Gln Leu Arg Arg Pro Ser Asp Gln Glu Val Ser Glu				
258	263	268	273	
tct atg gat ttt aga tat ctg cca gat gaa aaa gat act tac ggc aat				1041
Ser Met Asp Phe Arg Tyr Leu Pro Asp Glu Lys Asp Thr Tyr Gly Asn				
274	279	284	289	
aaa gca aag aaa caa aag aca act ctg ctt ttc cag aaa ctg tgc cag				1089
Lys Ala Lys Lys Gln Lys Thr Thr Leu Leu Phe Gln Lys Leu Cys Gln				
290	295	300	305	
gat cac gtt aat ttt cct gag aga cca aga cct ggt ctc ctc ggt tca				1137
Asp His Val Asn Phe Pro Glu Arg Pro Arg Pro Gly Leu Leu Gly Ser				
306	311	316	321	
att gga gaa gga aga tac ttc aaa aaa gaa cca aac ttg ttt tct cat				1185
Ile Gly Glu Gly Arg Tyr Phe Lys Lys Glu Pro Asn Leu Phe Ser His				
322	327	332	337	
gat gca gtt gtg aga gaa atg cct aca ggg gtt tca agt caa gca gaa				1233
Asp Ala Val Val Arg Glu Met Pro Thr Gly Val Ser Ser Gln Ala Glu				
338	343	348	353	
tcc tac tat ccc tca cct ggg ccc atc tca agt gga ttg tca cat cat				1281
Ser Tyr Tyr Pro Ser Pro Gly Pro Ile Ser Ser Gly Leu Ser His His				
354	359	364	369	
gcc tca atg gca cct ctg cct tct tca agc tgg tca tca gtg gcc cac				1329
Ala Ser Met Ala Pro Leu Pro Ser Ser Ser Trp Ser Ser Val Ala His				
370	375	380	385	
ccc acc cca cgc tca ggc aat aca aac cca ctg agt agt ttt tca aca				1377
Pro Thr Pro Arg Ser Gly Asn Thr Asn Pro Leu Ser Ser Phe Ser Thr				
386	391	396	401	
agg aca ctt cct tct aat tgc caa ggt atc cca cca ttc ctg aga ata				1425
Arg Thr Leu Pro Ser Asn Ser Gln Gly Ile Pro Pro Phe Leu Arg Ile				
402	407	412	417	
cct gtt ggg aat gat tta aat gct tct aat gct tgc att tac aac aat				1473
Pro Val Gly Asn Asp Leu Asn Ala Ser Asn Ala Cys Ile Tyr Asn Asn				
418	423	428	433	
gcc gat gac ata gtc gga atg gaa gcg tca tcc atg cca tca gca gat				1521
Ala Asp Asp Ile Val Gly Met Glu Ala Ser Ser Met Pro Ser Ala Asp				
434	439	444	449	
tta tat ggt att tct gat ccc aac atg ctg tct aat tgt tct gtg aat				1569
Leu Tyr Gly Ile Ser Asp Pro Asn Met Leu Ser Asn Cys Ser Val Asn				
450	455	460	465	

atg atg aca acc agc agt gac agc atg gga gag act gat aat cca aga	1617
Met Met Thr Thr Ser Ser Asp Ser Met Gly Glu Thr Asp Asn Pro Arg	
466 471 476 481	
ctt ctg agc atg aat ctt gaa aac ccc tca tgt aat tca gtg tta gac	1665
Leu Leu Ser Met Asn Leu Glu Asn Pro Ser Cys Asn Ser Val Leu Asp	
482 487 492 497	
cca aga gac ttg aga cag ctc cat cag atg tcc tct tcc agt atg tca	1713
Pro Arg Asp Leu Arg Gln Leu His Gln Met Ser Ser Ser Ser Met Ser	
498 503 508 513	
gca ggc gcc aat tcc aat act act gtt ttt gtt tca caa tca gat gca	1761
Ala Gly Ala Asn Ser Asn Thr Thr Val Phe Val Ser Gln Ser Asp Ala	
514 519 524 529	
ttt gag gga tct gac ttc agt tgt gca gat aac agc atg ata aat gag	1809
Phe Glu Gly Ser Asp Phe Ser Cys Ala Asp Asn Ser Met Ile Asn Glu	
530 535 540 545	
tcg gga cca tca aac agt act aat cca aac agt cat ggt ttt gtt caa	1857
Ser Gly Pro Ser Asn Ser Thr Asn Pro Asn Ser His Gly Phe Val Gln	
546 551 556 561	
gat agt cag tat tca ggt att ggc agt atg caa aat gag caa ttg agt	1905
Asp Ser Gln Tyr Ser Gly Ile Gly Ser Met Gln Asn Glu Gln Leu Ser	
562 567 572 577	
gac tcc ttt cca tat gaa ttt ttt caa gta taa cttgcaag atttaaattcc	1956
Asp Ser Phe Pro Tyr Glu Phe Phe Gln Val *	
578 583 588	
ttttaaatct tgataaccacc tatatagatg cagcattttg tatttgtcta actggggata	2016
taataactata tttatactgt atatataata ctgactgaga atataatact gtatttgaga	2076
atataaaaaa cttttttcag ggaagaagca tacaactttg gacatagcga atacaaaatt	2136
ggaagctgtc ataaaaagac aactcagagg ccaggcgcag gggctcacac ctgtaatcct	2196
agcacttttg gaggccaaagg cgggtggatc acttgagacc aggaattcga gaccagcctg	2256
gccaacatgg tgaaaccccg tctctactaa aaatacaaaa attagctgag catggtggta	2316
cgtgcctgta ctgtcagcta cttgggaggc tgaggcacaa taattgtttg aaccaggaa	2376
gcagaggttg cagtgaactg agatcacacc accgcactcc agcctgggtg acagagtga	2436
actctgtctc aaaaaaaaaa a	2457

<210> 224
 <211> 2335
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (105)..(1853)

<400> 224

```
gcacgagctc aaccgagttg tcgtgttgcc ctcgcttctc agatccccgc cggaagtgaa      60
gagagcaagc agatttgaac ctatctgctt tcaagctggg catc atg atg aaa ctt      116
                                     Met Met Lys Leu
                                     1
aga cac aaa aat aaa aag cca ggt gaa ggt tcc aag ggc cac aag aag      164
Arg His Lys Asn Lys Lys Pro Gly Glu Gly Ser Lys Gly His Lys Lys
  5                      10                      15                      20
ata agt tgg ccc tac cct cag cct gca aag caa aat ggg aag aaa gca      212
Ile Ser Trp Pro Tyr Pro Gln Pro Ala Lys Gln Asn Gly Lys Lys Ala
  21                      26                      31                      36
acc tcc aaa gtg ccc tct gca cct cat ttt gtt cac ccc aat gat cat      260
Thr Ser Lys Val Pro Ser Ala Pro His Phe Val His Pro Asn Asp His
  37                      42                      47                      52
gcc aat cga gag gct gaa tta aag aag aag tgg gtt gag gag atg agg      308
Ala Asn Arg Glu Ala Glu Leu Lys Lys Lys Trp Val Glu Glu Met Arg
  53                      58                      63                      68
gag aag cag caa gcc gcc cgg gag caa gaa aga caa aaa cgc agg acc      356
Glu Lys Gln Gln Ala Ala Arg Glu Gln Glu Arg Gln Lys Arg Arg Thr
  69                      74                      79                      84
att gag agc tac tgt cag gat gtc cta aga cgc cag gag gag ttt gag      404
Ile Glu Ser Tyr Cys Gln Asp Val Leu Arg Arg Gln Glu Glu Phe Glu
  85                      90                      95                      100
cat aag gag gaa gtt ttg cag gaa tta aat atg ttt cct cag ctg gat      452
His Lys Glu Glu Val Leu Gln Glu Leu Asn Met Phe Pro Gln Leu Asp
  101                      106                      111                      116
gac gag gcc acg agg aag gct tat tac aag gag ttc cgt aag gtg gtg      500
Asp Glu Ala Thr Arg Lys Ala Tyr Tyr Lys Glu Phe Arg Lys Val Val
  117                      122                      127                      132
gaa tac tct gat gtg att ctg gaa gtc ctg gat gcc aga gac cca tta      548
Glu Tyr Ser Asp Val Ile Leu Glu Val Leu Asp Ala Arg Asp Pro Leu
  133                      138                      143                      148
ggc tgc cgc tgc ttc caa atg gag gag gct gtc ctg cga gca caa ggc      596
Gly Cys Arg Cys Phe Gln Met Glu Glu Ala Val Leu Arg Ala Gln Gly
  149                      154                      159                      164
aac aag aag ctg gtc ctg gtc ttg aac aag att gac ctg gtc ccc aag      644
Asn Lys Lys Leu Val Leu Val Leu Asn Lys Ile Asp Leu Val Pro Lys
  165                      170                      175                      180
```

gag gtt gtg gag aaa tgg ctg gat tac ctt cgg aat gag ttg cca acc	692
Glu Val Val Glu Lys Trp Leu Asp Tyr Leu Arg Asn Glu Leu Pro Thr	
181 186 191 196	
gtg gct ttc aag gcc agt acc cag cat cag gtc aaa aac ctg aat cgt	740
Val Ala Phe Lys Ala Ser Thr Gln His Gln Val Lys Asn Leu Asn Arg	
197 202 207 212	
tgc agt gtg cca gta gat cag gcc tct gag tca ctg ctg aaa agc aaa	788
Cys Ser Val Pro Val Asp Gln Ala Ser Glu Ser Leu Leu Lys Ser Lys	
213 218 223 228	
gcc tgc ttt gga gct gaa aac ctc atg agg gtt ctg ggg aac tat tgc	836
Ala Cys Phe Gly Ala Glu Asn Leu Met Arg Val Leu Gly Asn Tyr Cys	
229 234 239 244	
cgc ctt ggt gaa gtg cgc acc cac att cgt gtg ggt gtt gtg ggt ctt	884
Arg Leu Gly Glu Val Arg Thr His Ile Arg Val Gly Val Val Gly Leu	
245 250 255 260	
ccc aat gtt ggg aag agc agc ctg atc aat agc ctg aag cgc agc cgc	932
Pro Asn Val Gly Lys Ser Ser Leu Ile Asn Ser Leu Lys Arg Ser Arg	
261 266 271 276	
gca tgc agc gtg gga gct gtt cct gga att acc aaa ttc atg cag gag	980
Ala Cys Ser Val Gly Ala Val Pro Gly Ile Thr Lys Phe Met Gln Glu	
277 282 287 292	
gtc tac ctg gac aag ttc atc cgg ctc ttg gat gct cca ggc att gtc	1028
Val Tyr Leu Asp Lys Phe Ile Arg Leu Leu Asp Ala Pro Gly Ile Val	
293 298 303 308	
cca ggg ccc aac tca gag gtg ggc acc atc ctg cgt aac tgc gtc cac	1076
Pro Gly Pro Asn Ser Glu Val Gly Thr Ile Leu Arg Asn Cys Val His	
309 314 319 324	
gtg cag aag ctg gca gac cct gtg acc cca gtg gag acc atc ctg cag	1124
Val Gln Lys Leu Ala Asp Pro Val Thr Pro Val Glu Thr Ile Leu Gln	
325 330 335 340	
cgc tgc aac ctg gag gag att tcc aac tat tat ggc gtc tct ggg ttc	1172
Arg Cys Asn Leu Glu Glu Ile Ser Asn Tyr Tyr Gly Val Ser Gly Phe	
341 346 351 356	
cag acc act gag cac ttt ctg acg gca gtg gcc cac cgt ttg ggg aag	1220
Gln Thr Thr Glu His Phe Leu Thr Ala Val Ala His Arg Leu Gly Lys	
357 362 367 372	
aag aag aag gga ggc tta tat agt cag gaa cag gcg gcc aaa gct gtc	1268
Lys Lys Lys Gly Gly Leu Tyr Ser Gln Glu Gln Ala Ala Lys Ala Val	
373 378 383 388	
cta gct gac tgg gtg agc ggg aag atc agc ttc tat ata cca cca cca	1316
Leu Ala Asp Trp Val Ser Gly Lys Ile Ser Phe Tyr Ile Pro Pro Pro	
389 394 399 404	
gcc act cac act ctg ccc acc cat ctc agt gct gag atc gtt aag gaa	1364

Ala Thr His Thr Leu Pro Thr His Leu Ser Ala Glu Ile Val Lys Glu	
405 410 415 420	
atg acc gag gtc ttt gac atc gag gat act gag cag gcc aat gaa gac	1412
Met Thr Glu Val Phe Asp Ile Glu Asp Thr Glu Gln Ala Asn Glu Asp	
421 426 431 436	
acc atg gaa tgc ttg gcc acc gga gaa tct gat gag ctg ttg ggt gac	1460
Thr Met Glu Cys Leu Ala Thr Gly Glu Ser Asp Glu Leu Leu Gly Asp	
437 442 447 452	
acg gac cca ctt gaa atg gag atc aag ttg ctc cat tct ccg atg acg	1508
Thr Asp Pro Leu Glu Met Glu Ile Lys Leu Leu His Ser Pro Met Thr	
453 458 463 468	
aaa ata gca gat gcc att gaa aat aaa acc acc gtg tat aag att gga	1556
Lys Ile Ala Asp Ala Ile Glu Asn Lys Thr Thr Val Tyr Lys Ile Gly	
469 474 479 484	
gat ctc act ggg tat tgc acc aat ccg aac cgt cat cag atg ggg tgg	1604
Asp Leu Thr Gly Tyr Cys Thr Asn Pro Asn Arg His Gln Met Gly Trp	
485 490 495 500	
gct aaa cgc aat gtg gac cac cgc cct aag agc aac agt atg gtg gat	1652
Ala Lys Arg Asn Val Asp His Arg Pro Lys Ser Asn Ser Met Val Asp	
501 506 511 516	
gtc tgc tca gtg gac cgc cgc tca gtg ctg cag agg atc atg gag acg	1700
Val Cys Ser Val Asp Arg Arg Ser Val Leu Gln Arg Ile Met Glu Thr	
517 522 527 532	
gac ccc ctg caa cag ggc cag gct ctg gca tct gcc ctg aaa aat aag	1748
Asp Pro Leu Gln Gln Gly Gln Ala Leu Ala Ser Ala Leu Lys Asn Lys	
533 538 543 548	
aag aag atg cag aaa cgt gca gat aaa atc gcc agc aag ctg tct gat	1796
Lys Lys Met Gln Lys Arg Ala Asp Lys Ile Ala Ser Lys Leu Ser Asp	
549 554 559 564	
tcc atg atg tct gct ctc gac ctc tct ggc aat gct gat gat ggt gtt	1844
Ser Met Met Ser Ala Leu Asp Leu Ser Gly Asn Ala Asp Asp Gly Val	
565 570 575 580	
ggt gac taa tcgactg atctcaacttc ccttcgcgtc caagcaccag ttccggtggt	1900
Gly Asp *	
581	
acgggggaat accagtgaaa tagtttggtt ctccctgaag catctgcata ttgaaagaac	1960
gctttcccca ctgtgtgtct tctccccctc ctccagtaaa aacagtcccg gctgggtgct	2020
gtggctcacg totgtaatcc cagcactttg ggaggccgag gtgggcggat cacctgaggt	2080
cgaggagttcg agaccagcct ggccaacatg gtgaaacccc gtctctacta aaaatacaaa	2140
aaaatttagc cgtgcttagt ggcacctata gtcccagcta cttgggaggc tgaggcagga	2200

aaa gtc aaa aca act agg gta acc cat taa c ccaggagaaa tcaagtgatc 617
 Lys Val Lys Thr Thr Arg Val Thr His *
 123 128

ctcaaggctg atgacattga acatgcgcat agaaacttaa ctcaactcct gaggtgatct 677
 tgaagatttt tataaccactt gaaagaggcg ctcaatagt 716

<210> 226
 <211> 6396
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (160)..(4983)

<400> 226

cccgcgaattc ccgggtcgac gattatctgg gcacccggca gccacagcgc agcgagagcg 60
 gacggtcgcc atggttcctt cccagccag tcccaggcgc ccggtgcact atgcggggca 120
 cgtgcgcccc ccagctctaa tctgcgcgct gacaggagc atg atc tgt gcc cag 174
 Met Ile Cys Ala Gln
 1

gcc agg gct ggc aag aat ctg tac cag aac agg ttt tta ggc ctg gcc 222
 Ala Arg Ala Gly Lys Asn Leu Tyr Gln Asn Arg Phe Leu Gly Leu Ala
 6 11 16 21

gcc atg gcg ttt cct tct aga aac tcc cag agc cta cgc cgg tgc aag 270
 Ala Met Ala Phe Pro Ser Arg Asn Ser Gln Ser Leu Arg Arg Cys Lys
 22 27 32 37

gag ccg atc cga tac agc tac aac ccc gac cag ttc cac aac atg gac 318
 Glu Pro Ile Arg Tyr Ser Tyr Asn Pro Asp Gln Phe His Asn Met Asp
 38 43 48 53

ctc agg ggc ggc ccc cac gat ggc gtc acc att ccc cgc tcc acc agc 366
 Leu Arg Gly Gly Pro His Asp Gly Val Thr Ile Pro Arg Ser Thr Ser
 54 59 64 69

gac act gac ctg gtc acc tcg gac agc cgc tcc acg ctc atg gtc agc 414
 Asp Thr Asp Leu Val Thr Ser Asp Ser Arg Ser Thr Leu Met Val Ser
 70 75 80 85

agc tcc tac tat tcc atc ggg cac tct cag gac ctg gtc atc cac tgg 462
 Ser Ser Tyr Tyr Ser Ile Gly His Ser Gln Asp Leu Val Ile His Trp
 86 91 96 101

gac ata aag gag gaa gtg gac gct ggg gac tgg att ggc atg tac ctc 510
 Asp Ile Lys Glu Glu Val Asp Ala Gly Asp Trp Ile Gly Met Tyr Leu
 102 107 112 117

att gat gag gtc ttg tcc gaa aac ttt ctg gac tat aaa aac cgt gga	558
Ile Asp Glu Val Leu Ser Glu Asn Phe Leu Asp Tyr Lys Asn Arg Gly	
118 123 128 133	
gtc aat ggt tct cat cgg ggc cag atc atc tgg aag atc gat gcc agc	606
Val Asn Gly Ser His Arg Gly Gln Ile Ile Trp Lys Ile Asp Ala Ser	
134 139 144 149	
tcg tac ttt gtg gaa cct gaa act aag atc tgc ttc aaa tac tac cat	654
Ser Tyr Phe Val Glu Pro Glu Thr Lys Ile Cys Phe Lys Tyr Tyr His	
150 155 160 165	
gga gtg agt ggg gcc ctg cga gca acc acc ccc agt gtc acg gtc aaa	702
Gly Val Ser Gly Ala Leu Arg Ala Thr Thr Pro Ser Val Thr Val Lys	
166 171 176 181	
aac tcg gca gct cct att ttt aaa agc att ggt gct gat gag acc gtc	750
Asn Ser Ala Ala Pro Ile Phe Lys Ser Ile Gly Ala Asp Glu Thr Val	
182 187 192 197	
caa gga caa gga agt cgg agg ctg atc agc ttc tct ctc tca gat ttc	798
Gln Gly Gln Gly Ser Arg Arg Leu Ile Ser Phe Ser Leu Ser Asp Phe	
198 203 208 213	
caa gcc atg ggg ttg aag aaa ggg atg ttt ttc aac cca gac cct tat	846
Gln Ala Met Gly Leu Lys Lys Gly Met Phe Phe Asn Pro Asp Pro Tyr	
214 219 224 229	
ctg aag att tcc att cag cct ggg aaa cac agc atc ttc ccc gcc ctc	894
Leu Lys Ile Ser Ile Gln Pro Gly Lys His Ser Ile Phe Pro Ala Leu	
230 235 240 245	
cct cac cat gga cag gag agg aga tcc aag atc ata ggc aac acc gtg	942
Pro His His Gly Gln Glu Arg Arg Ser Lys Ile Ile Gly Asn Thr Val	
246 251 256 261	
aac ccc atc tgg cag gcc gag caa ttc agt ttt gtg tcc ttg ccc act	990
Asn Pro Ile Trp Gln Ala Glu Gln Phe Ser Phe Val Ser Leu Pro Thr	
262 267 272 277	
gac gtg ctg gaa att gag gtg aag gac aag ttt gcc aag agc cgc ccc	1038
Asp Val Leu Glu Ile Glu Val Lys Asp Lys Phe Ala Lys Ser Arg Pro	
278 283 288 293	
atc atc aag cgc ttc ttg gga aag ctg tcg atg ccc gtt caa aga ctc	1086
Ile Ile Lys Arg Phe Leu Gly Lys Leu Ser Met Pro Val Gln Arg Leu	
294 299 304 309	
ctg gag aga cac gcc ata ggg gat agg gtg gtc agc tac aca ctt ggc	1134
Leu Glu Arg His Ala Ile Gly Asp Arg Val Val Ser Tyr Thr Leu Gly	
310 315 320 325	
cgc agg ctt cca aca gat cat gtg agt gga cag ctg caa ttc cga ttt	1182
Arg Arg Leu Pro Thr Asp His Val Ser Gly Gln Leu Gln Phe Arg Phe	
326 331 336 341	
gag atc act tcc tcc atc cac cca gat gat gag gag att tcc ctg agt	1230

Glu Ile Thr Ser Ser Ile His Pro Asp Asp Glu Glu Ile Ser Leu Ser	
342 347 352 357	
acc gag cct gag tca gcc caa att cag gac agc ccc atg aac aac ctg	1278
Thr Glu (Pro Glu Ser Ala Gln Ile Gln Asp Ser Pro Met Asn Asn Leu	
358 363 368 373	
atg gaa agc ggc agt ggg gaa cct cgg tct gag gca cca gag tcc tct	1326
Met Glu Ser Gly Ser Gly Glu Pro Arg Ser Glu Ala Pro Glu Ser Ser	
374 379 384 389	
gag agc tgg aag cca gag cag ctg ggt gag ggc agt gtc ccc gat cgt	1374
Glu Ser Trp Lys Pro Glu Gln Leu Gly Glu Gly Ser Val Pro Asp Arg	
390 395 400 405	
cca ggg aac caa agc ata gag ctt tcc aga cca gct gag gaa gca gca	1422
Pro Gly Asn Gln Ser Ile Glu Leu Ser Arg Pro Ala Glu Glu Ala Ala	
406 411 416 421	
gtc atc acg gag gca gga gac cag ggc atg gtc tct gtg gga cct gaa	1470
Val Ile Thr Glu Ala Gly Asp Gln Gly Met Val Ser Val Gly Pro Glu	
422 427 432 437	
ggg gct ggg gag ctc ctg gcc cag gtg caa aag gac atc cag cct gcc	1518
Gly Ala Gly Glu Leu Leu Ala Gln Val Gln Lys Asp Ile Gln Pro Ala	
438 443 448 453	
ccc agt gca gaa gag ctg gcc gag cag ctg gac ctg ggt gag gag gca	1566
Pro Ser Ala Glu Glu Leu Ala Glu Gln Leu Asp Leu Gly Glu Glu Ala	
454 459 464 469	
tca gca ctg ctg ctg gaa gac ggt gaa gcc cca gcc agc acc aag gag	1614
Ser Ala Leu Leu Leu Glu Asp Gly Glu Ala Pro Ala Ser Thr Lys Glu	
470 475 480 485	
gag ccc ttg gag gag gaa gca acg acc cag agc cgg gct gga agg gaa	1662
Glu Pro Leu Glu Glu Glu Ala Thr Thr Gln Ser Arg Ala Gly Arg Glu	
486 491 496 501	
gaa gag gag aag gag cag gag gag gag gga gat gtg tcc acc ctg gag	1710
Glu Glu Glu Lys Glu Gln Glu Glu Glu Gly Asp Val Ser Thr Leu Glu	
502 507 512 517	
cag gga gag ggc agg ctg cag ctg cgg gcc tcg gtg aag aga aaa agc	1758
Gln Gly Glu Gly Arg Leu Gln Leu Arg Ala Ser Val Lys Arg Lys Ser	
518 523 528 533	
agg ccc tgc tcc ttg cct gtg tcc gag ctg gag acg gtg atc gcg tca	1806
Arg Pro Cys Ser Leu Pro Val Ser Glu Leu Glu Thr Val Ile Ala Ser	
534 539 544 549	
gcc tgc ggg gac ccc gag acc ccg cgg aca cac tac atc cgc atc cac	1854
Ala Cys Gly Asp Pro Glu Thr Pro Arg Thr His Tyr Ile Arg Ile His	
550 555 560 565	
acc ctg ctg cac agc atg ccc tcc gcc cag ggc ggc agc gcg gca gag	1902
Thr Leu Leu His Ser Met Pro Ser Ala Gln Gly Gly Ser Ala Ala Glu	

566	571	576	581	
gag gag gac ggc gcg gag gag gag tcc acc ctc aag gac tcc tcg gag				1950
Glu Glu Asp Gly Ala Glu Glu Glu Ser Thr Leu Lys Asp Ser Ser Glu				
582	587	592	597	
aag gat ggg ctc agc gag gtg gac acg gtg gcc gct gac ccg tct gcc				1998
Lys Asp Gly Leu Ser Glu Val Asp Thr Val Ala Ala Asp Pro Ser Ala				
598	603	608	613	
ctg gaa gag gac aga gaa gag ccc gag ggg gct act cca ggc acg gcg				2046
Leu Glu Glu Asp Arg Glu Glu Pro Glu Gly Ala Thr Pro Gly Thr Ala				
614	619	624	629	
cac cct ggc cac tcc ggg ggc cac ttc ccc agc ctg gcc aat ggc gcg				2094
His Pro Gly His Ser Gly Gly His Phe Pro Ser Leu Ala Asn Gly Ala				
630	635	640	645	
gcc cag gat ggc gac acg cac ccc agc acc ggg agc gag agc gac tcc				2142
Ala Gln Asp Gly Asp Thr His Pro Ser Thr Gly Ser Glu Ser Asp Ser				
646	651	656	661	
agc ccc agg caa ggc ggg gac cac agt tgc gag ggc tgt gac gcg tcc				2190
Ser Pro Arg Gln Gly Gly Asp His Ser Cys Glu Gly Cys Asp Ala Ser				
662	667	672	677	
tgc tgc agc ccc tcg tgc tac agc tcc tcg tgc tac agc acg tcc tgc				2238
Cys Cys Ser Pro Ser Cys Tyr Ser Ser Ser Cys Tyr Ser Thr Ser Cys				
678	683	688	693	
tac agc agc tcg tgc tac agc gcc tcg tgc tac agc ccc tcc tgc tac				2286
Tyr Ser Ser Ser Cys Tyr Ser Ala Ser Cys Tyr Ser Pro Ser Cys Tyr				
694	699	704	709	
aac ggc aac agg ttc gcc agc cac acg cgc ttc tcc tcc gtg gac agc				2334
Asn Gly Asn Arg Phe Ala Ser His Thr Arg Phe Ser Ser Val Asp Ser				
710	715	720	725	
gcc aag atc tcc gag agc acg gtc ttc tcc tcg caa gac gac gag gag				2382
Ala Lys Ile Ser Glu Ser Thr Val Phe Ser Ser Gln Asp Asp Glu Glu				
726	731	736	741	
gag gag aac agc gcg ttc gag tcg gta ccc gac tcc atg cag agc cct				2430
Glu Glu Asn Ser Ala Phe Glu Ser Val Pro Asp Ser Met Gln Ser Pro				
742	747	752	757	
gag ctg gac ccg gag tcc acg aac ggc gct ggg ccg tgg caa gac gag				2478
Glu Leu Asp Pro Glu Ser Thr Asn Gly Ala Gly Pro Trp Gln Asp Glu				
758	763	768	773	
ctg gcc gcc cct agc ggg cac gtg gaa aga agc ccg gaa ggt ctg gaa				2526
Leu Ala Ala Pro Ser Gly His Val Glu Arg Ser Pro Glu Gly Leu Glu				
774	779	784	789	
tcc ccc gtg gca ggt cca agc aat cgg aga gaa ggt gaa tgt cct ata				2574
Ser Pro Val Ala Gly Pro Ser Asn Arg Arg Glu Gly Glu Cys Pro Ile				
790	795	800	805	

ctc cat aat tcc cag cca gta agc cag ctt cct tcc ctg agg cct gaa	2622
Leu His Asn Ser Gln Pro Val Ser Gln Leu Pro Ser Leu Arg Pro Glu	
806 811 816 821	
cat cat cac tac cca aca atc gat gag cct ctt cca cca aac tgg gaa	2670
His His His Tyr Pro Thr Ile Asp Glu Pro Leu Pro Pro Asn Trp Glu	
822 827 832 837	
gct cga att gac agc cac ggg cgg gtc ttt tat gtg gac cac gtg aac	2718
Ala Arg Ile Asp Ser His Gly Arg Val Phe Tyr Val Asp His Val Asn	
838 843 848 853	
cgc aca acc acc tgg cag cgt ccg acg gca gca gcc acc ccg gat ggc	2766
Arg Thr Thr Thr Trp Gln Arg Pro Thr Ala Ala Ala Thr Pro Asp Gly	
854 859 864 869	
atg cgg aga tcg ggg tcc atc cag cag atg gag caa ctc aac agg cgg	2814
Met Arg Arg Ser Gly Ser Ile Gln Gln Met Glu Gln Leu Asn Arg Arg	
870 875 880 885	
tat caa aac att cag cga acc att gca aca gag agg tcc gaa gaa gat	2862
Tyr Gln Asn Ile Gln Arg Thr Ile Ala Thr Glu Arg Ser Glu Glu Asp	
886 891 896 901	
tct ggc agc caa agc tgc gag caa gcc cca gca gga gga ggc gga ggt	2910
Ser Gly Ser Gln Ser Cys Glu Gln Ala Pro Ala Gly Gly Gly Gly Gly	
902 907 912 917	
gga ggg agt gac tca gaa gcc gaa tct tcc cag tcc agc tta gat cta	2958
Gly Gly Ser Asp Ser Glu Ala Glu Ser Ser Gln Ser Ser Leu Asp Leu	
918 923 928 933	
agg aga gag ggg tca ctt tct cca gtg aac tca caa aaa atc acc ttg	3006
Arg Arg Glu Gly Ser Leu Ser Pro Val Asn Ser Gln Lys Ile Thr Leu	
934 939 944 949	
ctg ctg cag tcc cca gcg gtc aag ttc atc acc aac ccc gag ttc ttc	3054
Leu Leu Gln Ser Pro Ala Val Lys Phe Ile Thr Asn Pro Glu Phe Phe	
950 955 960 965	
act gtg cta cat gcc aat tat agt gcc tac cga gtc ttc acc agt agc	3102
Thr Val Leu His Ala Asn Tyr Ser Ala Tyr Arg Val Phe Thr Ser Ser	
966 971 976 981	
acc tgc tta aag cac atg att ctg aaa gtc cga cgg gat gct cgc aat	3150
Thr Cys Leu Lys His Met Ile Leu Lys Val Arg Arg Asp Ala Arg Asn	
982 987 992 997	
ttt gaa cgc tac cag cac aac cgg gac ttg gtg aat ttc atc aac atg	3198
Phe Glu Arg Tyr Gln His Asn Arg Asp Leu Val Asn Phe Ile Asn Met	
998 1003 1008 1013	
ttc gca gac act cgg ctg gaa ctg ccc cgg ggc tgg gag atc aaa acg	3246
Phe Ala Asp Thr Arg Leu Glu Leu Pro Arg Gly Trp Glu Ile Lys Thr	
1014 1019 1024 1029	

gac cag cag gga aag tct ttt ttc gtg gac cac aac agt cga gct acc	3294
Asp Gln Gln Gly Lys Ser Phe Phe Val Asp His Asn Ser Arg Ala Thr	
1030 1035 1040 1045	
act ttc att gac ccc cga atc cct ctt cag aac ggt cgt ctt ccc aat	3342
Thr Phe Ile Asp Pro Arg Ile Pro Leu Gln Asn Gly Arg Leu Pro Asn	
1046 1051 1056 1061	
cat cta act cac cga cag cac ctc cag agg ctc cga agt tac agc gct	3390
His Leu Thr His Arg Gln His Leu Gln Arg Leu Arg Ser Tyr Ser Ala	
1062 1067 1072 1077	
gga gag gcc tca gaa gtt tct aga aac aga gga gcc tct tta ctg gcc	3438
Gly Glu Ala Ser Glu Val Ser Arg Asn Arg Gly Ala Ser Leu Leu Ala	
1078 1083 1088 1093	
agg cca gga cac agc tta gta gct gct att cga agc caa cat caa cat	3486
Arg Pro Gly His Ser Leu Val Ala Ala Ile Arg Ser Gln His Gln His	
1094 1099 1104 1109	
gag tca ttg cca ctg gca tat aat gac aag att gtg gca ttt ctt cgc	3534
Glu Ser Leu Pro Leu Ala Tyr Asn Asp Lys Ile Val Ala Phe Leu Arg	
1110 1115 1120 1125	
cag cca aac att ttt gaa atg ctg caa gag cgt cag cca agc tta gca	3582
Gln Pro Asn Ile Phe Glu Met Leu Gln Glu Arg Gln Pro Ser Leu Ala	
1126 1131 1136 1141	
aga aac cac aca ctc agg gag aaa atc cat tac att cgg act gag ggt	3630
Arg Asn His Thr Leu Arg Glu Lys Ile His Tyr Ile Arg Thr Glu Gly	
1142 1147 1152 1157	
aat cac ggg ctt gag aag ttg tcc tgt gat gcg gat ctg gtc att ttg	3678
Asn His Gly Leu Glu Lys Leu Ser Cys Asp Ala Asp Leu Val Ile Leu	
1158 1163 1168 1173	
ctg agt ctc ttt gaa gaa gag att atg tcc tac gtc ccc ctg cag gct	3726
Leu Ser Leu Phe Glu Glu Glu Ile Met Ser Tyr Val Pro Leu Gln Ala	
1174 1179 1184 1189	
gcc ttc cac cct ggg tat agc ttc tct ccc cgc tgt tca ccc tgt tct	3774
Ala Phe His Pro Gly Tyr Ser Phe Ser Pro Arg Cys Ser Pro Cys Ser	
1190 1195 1200 1205	
tca cct cag aac tcc cca ggt tta cag aga gcc agt gca aga gcc cct	3822
Ser Pro Gln Asn Ser Pro Gly Leu Gln Arg Ala Ser Ala Arg Ala Pro	
1206 1211 1216 1221	
tcc ccc tac cga aga gac ttt gag gcc aag ctc cgc aat ttc tac aga	3870
Ser Pro Tyr Arg Arg Asp Phe Glu Ala Lys Leu Arg Asn Phe Tyr Arg	
1222 1227 1232 1237	
aaa ctg gaa gcc aaa gga ttt ggt cag ggt ccg ggg aaa att aag ctc	3918
Lys Leu Glu Ala Lys Gly Phe Gly Gln Gly Pro Gly Lys Ile Lys Leu	
1238 1243 1248 1253	
att att cgc cgg gat cat ttg ttg gag gga acc ttc aat cag gtg atg	3966

Ile Ile Arg Arg Asp His Leu Leu Glu Gly Thr Phe Asn Gln Val Met	
1254 1259 1264 1269	
gcc tat tcg cgg aaa gag ctc cag cga aac aag ctc tac gtc acc ttt	4014
Ala Tyr Ser Arg Lys Glu Leu Gln Arg Asn Lys Leu Tyr Val Thr Phe	
1270 1275 1280 1285	
gtt gga gag gag ggc ctg gac tac agt ggc ccc tcg cgg gag ttc ttc	4062
Val Gly Glu Glu Gly Leu Asp Tyr Ser Gly Pro Ser Arg Glu Phe Phe	
1286 1291 1296 1301	
ttc ctt ctg tct cag gag ctc ttc aac cct tac tat gga ctc ttt gag	4110
Phe Leu Leu Ser Gln Glu Leu Phe Asn Pro Tyr Tyr Gly Leu Phe Glu	
1302 1307 1312 1317	
tac tcg gca aat gat act tac acg gtg cag atc agc ccc atg tcc gca	4158
Tyr Ser Ala Asn Asp Thr Tyr Thr Val Gln Ile Ser Pro Met Ser Ala	
1318 1323 1328 1333	
ttt gta gaa aac cat ctt gag tgg ttc agg ttt agc ggt cgc atc ctg	4206
Phe Val Glu Asn His Leu Glu Trp Phe Arg Phe Ser Gly Arg Ile Leu	
1334 1339 1344 1349	
ggt ctg gct ctg atc cat cag tac ctt ctt gac gct ttc ttc acg agg	4254
Gly Leu Ala Leu Ile His Gln Tyr Leu Leu Asp Ala Phe Phe Thr Arg	
1350 1355 1360 1365	
ccc ttc tac aag gca ctc ctg aga ctg ccc tgt gat ttg agt gac ctg	4302
Pro Phe Tyr Lys Ala Leu Leu Arg Leu Pro Cys Asp Leu Ser Asp Leu	
1366 1371 1376 1381	
gaa tat ttg gat gag gaa ttc cac cag agt ttg cag tgg atg aag gac	4350
Glu Tyr Leu Asp Glu Glu Phe His Gln Ser Leu Gln Trp Met Lys Asp	
1382 1387 1392 1397	
aac aac atc aca gac atc tta gac ctc act ttc act gtt aat gaa gag	4398
Asn Asn Ile Thr Asp Ile Leu Asp Leu Thr Phe Thr Val Asn Glu Glu	
1398 1403 1408 1413	
gtt ttt gga cag gtc acg gaa agg gag ttg aag tct gga gga gcc aac	4446
Val Phe Gly Gln Val Thr Glu Arg Glu Leu Lys Ser Gly Gly Ala Asn	
1414 1419 1424 1429	
aca cag gtg acg gag aaa aac aag aag gag tac atc gag cgc atg gtg	4494
Thr Gln Val Thr Glu Lys Asn Lys Lys Glu Tyr Ile Glu Arg Met Val	
1430 1435 1440 1445	
aag tgg cgg gtg gag cgc ggc gtg gta cag cag acc gag gcg ctg gtg	4542
Lys Trp Arg Val Glu Arg Gly Val Val Gln Gln Thr Glu Ala Leu Val	
1446 1451 1456 1461	
cgc ggc ttc tac gag gtt gta gac tcg agg ctg gtg tcc gtg ttt gat	4590
Arg Gly Phe Tyr Glu Val Val Asp Ser Arg Leu Val Ser Val Phe Asp	
1462 1467 1472 1477	
gcc agg gag ctg gag ctg gtg ata gct ggc acc gcg gaa atc gac cta	4638
Ala Arg Glu Leu Glu Leu Val Ile Ala Gly Thr Ala Glu Ile Asp Leu	

1478	1483	1488	1493	
aat gac tgg cgg aat aac act gag tac cgg gga ggt tac cac gat ggg				4686
Asn Asp Trp Arg Asn Asn Thr Glu Tyr Arg Gly Gly Tyr His Asp Gly				
1494	1499	1504	1509	
cat ctt gtg atc cgc tgg ttc tgg gct gcg gtg gag cgc ttc aat aat				4734
His Leu Val Ile Arg Trp Phe Trp Ala Ala Val Glu Arg Phe Asn Asn				
1510	1515	1520	1525	
gag cag agg ctg aga tta ctg cag ttt gtc acg gga aca tcc agc gtg				4782
Glu Gln Arg Leu Arg Leu Leu Gln Phe Val Thr Gly Thr Ser Ser Val				
1526	1531	1536	1541	
ccc tac gaa ggc ttc gca gcc ctc cgt ggg agc aat ggg ctt cgg cgc				4830
Pro Tyr Glu Gly Phe Ala Ala Leu Arg Gly Ser Asn Gly Leu Arg Arg				
1542	1547	1552	1557	
ttc tgc ata gag aaa tgg ggg aaa att act tct ctc ccc agg gca cac				4878
Phe Cys Ile Glu Lys Trp Gly Lys Ile Thr Ser Leu Pro Arg Ala His				
1558	1563	1568	1573	
aca tgc ttc aac cga ctg gat ctt cca ccg tat ccc tcg tac tcc atg				4926
Thr Cys Phe Asn Arg Leu Asp Leu Pro Pro Tyr Pro Ser Tyr Ser Met				
1574	1579	1584	1589	
ttg tat gaa aag ctg tta aca gca gta gag gaa acc agc acc ttt gga				4974
Leu Tyr Glu Lys Leu Leu Thr Ala Val Glu Glu Thr Ser Thr Phe Gly				
1590	1595	1600	1605	
ctt gag tga ggacatg gaacctcgcc tgacattttc ctggccagtg acatcaccc				5030
Leu Glu *				
1606				
tcctgggatg atccccctttt ccctttccct taatcaactc tcctttgatt ttggtattcc				5090
atgatttttta ttttcaaacc aaatcaggat tgacaaaagc tgtgcatgaa gaactgcctt				5150
cttctaagat ctaaccttca ggcttctctc ctctgttttc aatgaactgc tagcctgtat				5210
gcaatattaa aaaacagctg totcaaggctc tgtgtatata tccacatacc tccattacta				5270
acaatgaaat atgaatgcaa gttaagctac acttgaccaaa atggtaataa atgtttactt				5330
ccattttctat cattgaaggg aaaatgtgag cattaagcac tccaggcttt catatgcccc				5390
tgtcttctga gcagagccac catttttttat aatttctaata aaccaactcc agaactagga				5450
gctgatcaac tctttgtttt cctctccatc tacttttccc tgtgcataat atccatccaa				5510
aggacaacag tggcaaagct gaaattttta tacattcaac tcatgattca catgtggcat				5570
cagtcccatc agccggaact agcctagaca tacgggtgcaa atatgacact tctaacgatt				5630
aacaacagca agaaaacacc tgctgctgat gcaatgcaat gcatcccaat gggtgtgggg				5690
attgtgggct caactcaaga gaagtttagg agggggagca tccctagtga atactcacac				5750

Glu	Ala	Val	Leu	Arg	Thr	Leu	Arg	Asp	Thr	Pro	Met	Met	Val	His	Thr		
26					31					36					41		
ggc	ccc	tgc	tgc	tgc	tgc	ccc	tgc	tgt	cca	cgg	ctg	ctg	ctc	acc		555	
Gly	Pro	Cys	Cys	Cys	Cys	Pro	Cys	Cys	Pro	Arg	Leu	Leu	Leu	Thr			
42					47				52					57			
agg	aag	aag	ctt	cag	ctg	ctg	atg	ttg	ggc	cct	ttc	caa	tac	gcc	ttc	603	
Arg	Lys	Lys	Leu	Gln	Leu	Leu	Met	Leu	Gly	Pro	Phe	Gln	Tyr	Ala	Phe		
58					63				68					73			
ttg	aag	ata	acg	ctg	acc	ctg	gtg	ggc	ctg	ttt	ctc	atc	ccc	gac	ggc	651	
Leu	Lys	Ile	Thr	Leu	Thr	Leu	Val	Gly	Leu	Phe	Leu	Ile	Pro	Asp	Gly		
74					79				84					89			
atc	tat	gac	cca	gca	gac	att	tct	gag	ggg	agc	aca	gct	cta	tgg	atc	699	
Ile	Tyr	Asp	Pro	Ala	Asp	Ile	Ser	Glu	Gly	Ser	Thr	Ala	Leu	Trp	Ile		
90					95				100					105			
aac	act	ttc	ctc	ggc	gtg	tcc	aca	ctg	ctg	gct	ctc	tgg	acc	ctg	ggc	747	
Asn	Thr	Phe	Leu	Gly	Val	Ser	Thr	Leu	Leu	Ala	Leu	Trp	Thr	Leu	Gly		
106					111				116					121			
atc	att	tcc	cgt	caa	gcc	agg	cta	cac	ctg	ggg	gag	cag	aac	atg	gga	795	
Ile	Ile	Ser	Arg	Gln	Ala	Arg	Leu	His	Leu	Gly	Glu	Gln	Asn	Met	Gly		
122					127				132					137			
gcc	aaa	ttt	gct	ctg	ttc	cag	gtt	ctc	ctc	atc	ctg	act	gcc	cta	cag	843	
Ala	Lys	Phe	Ala	Leu	Phe	Gln	Val	Leu	Leu	Ile	Leu	Thr	Ala	Leu	Gln		
138					143				148					153			
ccc	tcc	atc	ttc	tca	gtc	ttg	gcc	aac	ggg	ggg	cag	att	gct	tgt	tcg	891	
Pro	Ser	Ile	Phe	Ser	Val	Leu	Ala	Asn	Gly	Gly	Gln	Ile	Ala	Cys	Ser		
154					159				164					169			
cct	ccc	tat	tcc	tct	aaa	acc	agg	tct	caa	gtg	atg	aat	tgc	cac	ctc	939	
Pro	Pro	Tyr	Ser	Ser	Lys	Thr	Arg	Ser	Gln	Val	Met	Asn	Cys	His	Leu		
170					175				180					185			
ctc	ata	ctg	gag	act	ttt	cta	atg	act	gtg	ctg	aca	cga	atg	tac	tac	987	
Leu	Ile	Leu	Glu	Thr	Phe	Leu	Met	Thr	Val	Leu	Thr	Arg	Met	Tyr	Tyr		
186					191				196					201			
cga	agg	aaa	gac	cac	aag	gtt	ggg	tat	gaa	act	ttc	tct	tct	cca	gac	1035	
Arg	Arg	Lys	Asp	His	Lys	Val	Gly	Tyr	Glu	Thr	Phe	Ser	Ser	Pro	Asp		
202					207				212					217			
ctg	gac	ttg	aac	ctc	aaa	gcc	taa	ggg	ggatggc	ttggacaatg	aaaggatgct					1089	
Leu	Asp	Leu	Asn	Leu	Lys	Ala	*										
218					223												
gtactcatta	gaatacaaga	ttcctttact	gtccctcaac	cttgaccaaa	tggaagcat											1149	
tcccccttgt	caacacaagc	tggcagatac	atttgactct	acagatgaag	gtgaacaatg											1209	
ttaggataaa	attgcttttg	atcttgccctg	gaagggtgtt	taagttttgt	aataaacaag											1269	

atgatgtctg aaaatgtgta actgggcacc ttgcctctgt ccatgtcact attaacccctt 1329
 caaggttgta tattgctggc taggtgcgac agctcatgcc tgctatccca gcactttggg 1389
 agcctgagggc gggaggatca cttgagccca ggaggttgag gccgcagtga gcaatggttg 1449
 tgccatacac tccagcctgg gtgatacagc cagaccctgc ctctggaaaa aaaagaaagc 1509
 ttactgagct ttccctaaagc agatgaaaag aagagtatat agtatt 1555

<210> 228
 <211> 955
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (80) .. (583)

<400> 228

ccggtgggttg attccccttg agaaacgcct tggcgtgaat ctgaatttag gtgacactat 60
 agaagagcta tgacgtcgc atg cac gcg tac gta agc ttg gat cct cta gag 112
 Met His Ala Tyr Val Ser Leu Asp Pro Leu Glu
 1 5
 cgg ccg cct act act act ata cgg ctg cga gaa gac gac aga agg gcg 160
 Arg Pro Pro Thr Thr Thr Ile Arg Leu Arg Glu Asp Asp Arg Arg Ala
 12 17 22 27
 act ctc acc tct cat gtg ctt ctg gcc agt agg tct ttg ttc tgg tcc 208
 Thr Leu Thr Ser His Val Leu Leu Ala Ser Arg Ser Leu Phe Trp Ser
 28 33 38 43
 aac gac agg agt agg ctt gta ttt aaa agc ggc ccc tcc tct cct gtg 256
 Asn Asp Arg Ser Arg Leu Val Phe Lys Ser Gly Pro Ser Ser Pro Val
 44 49 54 59
 gcc aca gaa cac agg cgt gct tgg att ctt gac aag cag ccc tgc tcc 304
 Ala Thr Glu His Arg Arg Ala Trp Ile Leu Asp Lys Gln Pro Cys Ser
 60 65 70 75
 tgc aga gga gac agc cac att tgg aat tgg gca ccg aga aga cct gag 352
 Cys Arg Gly Asp Ser His Ile Trp Asn Trp Ala Pro Arg Arg Pro Glu
 76 81 86 91
 aaa aac cca ctc tct ctt ttt ttt ttt gag acg gag tct tgc tct gtc 400
 Lys Asn Pro Leu Ser Leu Phe Phe Phe Glu Thr Glu Ser Cys Ser Val
 92 97 102 107
 acc cag gct gga gtg cag tgg cac gat ctc ggc tca ctg caa cct ccg 448
 Thr Gln Ala Gly Val Gln Trp His Asp Leu Gly Ser Leu Gln Pro Pro
 108 113 118 123

cct ccc aag ttc aag caa ttc tcc tgc ccc agc ctc ctg att agc tgg	496
Pro Pro Lys Phe Lys Gln Phe Ser Cys Pro Ser Leu Leu Ile Ser Trp	
124 129 134 139	
gat tac agg cgt gtg cca cca tgc cca gct aat ttt tgt gtt ttt agt	544
Asp Tyr Arg Arg Val Pro Pro Cys Pro Ala Asn Phe Cys Val Phe Ser	
140 145 150 155	
aga gac ggg gtt tca cca tgt tgg tca ggc tgg tct tga actcctgacg	593
Arg Asp Gly Val Ser Pro Cys Trp Ser Gly Trp Ser *	
156 161 166	
tggtgatcca cctgcctcgg cctcccaaag tgctgggatt acaggcgtga gccaccacgc	653
ctggccgaaa aaccactct cataacagaa gtgcagactc attgctagat tcagtgcctt	713
tgagtgtgcc agaggtcctc tgtgtttgag acaatcctgt gtgtgccagg aggctccgtg	773
tgcaccaggg gctctcagaa tcccgcttac ccagctggag accatgcctc tggcagcccc	833
atctcagcca gccctgctct ctccctcttc cctccaggtg aggcaaactt cataggaatc	893
tgtacctgaa tgtgagctcc tgataataaa actctgagggc tttggtgagc gcaaaaaaaaa	953
aa	955

<210> 229
 <211> 956
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (56) .. (823)

<400> 229	
agtgtgcgtg gaattcgctc agaacagcaa ctgctgagggc tgccttggga agagg atg	58
Met	
1	
atc cta aac aaa gct ctg atg ctg ggg gcc ctc gcc ctg acc acc gtg	106
Ile Leu Asn Lys Ala Leu Met Leu Gly Ala Leu Ala Leu Thr Thr Val	
2 7 12 17	
atg agc cct tgt gga ggt gaa gac att gtg gct gac cat gtt gcc tct	154
Met Ser Pro Cys Gly Gly Glu Asp Ile Val Ala Asp His Val Ala Ser	
18 23 28 33	
tac ggt gta aac ttg tac cag tct tat ggt ccc tct ggg cag tac agc	202
Tyr Gly Val Asn Leu Tyr Gln Ser Tyr Gly Pro Ser Gly Gln Tyr Ser	
34 39 44 49	
cat gaa ttt gat gga gac gag gag ttc tat gtg gac ctg gag agg aag	250
His Glu Phe Asp Gly Asp Glu Glu Phe Tyr Val Asp Leu Glu Arg Lys	

50	55	60	65	
gag act gtc tgg cag ttg cct ctg ttc cgc aga ttt aga aga ttt gac				298
Glu Thr Val Trp Gln Leu Pro Leu Phe Arg Arg Phe Arg Arg Phe Asp				
66	71	76	81	
ccg caa ttt gca ctg aca aac atc gct gtg cta aaa cat aac ttg aac				346
Pro Gln Phe Ala Leu Thr Asn Ile Ala Val Leu Lys His Asn Leu Asn				
82	87	92	97	
atc gtg att aaa cgc tcc aac tct acc gct gct acc aat gag gtt cct				394
Ile Val Ile Lys Arg Ser Asn Ser Thr Ala Ala Thr Asn Glu Val Pro				
98	103	108	113	
gag gtc aca gtg ttt tcc aag tct ccc gtg aca ctg ggt cag ccc aac				442
Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr Leu Gly Gln Pro Asn				
114	119	124	129	
acc ctc atc tgt ctt gtg gac aac atc ttt cct cct gtg gtc aac atc				490
Thr Leu Ile Cys Leu Val Asp Asn Ile Phe Pro Pro Val Val Asn Ile				
130	135	140	145	
acc tgg ctg agc aat ggg cac tca gtc aca gaa ggt gtt tct gag acc				538
Thr Trp Leu Ser Asn Gly His Ser Val Thr Glu Gly Val Ser Glu Thr				
146	151	156	161	
agc ttc ctc tcc aag agt gat cat tcc ttc ttc aag atc agt tac ctc				586
Ser Phe Leu Ser Lys Ser Asp His Ser Phe Phe Lys Ile Ser Tyr Leu				
162	167	172	177	
acc ttc ctc cct tct gct gat gag att tat gac tgc aag gtg gag cac				634
Thr Phe Leu Pro Ser Ala Asp Glu Ile Tyr Asp Cys Lys Val Glu His				
178	183	188	193	
tgg ggc ctg gat gag cct ctt ctg aaa cac tgg gag cct gag att cca				682
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Pro Glu Ile Pro				
194	199	204	209	
aca cct atg tca gag ctc aca gag act gtg gtc tgc gcc ctg ggg ttg				730
Thr Pro Met Ser Glu Leu Thr Glu Thr Val Val Cys Ala Leu Gly Leu				
210	215	220	225	
tct gtg ggc ctc gtg ggc att gtg gtg ggg acc gtc ttg atc atc cga				778
Ser Val Gly Leu Val Gly Ile Val Val Gly Thr Val Leu Ile Ile Arg				
226	231	236	241	
ggc ctg cgt tca gtt ggt gct tcc aga cac caa ggg ccc ttg tga atc				826
Gly Leu Arg Ser Val Gly Ala Ser Arg His Gln Gly Pro Leu *				
242	247	252		
ccatcctgaa aaggaagggtg ttacctacta agagatgcct ggggtaagcc gccagctac				886
ctaattcctc agtaacatcg atctaaaatc tccatggaag caataaatc cctttaagag				946
aaaaaaaaa				956

<210> 230
 <211> 1685
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (61)..(1338)

<400> 230
 aatgataccc gtgcggcacc ggcccggaat tcccgggtcg acccacgcgt ccggttgagg 60

atg gcc gga gcc gag ggc gcc gct ggg cgg cag tgc gag ctg gag ccc 108
 Met Ala Gly Ala Glu Gly Ala Ala Gly Arg Gln Ser Glu Leu Glu Pro
 1 5 10 15

gtg gta tgc ttg gtc gac gtc ctt gag gag gac gag gag ctg gag aat 156
 Val Val Ser Leu Val Asp Val Leu Glu Glu Asp Glu Glu Leu Glu Asn
 17 22 27 32

gag gcg tgc gct gtc ctg ggc ggc agc gac tcc gag aag tgc tcc tac 204
 Glu Ala Cys Ala Val Leu Gly Gly Ser Asp Ser Glu Lys Cys Ser Tyr
 33 38 43 48

tct cag ggc tca gta aag aga caa gca cta tat gcc tgt agt acc tgc 252
 Ser Gln Gly Ser Val Lys Arg Gln Ala Leu Tyr Ala Cys Ser Thr Cys
 49 54 59 64

acc cca gag gga gaa gaa cca gca gga att tgt tta gct tgc agt tat 300
 Thr Pro Glu Gly Glu Glu Pro Ala Gly Ile Cys Leu Ala Cys Ser Tyr
 65 70 75 80

gaa tgt cat gga agt cac aaa cta ttt gag cta tac aca aaa aga aat 348
 Glu Cys His Gly Ser His Lys Leu Phe Glu Leu Tyr Thr Lys Arg Asn
 81 86 91 96

ttt cgt tgt gat tgt gga aac agc aag ttt aaa aat ttg gaa tgc aaa 396
 Phe Arg Cys Asp Cys Gly Asn Ser Lys Phe Lys Asn Leu Glu Cys Lys
 97 102 107 112

tta ctt cct gac aaa gca aag gta aat tct ggc aat aag tac aat gac 444
 Leu Leu Pro Asp Lys Ala Lys Val Asn Ser Gly Asn Lys Tyr Asn Asp
 113 118 123 128

aac ttt ttt gga ttg tac tgc att tgc aag aga cct tat cct gat cct 492
 Asn Phe Phe Gly Leu Tyr Cys Ile Cys Lys Arg Pro Tyr Pro Asp Pro
 129 134 139 144

gaa gac gag att cca gat gag atg atc cag tgc gta gtc tgt gaa gac 540
 Glu Asp Glu Ile Pro Asp Glu Met Ile Gln Cys Val Val Cys Glu Asp
 145 150 155 160

tgg ttc cat gga agg cat ctt ggt gcc att ccc cct gag agt ggg gat 588
 Trp Phe His Gly Arg His Leu Gly Ala Ile Pro Pro Glu Ser Gly Asp
 161 166 171 176

ttt cag gag atg gta tgc cag gcc tgc atg aaa cgt tgt tct ttt ttg	636
Phe Gln Glu Met Val Cys Gln Ala Cys Met Lys Arg Cys Ser Phe Leu	
177 182 187 192	
tggt gct tat gct gca caa ttg gca gta acc aaa ata tcc act gag gat	684
Trp Ala Tyr Ala Ala Gln Leu Ala Val Thr Lys Ile Ser Thr Glu Asp	
193 198 203 208	
gat gga ttg gtg cgg aac att gat gga ata ggt gat cag gaa gtt atc	732
Asp Gly Leu Val Arg Asn Ile Asp Gly Ile Gly Asp Gln Glu Val Ile	
209 214 219 224	
aaa cct gaa aat gga gag cat caa gat agt acc ctg aaa gag gat gtt	780
Lys Pro Glu Asn Gly Glu His Gln Asp Ser Thr Leu Lys Glu Asp Val	
225 230 235 240	
cca gaa cag gga aag gat gat gtc cgg gag gtt aaa gta gag cag aac	828
Pro Glu Gln Gly Lys Asp Asp Val Arg Glu Val Lys Val Glu Gln Asn	
241 246 251 256	
agt gaa cca tgt gcc ggc tct agt tct gaa tct gat ctg cag aca gtg	876
Ser Glu Pro Cys Ala Gly Ser Ser Ser Glu Ser Asp Leu Gln Thr Val	
257 262 267 272	
ttt aag aat gaa agc ctg aac gca gaa tca aaa tct ggc tgc aaa ctt	924
Phe Lys Asn Glu Ser Leu Asn Ala Glu Ser Lys Ser Gly Cys Lys Leu	
273 278 283 288	
cag gag ctt aaa gct aag cag ctt ata aag aaa gac act gcc acc tat	972
Gln Glu Leu Lys Ala Lys Gln Leu Ile Lys Lys Asp Thr Ala Thr Tyr	
289 294 299 304	
tggt ccc ctg aac ttg cgt agc aag ttg tgt acc tgc caa gac tgt atg	1020
Trp Pro Leu Asn Trp Arg Ser Lys Leu Cys Thr Cys Gln Asp Cys Met	
305 310 315 320	
aaa atg tat gga gat cta gat gtc tta ttc ctg aca gat gaa tac gac	1068
Lys Met Tyr Gly Asp Leu Asp Val Leu Phe Leu Thr Asp Glu Tyr Asp	
321 326 331 336	
aca gtt ctg gct tat gaa aac aaa ggg aag att gcc cag gcc act gac	1116
Thr Val Leu Ala Tyr Glu Asn Lys Gly Lys Ile Ala Gln Ala Thr Asp	
337 342 347 352	
agg agc gat ccc cta atg gat acc ctt agc agc atg aat aga gtc cag	1164
Arg Ser Asp Pro Leu Met Asp Thr Leu Ser Ser Met Asn Arg Val Gln	
353 358 363 368	
caa gtg gaa ctg att tgt gaa tac aat gat ttg aag act gaa ctt aaa	1212
Gln Val Glu Leu Ile Cys Glu Tyr Asn Asp Leu Lys Thr Glu Leu Lys	
369 374 379 384	
gac tat ctg aag aga ttt gct gat gaa ggc acg gtt gtt aag aga gag	1260
Asp Tyr Leu Lys Arg Phe Ala Asp Glu Gly Thr Val Val Lys Arg Glu	
385 390 395 400	

gac att cag cag ttc ttt gaa gag ttt cag tca aaa aag aga aga aga 1308
 Asp Ile Gln Gln Phe Phe Glu Glu Phe Gln Ser Lys Lys Arg Arg Arg
 401 406 411 416

gtg gat ggg atg cag tat tac tgc agc tag a gtggagtatg aagctttctc 1359
 Val Asp Gly Met Gln Tyr Tyr Cys Ser *
 417 422

attcaagcca atgaaaatgc gcttcccatt cttggaataa aagaggtgtg gttcacattt 1419

ggcccccttt ccgtcctcct ctgtttggag aggcctcgcg ctcccttcat tctcttttagc 1479

tgcagtagcc accgtgtgga tgctgacttc acagccagcg tcctctgtga ctcagctgat 1539

gcagctcatt ccacagactt cgccagtgtg ctctactcc agtgcaccca gggttatttg 1599

catagttttt aagtttgatt ttgttttgag aaagcaaatt tgggtgtcttt gtttaatgat 1659

ctgttatttc actcccagat gtgtgt 1685

<210> 231
 <211> 1593
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (151) .. (1437)

<400> 231
 gcacaggact ttgcctcggg ccagctatgt gttcagcccg gaatctgaag tgtcagccca 60

ggcgtctctg aagaccgact aaagccccag gaaggggaagg gaagtgtgct aaggcgggat 120

gtgtcagtca aagcagcctc tgaacttctc atg aaa ctc tca gcg gaa agc 171
 Met Lys Leu Ser Ala Glu Ser
 1 5

tac aag gaa aca cag atg gtg aag att aaa gag gaa ccc atg gag gtt 219
 Tyr Lys Glu Thr Gln Met Val Lys Ile Lys Glu Glu Pro Met Glu Val
 8 13 18 23

gac atc cag gac tcc cat gtc tcg ata tca ccc agc cgg aat gtt ggc 267
 Asp Ile Gln Asp Ser His Val Ser Ile Ser Pro Ser Arg Asn Val Gly
 24 29 34 39

tac agc act tta atc ggg cga gag aaa acc gaa ccc tta cag aag atg 315
 Tyr Ser Thr Leu Ile Gly Arg Glu Lys Thr Glu Pro Leu Gln Lys Met
 40 45 50 55

cca gag ggc aga gta ccc cca gag aga aac ctc ttc agt cag gat atc 363
 Pro Glu Gly Arg Val Pro Pro Glu Arg Asn Leu Phe Ser Gln Asp Ile
 56 61 66 71

tct gtg aaa atg gct tcc gag ctc ctc ttt caa ctg tca gaa aaa gtg	411
Ser Val Lys Met Ala Ser Glu Leu Leu Phe Gln Leu Ser Glu Lys Val	
72 77 82 87	
agc aaa gag cac aat cat aca aaa gaa aac acc atc cgg acc acg acc	459
Ser Lys Glu His Asn His Thr Lys Glu Asn Thr Ile Arg Thr Thr Thr	
88 93 98 103	
agc cct ttc ttt tca gaa gac aca ttt aga caa tca cca ttc acc tcc	507
Ser Pro Phe Phe Ser Glu Asp Thr Phe Arg Gln Ser Pro Phe Thr Ser	
104 109 114 119	
aat tca aaa gaa ctg ctg ccc agt gac tcc gtg ctg cac gga aga ata	555
Asn Ser Lys Glu Leu Leu Pro Ser Asp Ser Val Leu His Gly Arg Ile	
120 125 130 135	
tca gct cca gaa aca gaa aag ata gtc cta gag gca gga aat gga tta	603
Ser Ala Pro Glu Thr Glu Lys Ile Val Leu Glu Ala Gly Asn Gly Leu	
136 141 146 151	
cca tcc tgg aaa ttc aat gac cag ctt ttt ccc tgt gac gtg tgt ggg	651
Pro Ser Trp Lys Phe Asn Asp Gln Leu Phe Pro Cys Asp Val Cys Gly	
152 157 162 167	
aaa gtg ttt ggc cga cag cag aca ttg tcc cga cac ctc tcg ctg cac	699
Lys Val Phe Gly Arg Gln Gln Thr Leu Ser Arg His Leu Ser Leu His	
168 173 178 183	
aca gag gaa aga aaa tac aaa tgc cac ttg tgc ccc tat gct gct aag	747
Thr Glu Glu Arg Lys Tyr Lys Cys His Leu Cys Pro Tyr Ala Ala Lys	
184 189 194 199	
tgc cgt gca aat ctg aac cag cac ttg acc gtc cat tcc gtg aag ctg	795
Cys Arg Ala Asn Leu Asn Gln His Leu Thr Val His Ser Val Lys Leu	
200 205 210 215	
gtg agt aca gac acc gag gac att gtc agc gcc gtc acc tct gaa ggc	843
Val Ser Thr Asp Thr Glu Asp Ile Val Ser Ala Val Thr Ser Glu Gly	
216 221 226 231	
agt gat ggg aag aaa cat cct tat tat tac agt tgt cac gtg tgt gga	891
Ser Asp Gly Lys Lys His Pro Tyr Tyr Tyr Ser Cys His Val Cys Gly	
232 237 242 247	
ttt gag acc gag ctc aat gtc cag ttt gtc agc cac atg tca ctc cac	939
Phe Glu Thr Glu Leu Asn Val Gln Phe Val Ser His Met Ser Leu His	
248 253 258 263	
gtg gac aag gag cag tgg atg ttt tcg atc tgc tgc act gcc tgc gac	987
Val Asp Lys Glu Gln Trp Met Phe Ser Ile Cys Cys Thr Ala Cys Asp	
264 269 274 279	
ttc gtc acc atg gag gaa gca gag ata aag act cac att ggc acc aag	1035
Phe Val Thr Met Glu Glu Ala Glu Ile Lys Thr His Ile Gly Thr Lys	
280 285 290 295	
cac aca ggg gaa gac agg aag acc ccc agc gaa tca aat agc ccc tct	1083

His Thr Gly Glu Asp Arg Lys Thr Pro Ser Glu Ser Asn Ser Pro Ser	
296 301 306 311	
tca tcc tcc ctc tca gct ctg agt gat tca gcc aac agc aaa gat gat	1131
Ser Ser Ser Leu Ser Ala Leu Ser Asp Ser Ala Asn Ser Lys Asp Asp	
312 317 322 327	
tca gat ggc tcc cag aaa aac aag ggc ggg aac aat ctg ctg gtc atc	1179
Ser Asp Gly Ser Gln Lys Asn Lys Gly Gly Asn Asn Leu Leu Val Ile	
328 333 338 343	
tct gtc atg cct ggg agc cag ccc tca ctg aac agt gag gaa aag cca	1227
Ser Val Met Pro Gly Ser Gln Pro Ser Leu Asn Ser Glu Glu Lys Pro	
344 349 354 359	
gag aaa ggg ttc gaa tgt gtt ttt tgc aac ttt gtc tgc aag acg aag	1275
Glu Lys Gly Phe Glu Cys Val Phe Cys Asn Phe Val Cys Lys Thr Lys	
360 365 370 375	
aac atg ttt gag cgt cat ctg cag ata cac ctc atc acc cgg atg ttt	1323
Asn Met Phe Glu Arg His Leu Gln Ile His Leu Ile Thr Arg Met Phe	
376 381 386 391	
gag tgt gat gtg tgc cac aag ttc atg aag acc ccc gaa cag ctg ctg	1371
Glu Cys Asp Val Cys His Lys Phe Met Lys Thr Pro Glu Gln Leu Leu	
392 397 402 407	
gag cat aag aaa tgc cac act gtc ccc acc ggt ggg ctc aat tta tgt	1419
Glu His Lys Lys Cys His Thr Val Pro Thr Gly Gly Leu Asn Leu Cys	
408 413 418 423	
tct agg atg acc aag tag aagaat actttgaaaa aattgataat gccttctggc	1473
Ser Arg Met Thr Lys *	
424 429	
tatacagtgc ccattctgca ttattccac caaccgcccc gctgccatgg agtgccacct	1533
caagaccac tacaagatgg agtacaagtg ccggatctgc cagacggtga aggccaaccc	1593

<210> 232
 <211> 1234
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (342) .. (1046)

<400> 232	
tcttgggttg acccagcgt cccatgccac gtctgtctet gttgaacacg gatgtgtgca	60
gagcattctc tttctttaca aatctgatgt ggggagagga aagatgaatt tttatttcat	120
aaagccacta gatcagcaat tctgaccct gtgaccacag agttcccatc cacgcggctg	180

gtc gac ctg ccc aag gcc atc gct ggc ggg tcc gcc tgt gtc tgc gcc 977
Val Asp Leu Pro Lys Ala Ile Ala Gly Gly Ser Ala Cys Val Cys Ala
197 202 207 212

ctg gag cca cgg cca gag gac aag aag aag aaa ggc aaa ggc aag agg 1025
Leu Glu Pro Arg Pro Glu Asp Lys Lys Lys Lys Gly Lys Gly Lys Arg
213 218 223 228

cac cag gac cgg ggc cag tga cc ctagctgcgc ctcttgggac catcctcacc 1078
His Gln Asp Arg Gly Gln *
229 234

gtcacctccc agggctctgt agaccagcag caacttctta gtattccgga aacattatgt 1138

acaacttagc agcttttttt acttttatga ttattgggat ttctatgata tcacagtaac 1198

caattaaata ctatctgtaa ctttaaaaaa aaaaaa 1234

<210> 233
<211> 3542
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) .. (3168)

<400> 233

atg gag gcg gag gcg gcg gca gct cct gag cgg gaa ggc ggg agc tgc 48
Met Glu Ala Glu Ala Ala Ala Ala Pro Glu Arg Glu Gly Gly Ser Cys
1 5 10

gtg ctg tgc tgc gga gac ctg gag gcc acg gcg ctg ggg ccg ctg cga 96
Val Leu Cys Cys Gly Asp Leu Glu Ala Thr Ala Leu Gly Pro Leu Arg
17 22 27 32

cca ccc ggt gtg cta ccg ctg ctc tac caa gat gcg ggt gct ctg cga 144
Pro Pro Gly Val Leu Pro Leu Leu Tyr Gln Asp Ala Gly Ala Leu Arg
33 38 43 48

gca gcg cta ctg cgc cgt gtg ccg cga gga gct gcg cca gct gct ggc 192
Ala Ala Leu Leu Arg Arg Val Pro Arg Gly Ala Ala Pro Ala Ala Gly
49 54 59 64

tgt ggg cac ctg gct gga gcc cgt tgg ttt gct gag ctt aga gat ttg 240
Cys Gly His Leu Ala Gly Ala Arg Trp Phe Ala Glu Leu Arg Asp Leu
65 70 75 80

ttt gct tcc agc att gtg aaa ttc ccc cgg ttt gtt cat aga agg ctt 288
Phe Ala Ser Ser Ile Val Lys Phe Pro Arg Phe Val His Arg Arg Leu
81 86 91 96

cgg ctg gtg aca tct gcc agg aat cta act ttc ttc tcc cca gaa gtg 336
Arg Leu Val Thr Ser Ala Arg Asn Leu Thr Phe Phe Ser Pro Glu Val

97	102	107	112	
atg cag agc agt att gag gca gac act ggc ttc ctc gcc cgc ctg cct				384
Met Gln Ser Ser Ile Glu Ala Asp Thr Gly Phe Leu Ala Arg Leu Pro				
113	118	123	128	
gct gct tcg gga gct gtg gtg ggg aag tgg ccc tgt ctg gtt ccc ggg				432
Ala Ala Ser Gly Ala Val Val Gly Lys Trp Pro Cys Leu Val Pro Gly				
129	134	139	144	
agt cca ggt act cag ctc ccc gag gag gct cgc gct ctg cgt ccc agc				480
Ser Pro Gly Thr Gln Leu Pro Glu Glu Ala Arg Ala Leu Arg Pro Ser				
145	150	155	160	
agc acc ctg agt ggc tcc gct cag ctc ccc gag gag gct cgt gct ctg				528
Ser Thr Leu Ser Gly Ser Ala Gln Leu Pro Glu Glu Ala Arg Ala Leu				
161	166	171	176	
ggc ccc agc agc acc ctg agt ggc tgc aca gat tgc gcc tgt gag ggt				576
Gly Pro Ser Ser Thr Leu Ser Gly Cys Thr Asp Cys Ala Cys Glu Gly				
177	182	187	192	
cgg gct gga gag gcg ccc ttg gga gtg gtc ttt ggg aag aag ctt cct				624
Arg Ala Gly Glu Ala Pro Leu Gly Val Val Phe Gly Lys Lys Leu Pro				
193	198	203	208	
gcc ttt gcc acc atc ccc atc cac cag ctg cag cat gag aag aaa tat				672
Ala Phe Ala Thr Ile Pro Ile His Gln Leu Gln His Glu Lys Lys Tyr				
209	214	219	224	
gat atc tac ttt gca gat gga aag gtg tac gca ttg tac agg cag ctg				720
Asp Ile Tyr Phe Ala Asp Gly Lys Val Tyr Ala Leu Tyr Arg Gln Leu				
225	230	235	240	
ctg cag cac gag tgc ccg cgg tgc ccc gag ctg cca cct ttc agc ctc				768
Leu Gln His Glu Cys Pro Arg Cys Pro Glu Leu Pro Pro Phe Ser Leu				
241	246	251	256	
ttc ggg gac ctg gag cag cac atg cgg agg cag cat gag ctc ttc tgc				816
Phe Gly Asp Leu Glu Gln His Met Arg Arg Gln His Glu Leu Phe Cys				
257	262	267	272	
tgc cgt ctg tgc ctc cag cac ctc cag atc ttc aca tat gag cgc aag				864
Cys Arg Leu Cys Leu Gln His Leu Gln Ile Phe Thr Tyr Glu Arg Lys				
273	278	283	288	
tgg tac tcg cgc aag gac ctg gcc cgg cat cgc atg cag ggt gac ccc				912
Trp Tyr Ser Arg Lys Asp Leu Ala Arg His Arg Met Gln Gly Asp Pro				
289	294	299	304	
gat gac acg tcg cac cgt ggg cac ccg ctc tgc aag ttc tgt gac gag				960
Asp Asp Thr Ser His Arg Gly His Pro Leu Cys Lys Phe Cys Asp Glu				
305	310	315	320	
cgc tac ctg gac aat gat gag ctg ctt aag cac ctg cgc cgc gac cac				1008
Arg Tyr Leu Asp Asn Asp Glu Leu Leu Lys His Leu Arg Arg Asp His				
321	326	331	336	

tac ttc tgc cac ttc tgc gac tcg gac ggg gcc cag gac tac tac agc	1056
Tyr Phe Cys His Phe Cys Asp Ser Asp Gly Ala Gln Asp Tyr Tyr Ser	
337 342 347 352	
gac tat gcc tac ctg cgt gag cac ttc cgg gag aag cac ttt ctg tgt	1104
Asp Tyr Ala Tyr Leu Arg Glu His Phe Arg Glu Lys His Phe Leu Cys	
353 358 363 368	
gag gaa ggc cgc tgc agc acg gag cag ttc acc cac gcc ttc cgc acc	1152
Glu Glu Gly Arg Cys Ser Thr Glu Gln Phe Thr His Ala Phe Arg Thr	
369 374 379 384	
gag atc gac ctc aag gcc cac agg acg gcc tgc cac agt cgc agc cgc	1200
Glu Ile Asp Leu Lys Ala His Arg Thr Ala Cys His Ser Arg Ser Arg	
385 390 395 400	
gcc gag gca cgc cag aac cgc cac atc gac ctg cag ttc agc tac gcg	1248
Ala Glu Ala Arg Gln Asn Arg His Ile Asp Leu Gln Phe Ser Tyr Ala	
401 406 411 416	
cca cgg cac tcg cgc cgg aac gag ggt gag cag gca cct ggc ctg gat	1296
Pro Arg His Ser Arg Arg Asn Glu Gly Glu Gln Ala Pro Gly Leu Asp	
417 422 427 432	
gcc ccc agg cct gtt cct cct att gtc gtc ccg ggg tcc cgg gaa gtg	1344
Ala Pro Arg Pro Val Pro Pro Ile Val Val Pro Gly Ser Arg Glu Val	
433 438 443 448	
acg ggc tgt ctg ctg gcc gca ggg gtc gtt ggt ggc gaa gac tac gag	1392
Thr Gly Cys Leu Leu Ala Ala Gly Val Val Gly Gly Glu Asp Tyr Glu	
449 454 459 464	
gag gtg gac agg tac agc cgc cag ggc cga gtg gcc cgg gct ggc act	1440
Glu Val Asp Arg Tyr Ser Arg Gln Gly Arg Val Ala Arg Ala Gly Thr	
465 470 475 480	
cgc gga gcc cag cag agc cgc cga gga agc tgg agg tac aaa agg gaa	1488
Arg Gly Ala Gln Gln Ser Arg Arg Gly Ser Trp Arg Tyr Lys Arg Glu	
481 486 491 496	
gaa gag gac cga gaa gta gca gct gct gtc cgg gcc tcc gtg gcc gca	1536
Glu Glu Asp Arg Glu Val Ala Ala Ala Val Arg Ala Ser Val Ala Ala	
497 502 507 512	
cag cag cag gag gag gct cgc agg agt gag gat cag gag gaa ggc ggt	1584
Gln Gln Gln Glu Glu Ala Arg Arg Ser Glu Asp Gln Glu Glu Gly Gly	
513 518 523 528	
agg ccc aag aag gag gag gca gcg gcg cgg gga cct gag gat ccc cgt	1632
Arg Pro Lys Lys Glu Glu Ala Ala Ala Arg Gly Pro Glu Asp Pro Arg	
529 534 539 544	
ggc ccc cgg cgc tca ccc cgg act cag ggc gaa ggc cca ggc ccc aag	1680
Gly Pro Arg Arg Ser Pro Arg Thr Gln Gly Glu Gly Pro Gly Pro Lys	
545 550 555 560	

gaa acc tcg aca aat ggt cct gta agc caa gaa gcc ttc tcg gtg aca	1728
Glu Thr Ser Thr Asn Gly Pro Val Ser Gln Glu Ala Phe Ser Val Thr	
561 566 571 576	
ggc cca gcc gcc cca ggc gcc ctc cca cca ccc agc ccg aag ctc aag	1776
Gly Pro Ala Ala Pro Gly Ala Leu Pro Pro Pro Ser Pro Lys Leu Lys	
577 582 587 592	
gac gaa gac ttc ccc agc ctc tct gcc tcc act tcc tcc tcc tgc tcc	1824
Asp Glu Asp Phe Pro Ser Leu Ser Ala Ser Thr Ser Ser Ser Cys Ser	
593 598 603 608	
act gca gca acc ccg ggc cct gtg ggg ttg gcg ctg ccg tac gcc atc	1872
Thr Ala Ala Thr Pro Gly Pro Val Gly Leu Ala Leu Pro Tyr Ala Ile	
609 614 619 624	
cct gcc aga ggc agg agt gcc ttc cag gag gag gac ttc ccc gcc ctg	1920
Pro Ala Arg Gly Arg Ser Ala Phe Gln Glu Glu Asp Phe Pro Ala Leu	
625 630 635 640	
gtg tcc tcg gtg ccc aag cct ggc acc gcc ccc acc agc ctt gtc tct	1968
Val Ser Ser Val Pro Lys Pro Gly Thr Ala Pro Thr Ser Leu Val Ser	
641 646 651 656	
gcc tgg aac agc agc agt agc agc aag aag gta gca cag ccc cca ctc	2016
Ala Trp Asn Ser Ser Ser Ser Ser Lys Lys Val Ala Gln Pro Pro Leu	
657 662 667 672	
tcg gcg cag gct acc ggc agc ggc cag ccc acc agg aag gct ggg aag	2064
Ser Ala Gln Ala Thr Gly Ser Gly Gln Pro Thr Arg Lys Ala Gly Lys	
673 678 683 688	
ggg agc agg ggc ggc agg aag ggc ggc ccg ccc ttc aca cag gag gag	2112
Gly Ser Arg Gly Gly Arg Lys Gly Gly Pro Pro Phe Thr Gln Glu Glu	
689 694 699 704	
gag gag gac ggc ggc ccg gcc ctg cag gag ctt ctg agc aca cgc ccc	2160
Glu Glu Asp Gly Gly Pro Ala Leu Gln Glu Leu Leu Ser Thr Arg Pro	
705 710 715 720	
acg ggc tcc gtc tcc tcc aca ctg ggg ctg gcc tcc atc caa ccc tct	2208
Thr Gly Ser Val Ser Ser Thr Leu Gly Leu Ala Ser Ile Gln Pro Ser	
721 726 731 736	
aaa gtt ggg aag aag aag aaa gtg ggc tcg gag aag cca ggc acc aca	2256
Lys Val Gly Lys Lys Lys Lys Val Gly Ser Glu Lys Pro Gly Thr Thr	
737 742 747 752	
ttg cca cag ccc ccg ccc gct acc tgt ccc cca ggg gct ttg cag gcc	2304
Leu Pro Gln Pro Pro Pro Ala Thr Cys Pro Pro Gly Ala Leu Gln Ala	
753 758 763 768	
ccg gaa gct cct gcc agc aga gcc gag ggg cca gtt gcc gtc gtc gtt	2352
Pro Glu Ala Pro Ala Ser Arg Ala Glu Gly Pro Val Ala Val Val Val	
769 774 779 784	
aat gga cac acg gag ggc ccg gcc cct gct cgg agt gcc ccc aag gaa	2400

Asn Gly His Thr Glu Gly Pro Ala Pro Ala Arg Ser Ala Pro Lys Glu	
785 790 795 800	
ccc cct ggg ctc cca agg ccc ctg ggg tcc ttc ccc tgc ccc acg cca	2448
Pro Pro Gly Leu Pro Arg Pro Leu Gly Ser Phe Pro Cys Pro Thr Pro	
801 806 811 816	
cag gag gac ttc cca gcg ctc ggc ggc ccc tgc cca ccc cgg atg ccg	2496
Gln Glu Asp Phe Pro Ala Leu Gly Gly Pro Cys Pro Pro Arg Met Pro	
817 822 827 832	
ccg ccc cca ggc ttc agc gct gtg gtg ctc ctg aag ggc acg cct ccc	2544
Pro Pro Pro Gly Phe Ser Ala Val Val Leu Leu Lys Gly Thr Pro Pro	
833 838 843 848	
cca ccc ccg ccg ggc ctg gtg ccc cca atc agc aag ccg ccc cct ggc	2592
Pro Pro Pro Pro Gly Leu Val Pro Pro Ile Ser Lys Pro Pro Pro Gly	
849 854 859 864	
ttc tct ggc ctt ctg cct agc ccc cac ccg gcc tgt gtc ccc agc ccc	2640
Phe Ser Gly Leu Leu Pro Ser Pro His Pro Ala Cys Val Pro Ser Pro	
865 870 875 880	
gcc acc acc acc acc aca aaa gca ccc agg ctg ctg cct gcc cca ccg	2688
Ala Thr Thr Thr Thr Thr Lys Ala Pro Arg Leu Leu Pro Ala Pro Arg	
881 886 891 896	
gcc tac cta gtc ccc gag aac ttc ccg gag agg aac ctt cag ctc atc	2736
Ala Tyr Leu Val Pro Glu Asn Phe Arg Glu Arg Asn Leu Gln Leu Ile	
897 902 907 912	
cag tcc atc agg gac ttc ctg cag agc gac gag gcc cgc ttc agc gag	2784
Gln Ser Ile Arg Asp Phe Leu Gln Ser Asp Glu Ala Arg Phe Ser Glu	
913 918 923 928	
ttc aag agc cac tca ggg gag ttc aga cag gcc ctg atc tcc gca gcc	2832
Phe Lys Ser His Ser Gly Glu Phe Arg Gln Gly Leu Ile Ser Ala Ala	
929 934 939 944	
cag tat tac aag agt tgc ccg gac ctg ctg ggg gag aat ttc cag aag	2880
Gln Tyr Tyr Lys Ser Cys Arg Asp Leu Leu Gly Glu Asn Phe Gln Lys	
945 950 955 960	
gtc ttt aat gag ctg ctg gtc ctg ctg ccc gac acg gcc aag cag cag	2928
Val Phe Asn Glu Leu Leu Val Leu Leu Pro Asp Thr Ala Lys Gln Gln	
961 966 971 976	
gag ctc ctg tct gca cac acg gac ttc tgc aac cgc gag aag cct ctg	2976
Glu Leu Leu Ser Ala His Thr Asp Phe Cys Asn Arg Glu Lys Pro Leu	
977 982 987 992	
agc acc aag tcc aag aag aac aag aag agc gcg tgg cag gcc acc acc	3024
Ser Thr Lys Ser Lys Lys Asn Lys Lys Ser Ala Trp Gln Ala Thr Thr	
993 998 1003 1008	
cag cag gcg ggc ctg gac tgc cgt gtg tgc ccc acc tgc cag cag gtg	3072
Gln Gln Ala Gly Leu Asp Cys Arg Val Cys Pro Thr Cys Gln Gln Val	

1009	1014	1019	1024	
ctc gcg cat ggc gat gcc agc agc cac cag gcg ctg cat gct gcc cgg				3120
Leu Ala His Gly Asp Ala Ser Ser His Gln Ala Leu His Ala Ala Arg				
1025	1030	1035	1040	
gac gac gac ttc ccc tcc ctg caa gcc atc gcc agg atc atc acg tag				3168
Asp Asp Asp Phe Pro Ser Leu Gln Ala Ile Ala Arg Ile Ile Thr *				
1041	1046	1051	1056	
ctccccgccag cgtggccaga gctgtgcac cgtgagcgtc cttcctcctt cctctccggg				3228
ctgccaggca gccaggtaag gcttgatttg ggccctccca aagctgaggg ctgcagcccg				3288
tggggcctca gagctgaaag ctgcccgcgc actggtgcc aagtcagatg tcacagatgt				3348
gttgtgtaaa cagttggctg tttcatgctt caagaatgtt caggattaaa agcagacaag				3408
aaattgtgct acttgaagtt gaatttttt atgagacaag ctgaatctgg gatctcaa				3468
tgctctgac cttttataag acagtttatt ttcaaataaa tttattttgc aataccacgc				3528
aaaaaaaaaaaa				3542

<210> 234
 <211> 677
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (293)..(571)

<400> 234				
attgaaacct tgtggtaccg cctcggaatt cccgggtcga cccacgcgtc cgctcgcttc				60
ttacctcaca taattcctgc cttaaaatgt ttaaaagtag gaaaagccct ttgtttgggg				120
ctcagacttt ctggacatat gtccagctgg gccagtgatg accttaatag actctcctga				180
accttttttg gtctctccag tctttgattg tctgttaaca tttctggggg cttatccggg				240
attggagatg gcagattttc tgtcttcttt gcctgtgggc tagagcccca gg				295
			atg	
			Met	
			1	
tgg gag atc tgg ggt cct tgg cac cgc tgg gag agt ttc agc ctg gaa				343
Trp Glu Ile Trp Gly Pro Trp His Arg Trp Glu Ser Phe Ser Leu Glu				
2	7	12	17	
gga gaa tgg ccc tcc cgc att cca gag cct tcc cct gac agc acc aaa				391
Gly Glu Trp Pro Ser Arg Ile Pro Glu Pro Ser Pro Asp Ser Thr Lys				
18	23	28	33	

gga acc agt gga aag ggt tgc agg aca gtc aca gga gca gtg cac aga	439
Gly Thr Ser Gly Lys Gly Cys Arg Thr Val Thr Gly Ala Val His Arg	
34 39 44 49	
cat ctg aac cat gtt gca ggt atc ata cct tgg gtt ctt cat agc cag	487
His Leu Asn His Val Ala Gly Ile Ile Pro Trp Val Leu His Ser Gln	
50 55 60 65	
ctg aaa cca aca gca gcc act gcc cag gac cag tgg acc agt caa caa	535
Leu Lys Pro Thr Ala Ala Thr Ala Gln Asp Gln Trp Thr Ser Gln Gln	
66 71 76 81	
tac cca gac cac cca aca cgg ctg atc cta cag tga aatc aagccactgc	585
Tyr Pro Asp His Pro Thr Arg Leu Ile Leu Gln *	
82 87 92	
tgacaagaac aactgaacaa ctgccctgct ccaaccacac cagaggctgg gtcagtccac	645
gcatggctga agcttaagga aacatcgagc cc	677

<210> 235
 <211> 1789
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (706)..(966)

<400> 235	
ttgggggtgtc acccaccatt gaaaatgagt ttttttttta acctgtaaaa ctaggctgat	60
tttgaattcc agggctagtc ctgagaatta agtgagagaa tacatgtaaa gtcgtgtaac	120
tggagaagtt atatgcactt gctgggtatg actacaggac tggcatttac ggattgttta	180
tagaggtctg ggcattgggt tatggtttgg gatttgactg tcacttgaca gccacggccg	240
ctgtgaatga cagaaatgag gttcttgacc ctcccttacc ggtcagctgt atgcagtgtg	300
gtgggtattgt cctagatggt ttgcataaca gacctgtcat catacagatg aggaaactga	360
ggctcagaaa ggctaagccg cttaccaga agtcacatag ctactaagac caagttaggt	420
tttgaatcta gacttctgac tcctaagctc accagatctt aacctacttg gaaccactg	480
cttggtagtg aattataata aaatattaac tgtgtttcta accaaatcag tgcttgagat	540
ttaaaaattc atacacacgc ctcaaacctc cagattctga aacgacttct ttgggattaa	600
agaagtgtat gtttctagaa gactgcggaa aacatcattt ctttggctgt gactttcttg	660
gagcaggcag tgggtagcaa ggagtgtgtc cccgtggacc agttc atg gag cac	714
	Met Glu His

ctg ctt ccc agc ctc ctg agc ctc gca tca gat cct gtg ccc aac gtg	762
Leu Leu Pro Ser Leu Leu Ser Leu Ala Ser Asp Pro Val Pro Asn Val	
4 9 14 19	
agg gtt ctg cta gcc aag gcc cta agg cag atg ctg ttg gaa aag gcg	810
Arg Val Leu Leu Ala Lys Ala Leu Arg Gln Met Leu Leu Glu Lys Ala	
20 25 30 35	
tat ttt aga aat gct ggt aac cct cat ctt gaa gtc att gaa gag acc	858
Tyr Phe Arg Asn Ala Gly Asn Pro His Leu Glu Val Ile Glu Glu Thr	
36 41 46 51	
atc tta gca ttg cag tca gac cgg gac caa gat gtt tcc ttt ttt gca	906
Ile Leu Ala Leu Gln Ser Asp Arg Asp Gln Asp Val Ser Phe Phe Ala	
52 57 62 67	
gcc cta gaa cca aag cgg cgg aat atc ata gac act gct gta cta gaa	954
Ala Leu Glu Pro Lys Arg Arg Asn Ile Ile Asp Thr Ala Val Leu Glu	
68 73 78 83	
aaa cag aat taa cta cttccgtgat gagttgcaat ctgattatatt catgcttggc	1009
Lys Gln Asn *	
84	
acatatggct taccataact tgaaggggaa ctgattgtat tataccagct gggggagatt	1069
ttggaacctt tcatactatg cactcagtga ttgacgcctt ttccatctgt accccgaagg	1129
gactgaacct gatgggggct ttttctggat ggctggggcca tcctgatcaa gcctgatcag	1189
taagtctgtg gaaagattgc agaccaggtg gctaactggg cactggagcc tctgaacct	1249
caggctgtct gccagcaagt tcttttctcc atggcagact gtatgatctg aagtcccccc	1309
aacctctctcc aagtaaagta gtttattaga agctcttaag tctttaatag acctgcatat	1369
ttccttcctt tatgatttcc tataaaatat agtttatggg gttatatttt taactgaaat	1429
actgtacata tgtaaataac tcttgacagg aagaaaatat attaattgtag tatttgcccc	1489
ctatcagtga gctgaacaaa tacatcattt aaatctatgc tgcactttga gttgctacaa	1549
atatggttcg atttgtttat ttttgaaaaa tgtgataaag aaatctaaag aatgattgat	1609
ggcagtcttt ctaatatgtt gcctttgtta taaactactt ggaacttttc ctcaggcact	1669
cactcctccc tgctgacag gaactgtttc catgaagata tgtgttggcc tttgatagag	1729
gcataaagct gaaagatttt tcatttttat atggatatgc tgtcatatgt ttaagaactg	1789

<210> 236

<211> 1935

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (175)..(1872)

<400> 236

```

ccgaggctat aagagggcgc acaagtggcg cggcgcagga gccgccgcca gtggaggggcc      60
gggcgctgcg gccgcggccg gggcgggcgc agggccgagc ggacgggggg gcgcggggccc      120
cccgggaggc cgcggccact ccccccggg ccggcgcggc gggggaggcg gagg   atg      177
                                           Met
                                           1

gaa aca ccc ttc tac ggc gat gag gcg ctg agc ggc ctg ggc ggc ggc      225
Glu Thr Pro Phe Tyr Gly Asp Glu Ala Leu Ser Gly Leu Gly Gly Gly
  2              7              12              17

gcc agt ggc agc ggc ggc agc ttc gcg tcc ccg ggc cgc ttg ttc ccc      273
Ala Ser Gly Ser Gly Gly Ser Phe Ala Ser Pro Gly Arg Leu Phe Pro
  18              23              28              33

ggg gcg ccc ccg acg gcc gcg gcc ggc agc atg atg aag aag gac gcg      321
Gly Ala Pro Pro Thr Ala Ala Ala Gly Ser Met Met Lys Lys Asp Ala
  34              39              44              49

ctg acg ctg agc ctg agt gag cag gtg gcg gca gcg ctc aag cct gcg      369
Leu Thr Leu Ser Leu Ser Glu Gln Val Ala Ala Ala Leu Lys Pro Ala
  50              55              60              65

gcc gcg ccc gcc tcc tac ccc cct gcg cgc cga cgg cgc ccc cag cgc      417
Ala Ala Pro Ala Ser Tyr Pro Pro Ala Arg Arg Arg Arg Pro Gln Arg
  66              71              76              81

ggc acc ccc cga cgg cct gct cgc ctc tcc cga cct ggg gct gct gaa      465
Gly Thr Pro Arg Arg Pro Ala Arg Leu Ser Arg Pro Gly Ala Ala Glu
  82              87              92              97

gct ggc ctc ccc cga gct cga gcg cct cat cat cca gtc caa cgg gct      513
Ala Gly Leu Pro Arg Ala Arg Ala Pro His His Pro Val Gln Arg Ala
  98              103              108              113

ggt cac cac cac gcc gac gag ctc aca gtt cct cta ccc caa ggt ggc      561
Gly His His His Ala Asp Glu Leu Thr Val Pro Leu Pro Gln Gly Gly
  114              119              124              129

ggc cag cga gga gca gga gtt cgc cga ggg ctt cgt caa ggc cct gga      609
Gly Gln Arg Gly Ala Gly Val Arg Arg Gly Leu Arg Gln Gly Pro Gly
  130              135              140              145

gga ttt aca caa gca gaa cca gct cgg cgc ggg cgc ggc cgc tgc cgc      657
Gly Phe Thr Gln Ala Glu Pro Ala Arg Arg Gly Arg Gly Arg Cys Arg
  146              151              156              161

cgc cgc cgc cgc cgc cgg ggg gcc ctc ggg cac ggc cac ggg ctc cgc      705

```

Arg	Arg	Arg	Arg	Arg	Arg	Gly	Ala	Leu	Gly	His	Gly	His	Gly	Leu	Arg	
162						167				172					177	
gcc	ccc	cgg	cga	gct	ggc	ccc	ggc	ggc	ggc	cgc	gcc	cga	agc	gcc	tgt	753
Ala	Pro	Arg	Arg	Ala	Gly	Pro	Gly	Gly	Gly	Arg	Ala	Arg	Ser	Ala	Cys	
178					183					188					193	
cta	cgc	gaa	cct	gag	cag	cta	cgc	ggg	cgg	cgc	cgg	ggg	cgc	ggg	ggg	801
Leu	Arg	Glu	Pro	Glu	Gln	Leu	Arg	Gly	Arg	Arg	Arg	Gly	Arg	Gly	Gly	
194					199					204					209	
cgc	cgc	gac	ggg	cgc	ctt	cgc	tgc	cga	acc	tgt	gcc	ctt	ccc	gcc	gcc	849
Arg	Arg	Asp	Gly	Arg	Leu	Arg	Cys	Arg	Thr	Cys	Ala	Leu	Pro	Ala	Ala	
210					215					220					225	
gcc	acc	ccc	agg	cgc	gtt	ggg	gcc	gcc	gcg	cct	ggc	tgc	gct	caa	gga	897
Ala	Thr	Pro	Arg	Arg	Val	Gly	Ala	Ala	Ala	Pro	Gly	Cys	Ala	Gln	Gly	
226					231					236					241	
cga	gcc	aca	gac	ggg	gcc	cga	cgt	gcc	gag	ctt	cgg	cga	gag	ccc	gcc	945
Arg	Ala	Thr	Asp	Gly	Ala	Arg	Arg	Ala	Glu	Leu	Arg	Arg	Glu	Pro	Ala	
242					247					252					257	
gtt	gtc	gcc	cat	cga	cat	gga	cac	gca	gga	gcg	cat	caa	ggc	gga	gcg	993
Val	Val	Ala	His	Arg	His	Gly	His	Ala	Gly	Ala	His	Gln	Gly	Gly	Ala	
258					263					268					273	
caa	gcg	gct	gcg	caa	ccg	cat	cgc	cgc	ctc	caa	gtg	ccg	caa	gcg	caa	1041
Gln	Ala	Ala	Ala	Gln	Pro	His	Arg	Arg	Leu	Gln	Val	Pro	Gln	Ala	Gln	
274					279					284					289	
gct	gga	gcg	cat	ctc	gcg	cct	gga	aga	gaa	agt	gaa	gac	cct	caa	gag	1089
Ala	Gly	Ala	His	Leu	Ala	Pro	Gly	Arg	Glu	Ser	Glu	Asp	Pro	Gln	Glu	
290					295					300					305	
tca	gaa	cac	gga	gct	ggc	gtc	cac	ggc	gag	cct	gct	gcg	cga	gca	ggg	1137
Ser	Glu	His	Gly	Ala	Gly	Val	His	Gly	Glu	Pro	Ala	Ala	Arg	Ala	Gly	
306					311					316					321	
ggc	gca	gct	caa	gca	gaa	agt	cct	cag	cca	cgt	caa	cag	cgg	ctg	cca	1185
Gly	Ala	Ala	Gln	Ala	Glu	Ser	Pro	Gln	Pro	Arg	Gln	Gln	Arg	Leu	Pro	
322					327					332					337	
gct	gct	gcc	cca	gca	cca	ggg	gcc	cgc	gta	ctg	agt	ccg	cgc	gcg	ggg	1233
Ala	Ala	Ala	Pro	Ala	Pro	Gly	Ala	Arg	Val	Leu	Ser	Pro	Arg	Ala	Gly	
338					343					348					353	
cgc	atg	cgc	ggc	cac	cct	ccc	caa	ggg	gcg	ggc	tgc	cgg	ggg	ggg	gtc	1281
Arg	Met	Arg	Gly	His	Pro	Pro	Gln	Gly	Ala	Gly	Ser	Arg	Gly	Gly	Val	
354					359					364					369	
gtg	ggc	gcc	ccg	gac	ttg	gag	agg	gtg	cgg	ccc	tgg	gga	ccc	ccc	cct	1329
Val	Gly	Ala	Pro	Asp	Leu	Glu	Arg	Val	Arg	Pro	Trp	Gly	Pro	Pro	Pro	
370					375					380					385	
ccc	cga	gtg	tgc	cca	gga	act	cag	aga	ggg	cgc	ggc	ccc	cgg	gga	ttc	1377
Pro	Arg	Val	Cys	Pro	Gly	Thr	Gln	Arg	Gly	Arg	Gly	Pro	Arg	Gly	Phe	

386	391	396	401	
ccc ccc gag ggt gcc cag gac tcg gaa ggg gcg ccc cgg act cga caa				1425
Pro Pro Glu Gly Ala Gln Asp Ser Glu Gly Ala Pro Arg Thr Arg Gln				
402	407	412	417	
gct gga ccc cct gct ccc ggg ggg ggc gag cgc atg acc ccc ccg ccc				1473
Ala Gly Pro Pro Ala Pro Gly Gly Gly Glu Arg Met Thr Pro Pro Pro				
418	423	428	433	
tcg cgc tgc ctc ttt ccc ccg cgc ggc cgc ccc gtg ttg cac aaa ccc				1521
Ser Arg Cys Leu Phe Pro Pro Arg Gly Arg Pro Val Leu His Lys Pro				
434	439	444	449	
gcg cgt ctc ggc tgc ccc ttt gta cac cgc gcc gcg gaa ggg ggc tcc				1569
Ala Arg Leu Gly Cys Pro Phe Val His Arg Ala Ala Glu Gly Gly Ser				
450	455	460	465	
gag ggg gcg cag cct caa acc ctg cct ttc ctt tac ttt tac ttt ttt				1617
Glu Gly Ala Gln Pro Gln Thr Leu Pro Phe Leu Tyr Phe Tyr Phe Phe				
466	471	476	481	
ttt ttt ttt ctt tgg aag aga gaa gaa cag agt gtt cga ttc tgc cct				1665
Phe Phe Phe Leu Trp Lys Arg Glu Glu Gln Ser Val Arg Phe Cys Pro				
482	487	492	497	
att tat gtt tct act cgg gaa caa acg ttg gtt gtg tgt gtg tgt gtt				1713
Ile Tyr Val Ser Thr Arg Glu Gln Thr Leu Val Val Cys Val Cys Val				
498	503	508	513	
ttc ttg tgt tgg ttt ttt aaa gaa atg gga aga aga aaa aaa aat tct				1761
Phe Leu Cys Trp Phe Phe Lys Glu Met Gly Arg Arg Lys Lys Asn Ser				
514	519	524	529	
ccg ccc ctt tcc tcg atc tcg ctc ccc cct tcg gtt ctt tcg acc ggt				1809
Pro Pro Leu Ser Ser Ile Ser Leu Pro Pro Ser Val Leu Ser Thr Gly				
530	535	540	545	
ccc ccc tcc ctt ttt tgt tct gtt ttg ttt tgt ttt gct acg agt cca				1857
Pro Pro Ser Leu Phe Cys Ser Val Leu Phe Cys Phe Ala Thr Ser Pro				
546	551	556	561	
cat tcc tgt ttg taa tocttggttc gcccggtttt ctgttttcag taaagtctcg				1912
His Ser Cys Leu *				
562				
ttacgccaaa aaaaaaaaaa aaa				1935

<210> 237
 <211> 6098
 <212> DNA
 <213> Homo sapiens
 <220>

<221> CDS

<222> (58)..(4251)

<400> 237

acgtcagtgc aggggggactc ccaggggcacc cccacctcca gccaggggcag catcaat	57
atg gag cac tgg atc agc cag gcc atc cac ggc tcc acc acg tcc acc	105
Met Glu His Trp Ile Ser Gln Ala Ile His Gly Ser Thr Thr Ser Thr	
1 5 10 15	
acc tcc tcg tcc tct acg cag agc ggg ggc agc ggg gct gcc cac agg	153
Thr Ser Ser Ser Ser Thr Gln Ser Gly Gly Ser Gly Ala Ala His Arg	
17 22 27 32	
ctg gcg gat gtc atg gct cag acc cac ata gaa aat cat tct gca cct	201
Leu Ala Asp Val Met Ala Gln Thr His Ile Glu Asn His Ser Ala Pro	
33 38 43 48	
cct gac gta acc acg tac acc tca gag cac tcg ata cag gtg gag aga	249
Pro Asp Val Thr Thr Tyr Thr Ser Glu His Ser Ile Gln Val Glu Arg	
49 54 59 64	
ccg cag ggt tcc acg ggg tcc cgg aca gcg ccc aag tac ggc aac gcc	297
Pro Gln Gly Ser Thr Gly Ser Arg Thr Ala Pro Lys Tyr Gly Asn Ala	
65 70 75 80	
gag ctc atg gag acc ggg gat gga gta cca gta agt agc cgg gtg tca	345
Glu Leu Met Glu Thr Gly Asp Gly Val Pro Val Ser Ser Arg Val Ser	
81 86 91 96	
gca aaa atc cag cag ctt gtc aat acc ctc aaa cga ccg aaa cga cca	393
Ala Lys Ile Gln Gln Leu Val Asn Thr Leu Lys Arg Pro Lys Arg Pro	
97 102 107 112	
cct tta cga gaa ttc ttt gtc gat gac ttt gaa gaa tta tta gaa gtt	441
Pro Leu Arg Glu Phe Phe Val Asp Asp Phe Glu Glu Leu Leu Glu Val	
113 118 123 128	
caa caa ccg gat ccg aac caa cca aag ccg gag ggg gcc cag atg ctg	489
Gln Gln Pro Asp Pro Asn Gln Pro Lys Pro Glu Gly Ala Gln Met Leu	
129 134 139 144	
gcc atg cgc gga gag cag ctg ggc gtg gtc acg aac tgg ccg ccg tcg	537
Ala Met Arg Gly Glu Gln Leu Gly Val Val Thr Asn Trp Pro Pro Ser	
145 150 155 160	
ctg gag gcc gca ctg cag agg tgg ggc acc atc tcg ccc aag gcg ccc	585
Leu Glu Ala Ala Leu Gln Arg Trp Gly Thr Ile Ser Pro Lys Ala Pro	
161 166 171 176	
tgc ctg acc acc atg gac acc aac ggg aag ccc ctc tac atc ctc act	633
Cys Leu Thr Thr Met Asp Thr Asn Gly Lys Pro Leu Tyr Ile Leu Thr	
177 182 187 192	
tac ggc aag ctg tgg aca aga agt atg aag gtc gct tac agc att cta	681
Tyr Gly Lys Leu Trp Thr Arg Ser Met Lys Val Ala Tyr Ser Ile Leu	
193 198 203 208	

cac aaa tta ggc aca aag cag gaa ccc atg gtc cgg cct gga gat agg	729
His Lys Leu Gly Thr Lys Gln Glu Pro Met Val Arg Pro Gly Asp Arg	
209 214 219 224	
gtg gca ctg gtg ttc ccc aac aat gat ccg gct gcc ttc atg gcg gct	777
Val Ala Leu Val Phe Pro Asn Asn Asp Pro Ala Ala Phe Met Ala Ala	
225 230 235 240	
ttc tac ggc tgc ctg ctg gcc gag gtg gtc ccc gtg ccc atc gag gtg	825
Phe Tyr Gly Cys Leu Leu Ala Glu Val Val Pro Val Pro Ile Glu Val	
241 246 251 256	
cca ctc acc agg aag gac gca ggg agc cag cag ata ggt ttc ttg ctt	873
Pro Leu Thr Arg Lys Asp Ala Gly Ser Gln Gln Ile Gly Phe Leu Leu	
257 262 267 272	
gga agc tgt gga gtt act gta gcc ttg act agt gac gcc tgc cat aaa	921
Gly Ser Cys Gly Val Thr Val Ala Leu Thr Ser Asp Ala Cys His Lys	
273 278 283 288	
gga ctt cca aaa agc cca acg gga gag atc cca cag ttt aaa ggt tgg	969
Gly Leu Pro Lys Ser Pro Thr Gly Glu Ile Pro Gln Phe Lys Gly Trp	
289 294 299 304	
cca aag ctg ctg tgg ttt gtc aca gag tct aaa cat ctc tcc aaa ccg	1017
Pro Lys Leu Leu Trp Phe Val Thr Glu Ser Lys His Leu Ser Lys Pro	
305 310 315 320	
ccc cga gac tgg ttc cca cac att aaa gat gcc aat aac gac act gcg	1065
Pro Arg Asp Trp Phe Pro His Ile Lys Asp Ala Asn Asn Asp Thr Ala	
321 326 331 336	
tat att gag tac aag acg tgt aag gat ggc agt gtg ctg ggt gtg acg	1113
Tyr Ile Glu Tyr Lys Thr Cys Lys Asp Gly Ser Val Leu Gly Val Thr	
337 342 347 352	
gta acg agg act gcg ctg ctg aca cac tgc cag gcc ctg acg cag gcg	1161
Val Thr Arg Thr Ala Leu Leu Thr His Cys Gln Ala Leu Thr Gln Ala	
353 358 363 368	
tgt ggc tac acg gaa gct gaa acc att gtg aat gtg ctg gat ttc aag	1209
Cys Gly Tyr Thr Glu Ala Glu Thr Ile Val Asn Val Leu Asp Phe Lys	
369 374 379 384	
aag gac gtc ggg ctc tgg cat ggc atc ctg aca agc gtc atg aac atg	1257
Lys Asp Val Gly Leu Trp His Gly Ile Leu Thr Ser Val Met Asn Met	
385 390 395 400	
atg cat gtg atc agc atc ccg tac tcg ctg atg aag gtg aac cct ctc	1305
Met His Val Ile Ser Ile Pro Tyr Ser Leu Met Lys Val Asn Pro Leu	
401 406 411 416	
tcc tgg atc cag aag gtc tgc cag tac aaa gca aaa gtg gcg tgt gtg	1353
Ser Trp Ile Gln Lys Val Cys Gln Tyr Lys Ala Lys Val Ala Cys Val	
417 422 427 432	
aaa tcg agg gat atg cat tgg gca tta gta gca cac aga gat cag aga	1401

Lys	Ser	Arg	Asp	Met	His	Trp	Ala	Leu	Val	Ala	His	Arg	Asp	Gln	Arg		
433					438					443					448		
gac	atc	aac	ctc	tcc	tct	ctg	cga	atg	ctg	ata	gtg	gcg	gac	ggc	gcg		1449
Asp	Ile	Asn	Leu	Ser	Ser	Leu	Arg	Met	Leu	Ile	Val	Ala	Asp	Gly	Ala		
449					454					459					464		
aac	ccc	tgg	tct	att	tct	tct	tgc	gat	gca	ttt	ctc	aat	gtc	ttc	caa		1497
Asn	Pro	Trp	Ser	Ile	Ser	Ser	Cys	Asp	Ala	Phe	Leu	Asn	Val	Phe	Gln		
465					470					475					480		
agt	aaa	ggc	ctt	cga	cag	gag	gtc	atc	tgt	cct	tgt	gcc	agc	tcg	cca		1545
Ser	Lys	Gly	Leu	Arg	Gln	Glu	Val	Ile	Cys	Pro	Cys	Ala	Ser	Ser	Pro		
481					486					491					496		
gag	gcc	ctc	act	gtg	gcc	atc	cgg	agg	ccc	acg	gat	gac	agt	aac	cag		1593
Glu	Ala	Leu	Thr	Val	Ala	Ile	Arg	Arg	Pro	Thr	Asp	Asp	Ser	Asn	Gln		
497					502					507					512		
ccc	ccg	ggc	cgg	ggt	gtc	ctc	tcc	atg	cat	gga	ctg	acc	tat	ggg	gtc		1641
Pro	Pro	Gly	Arg	Gly	Val	Leu	Ser	Met	His	Gly	Leu	Thr	Tyr	Gly	Val		
513					518					523					528		
att	cgt	gtg	gac	tcg	gaa	gag	aag	ctg	tcc	gtg	ctc	acc	gtg	cag	gat		1689
Ile	Arg	Val	Asp	Ser	Glu	Glu	Lys	Leu	Ser	Val	Leu	Thr	Val	Gln	Asp		
529					534					539					544		
gtc	ggc	ctc	gtg	atg	cct	gga	gcc	atc	atg	tgt	tca	gtg	aag	cca	gac		1737
Val	Gly	Leu	Val	Met	Pro	Gly	Ala	Ile	Met	Cys	Ser	Val	Lys	Pro	Asp		
545					550					555					560		
ggg	gtt	cct	cag	ctg	tgc	aga	acg	gat	gag	atc	ggg	gag	ctg	tgt	gtg		1785
Gly	Val	Pro	Gln	Leu	Cys	Arg	Thr	Asp	Glu	Ile	Gly	Glu	Leu	Cys	Val		
561					566					571					576		
tgt	gca	gtt	gcg	acg	ggc	acg	tcc	tac	tat	ggc	ctc	tct	ggc	atg	acc		1833
Cys	Ala	Val	Ala	Thr	Gly	Thr	Ser	Tyr	Tyr	Gly	Leu	Ser	Gly	Met	Thr		
577					582					587					592		
aag	aac	acc	ttt	gag	gtg	ttt	ccc	atg	aca	agc	tcc	ggg	gct	ccg	atc		1881
Lys	Asn	Thr	Phe	Glu	Val	Phe	Pro	Met	Thr	Ser	Ser	Gly	Ala	Pro	Ile		
593					598					603					608		
agt	gaa	tac	cca	ttc	ata	agg	aca	ggc	ttg	ctg	ggg	ttc	gtg	ggt	ccc		1929
Ser	Glu	Tyr	Pro	Phe	Ile	Arg	Thr	Gly	Leu	Leu	Gly	Phe	Val	Gly	Pro		
609					614					619					624		
gga	ggc	ctc	gtc	ttc	gtg	gtg	ggc	aag	atg	gat	ggc	ctc	atg	gtg	gtc		1977
Gly	Gly	Leu	Val	Phe	Val	Val	Gly	Lys	Met	Asp	Gly	Leu	Met	Val	Val		
625					630					635					640		
agc	ggg	cgc	agg	cac	aac	gcc	gac	gac	atc	gtg	gcc	act	gcg	ctg	gcc		2025
Ser	Gly	Arg	Arg	His	Asn	Ala	Asp	Asp	Ile	Val	Ala	Thr	Ala	Leu	Ala		
641					646					651					656		
gta	gaa	ccc	atg	aag	ttt	gtc	tac	cgg	gga	agg	ata	gcc	gtg	ttc	tcg		2073
Val	Glu	Pro	Met	Lys	Phe	Val	Tyr	Arg	Gly	Arg	Ile	Ala	Val	Phe	Ser		

657	662	667	672	
gtg acc gtg ctg cac gac gag agg atc gtg atc gtg gct gag cag agg				2121
Val Thr Val Leu His Asp Glu Arg Ile Val Ile Val Ala Glu Gln Arg				
673	678	683	688	
cct gac tcc acg gaa gag gac agt ttc cag tgg atg agc cgt gtg ctg				2169
Pro Asp Ser Thr Glu Glu Asp Ser Phe Gln Trp Met Ser Arg Val Leu				
689	694	699	704	
cag gcg att gac agt ata cat caa gtt gga gtt tat tgc ctg gcc ttg				2217
Gln Ala Ile Asp Ser Ile His Gln Val Gly Val Tyr Cys Leu Ala Leu				
705	710	715	720	
gtg cca gca aac acc ctc ccc aaa acc ccg ctt ggt ggg atc cat tta				2265
Val Pro Ala Asn Thr Leu Pro Lys Thr Pro Leu Gly Gly Ile His Leu				
721	726	731	736	
tca gaa aca aaa cag ctt ttt ctg gag ggc tct ctg cac ccc tgc aat				2313
Ser Glu Thr Lys Gln Leu Phe Leu Glu Gly Ser Leu His Pro Cys Asn				
737	742	747	752	
gtc cta atg tgc ccc cac acc tgc gtc aca aac ttg cct aag cct cga				2361
Val Leu Met Cys Pro His Thr Cys Val Thr Asn Leu Pro Lys Pro Arg				
753	758	763	768	
cag aag cag cca gaa atc ggc cct gcc tct gtg atg gtg ggg aac ctg				2409
Gln Lys Gln Pro Glu Ile Gly Pro Ala Ser Val Met Val Gly Asn Leu				
769	774	779	784	
gtc tct ggg aag aga atc gcc cag gcc agt ggc aga gac ctg ggt cag				2457
Val Ser Gly Lys Arg Ile Ala Gln Ala Ser Gly Arg Asp Leu Gly Gln				
785	790	795	800	
atc gaa gat aac gac cag gca cgc aag ttc ctg ttc ctc tca gag gtc				2505
Ile Glu Asp Asn Asp Gln Ala Arg Lys Phe Leu Phe Leu Ser Glu Val				
801	806	811	816	
ttg cag tgg aga gca cag acc acc ccg gac cac atc ctc tac acg ctg				2553
Leu Gln Trp Arg Ala Gln Thr Thr Pro Asp His Ile Leu Tyr Thr Leu				
817	822	827	832	
ctc aac tgt cgg ggt gcg ata gcg aac tcg ctg acc tgc gtg cag ctg				2601
Leu Asn Cys Arg Gly Ala Ile Ala Asn Ser Leu Thr Cys Val Gln Leu				
833	838	843	848	
cac aag aga gct gag aag atc gcc gtg atg ctg atg gag agg ggc cac				2649
His Lys Arg Ala Glu Lys Ile Ala Val Met Leu Met Glu Arg Gly His				
849	854	859	864	
ctt cag gac ggc gac cac gtg gcc ttg gtc tac ccc cca gga ata gac				2697
Leu Gln Asp Gly Asp His Val Ala Leu Val Tyr Pro Pro Gly Ile Asp				
865	870	875	880	
ctg ata gca gcg ttt tat ggt tgc ctg tac gca ggc tgt gtg cca ata				2745
Leu Ile Ala Ala Phe Tyr Gly Cys Leu Tyr Ala Gly Cys Val Pro Ile				
881	886	891	896	

acc gtc cgt ccc ccg cac cca cag aac atc gcg acg acg ttg cct acc	2793
Thr Val Arg Pro Pro His Pro Gln Asn Ile Ala Thr Thr Leu Pro Thr	
897 902 907 912	
gtc aag atg att gtg gag gtg agt cgc tct gcc tgt ctg atg acg aca	2841
Val Lys Met Ile Val Glu Val Ser Arg Ser Ala Cys Leu Met Thr Thr	
913 918 923 928	
cag ctg atc tgt aag ttg ctg cgg tcc agg gag gcg gcg gcg gct gtg	2889
Gln Leu Ile Cys Lys Leu Leu Arg Ser Arg Glu Ala Ala Ala Ala Val	
929 934 939 944	
gac gtc agg acg tgg ccc ctc atc ctg gac aca gat gat ttg cca aag	2937
Asp Val Arg Thr Trp Pro Leu Ile Leu Asp Thr Asp Asp Leu Pro Lys	
945 950 955 960	
aag cgg cct gcc cag atc tgc aaa cct tgc aac cca gac act ctt gca	2985
Lys Arg Pro Ala Gln Ile Cys Lys Pro Cys Asn Pro Asp Thr Leu Ala	
961 966 971 976	
tat ctc gac ttc agc gtg tcc aca act ggg atg cta gct ggc gta aag	3033
Tyr Leu Asp Phe Ser Val Ser Thr Thr Gly Met Leu Ala Gly Val Lys	
977 982 987 992	
atg tct cac gca gcc acc agt gcc ttc tgc cgt tcc att aag ctg cag	3081
Met Ser His Ala Ala Thr Ser Ala Phe Cys Arg Ser Ile Lys Leu Gln	
993 998 1003 1008	
tgt gaa ctt tac ccc tct aga gaa gtg gcc atc tgc ctg gac cct tac	3129
Cys Glu Leu Tyr Pro Ser Arg Glu Val Ala Ile Cys Leu Asp Pro Tyr	
1009 1014 1019 1024	
tgt gga ctg gga ttt gtc ctc tgg tgc ctc tgc agt gtg tat tct ggg	3177
Cys Gly Leu Gly Phe Val Leu Trp Cys Leu Cys Ser Val Tyr Ser Gly	
1025 1030 1035 1040	
cac cag tcc atc ctg atc ccg ccc tct gag ctg gaa acc aac ccc gcc	3225
His Gln Ser Ile Leu Ile Pro Pro Ser Glu Leu Glu Thr Asn Pro Ala	
1041 1046 1051 1056	
ttg tgg ctt ctt gcc gtg agt cag tac aaa gtc cga gac acg ttt tgc	3273
Leu Trp Leu Leu Ala Val Ser Gln Tyr Lys Val Arg Asp Thr Phe Cys	
1057 1062 1067 1072	
tcc tac tcc gtg atg gag ctg tgc acc aag ggg ctg ggc tog caa aca	3321
Ser Tyr Ser Val Met Glu Leu Cys Thr Lys Gly Leu Gly Ser Gln Thr	
1073 1078 1083 1088	
gag tcc ctc aag gcg cga ggg ctg gac ttg tcc cga gtg agg acc tgc	3369
Glu Ser Leu Lys Ala Arg Gly Leu Asp Leu Ser Arg Val Arg Thr Cys	
1089 1094 1099 1104	
gtg gtt gtg gcg gaa gag agg cct cgg atc gca ctc aca cag tog ttc	3417
Val Val Val Ala Glu Glu Arg Pro Arg Ile Ala Leu Thr Gln Ser Phe	
1105 1110 1115 1120	

tca aag ctg ttt aag gac ctg ggc ctt cac ccg cgg gcc gtc agc acc	3465
Ser Lys Leu Phe Lys Asp Leu Gly Leu His Pro Arg Ala Val Ser Thr	
1121 1126 1131 1136	
tcg ttc ggt tgc agg gtg aac ctg gcg att tgc ttg cag gga acc tca	3513
Ser Phe Gly Cys Arg Val Asn Leu Ala Ile Cys Leu Gln Gly Thr Ser	
1137 1142 1147 1152	
gga cct gac cca acc act gtc tac gtg gac atg aga gcc ctg aga cac	3561
Gly Pro Asp Pro Thr Thr Val Tyr Val Asp Met Arg Ala Leu Arg His	
1153 1158 1163 1168	
gac aga gtc cgc tta gtg gaa aga gga tcc cct cat agt ctg ccc ctg	3609
Asp Arg Val Arg Leu Val Glu Arg Gly Ser Pro His Ser Leu Pro Leu	
1169 1174 1179 1184	
atg gaa tcg gga aag ata ctt cca ggg gtt cgg att ata att gcc aac	3657
Met Glu Ser Gly Lys Ile Leu Pro Gly Val Arg Ile Ile Ile Ala Asn	
1185 1190 1195 1200	
cca gaa aca aaa gga ccg ctg ggg gac tca cac ctt gga gag att tgg	3705
Pro Glu Thr Lys Gly Pro Leu Gly Asp Ser His Leu Gly Glu Ile Trp	
1201 1206 1211 1216	
gtt cac agt gcc cac aat gcc agc ggt tat ttc act att tac gga gac	3753
Val His Ser Ala His Asn Ala Ser Gly Tyr Phe Thr Ile Tyr Gly Asp	
1217 1222 1227 1232	
gaa tcc ctc cag tca gat cac ttc aac tca aga cta agt ttt gga gac	3801
Glu Ser Leu Gln Ser Asp His Phe Asn Ser Arg Leu Ser Phe Gly Asp	
1233 1238 1243 1248	
acc cag acc atc tgg gca cgc aca ggc tac ttg ggg ttc ctg cgg aga	3849
Thr Gln Thr Ile Trp Ala Arg Thr Gly Tyr Leu Gly Phe Leu Arg Arg	
1249 1254 1259 1264	
act gag ctc aca gat gca aat gga gag cgc cat gat gcc ctc tac gtg	3897
Thr Glu Leu Thr Asp Ala Asn Gly Glu Arg His Asp Ala Leu Tyr Val	
1265 1270 1275 1280	
gta ggg gca ctg gac gaa gcc atg gag ctg cgg ggc atg cgg tac cac	3945
Val Gly Ala Leu Asp Glu Ala Met Glu Leu Arg Gly Met Arg Tyr His	
1281 1286 1291 1296	
cca atc gac att gag acc tcg gtc atc aga gcc cat aaa agc gtt acg	3993
Pro Ile Asp Ile Glu Thr Ser Val Ile Arg Ala His Lys Ser Val Thr	
1297 1302 1307 1312	
gaa tgt gct gtg ttt acc tgg aca aat ttg ttg gtg gtt gtg gtt gag	4041
Glu Cys Ala Val Phe Thr Trp Thr Asn Leu Leu Val Val Val Val Glu	
1313 1318 1323 1328	
ctg gat ggg tcg gaa caa gaa gcc ttg gac ctg gtt ccc ttg gtg acc	4089
Leu Asp Gly Ser Glu Gln Glu Ala Leu Asp Leu Val Pro Leu Val Thr	
1329 1334 1339 1344	
aac gtg gtc ctg gag gag cac tac ctg atc gtc gga gtg gtg gtc gtg	4137

Asn Val Val Leu Glu Glu His Tyr Leu Ile Val Gly Val Val Val Val
 1345 1350 1355 1360

gtg gac atc ggc gtc atc ccc atc aac tcc cgt ggg gag aag cag cgc 4185
 Val Asp Ile Gly Val Ile Pro Ile Asn Ser Arg Gly Glu Lys Gln Arg
 1361 1366 1371 1376

atg cac ctg cga gac ggg ttt ttg gca gac cag cta gac ccc atc tat 4233
 Met His Leu Arg Asp Gly Phe Leu Ala Asp Gln Leu Asp Pro Ile Tyr
 1377 1382 1387 1392

gtg gcc tac aac atg tag tctcgt ctcttggtt ccatggactt ttctagagat 4287
 Val Ala Tyr Asn Met *
 1393 1398

gtagacattg ttctccgtgt ccactgaagc gtgcagacac agggcaacac tcaccagaat 4347

acagccattt gtggtgagag tggaggagga agaggaggag gaagaggact tctcacagca 4407

gccacgattg gcatgggggt gaaatgtgaa tttaccactg aatttcgctc agaaggactt 4467

tggattactg ccttcagttt gttggaaaag cccatttcaa aaactttctt ttcttttctt 4527

tcttttttaa ttattggata ataagtgtt tcttcgtaaa tgtggtattt tgttaagccg 4587

aaatagcaat taaaaaata tcttgcctc cagatgggtt cttttaaaca atttatgtag 4647

tgtgacaaag aattgtttt tctgttttaa tgtgtcatga aatcttaatg acatggatct 4707

gttactaatt taagccattg ctagatctca tcttttagg aaagtttgag gtacgagaaa 4767

accttccaaa tagcacctt caattagata atagcagctt tctttgtcag aaatgtgctg 4827

aagaaacaaa ggctggtata cggccttcga agttagtata gaatgagaag aaattataaa 4887

taaggtgtat ttcggcaatt atcttgcaaa tatctttgta ctaaactaaa aagataaaat 4947

aagttaactt cctcaatatg taattatgta caaaacgttt aatttatttt gatctcttta 5007

gaactataaa agagaaaaac attcaagaat attaaagtct tgtaatgttt gctaataata 5067

aaaagtgttg tattatcttg cgtggatagt atcacaacaa atatatatat atgaaatata 5127

aattcactaa tgaacaaagg agatttttaa gtttaagatg cagaacttgt cacttgcatg 5187

gtgtgcccc cgtactcaca tacactctgc tgttgccagc agtcgcagac cgcaggagcc 5247

ctgtctaaaa gtttcttcta gaaccagaga ccagcaagtg aaattattgc catctcaagg 5307

atggcaaaaag aattcaaagc tcaatgtgca ctattttttt ctttgctgtg ggacaacagt 5367

gaatgtgttt atgccagcgt gtgctgatga tactgagggg ctttaggttg gcaaatagca 5427

ctgttttctt agctgcaaga attcattgca caatgttttt catcattttt gttaatgtca 5487

tctttttttg gtccttgcta cgaaaaggaa tgcgattctg tggtcattcg cactgggttg 5547

cattgattcc cctctgatg gccaatgtgg agtggacaaa gtgtccggaa ctacatcgg 5607
 tgatcgcccc ctogtcttaa gaccagccc gctctgtgtg agcctctggg gtcctctgc 5667
 tcagtgaagca cagttccccg ggggttcatt ccagagctcc ggctgaagca agaagtcctc 5727
 cagctgcgtc gtttgccgcc tgtggacgag tgcgccccag tttctgccct ggcagctcct 5787
 ggccacacct tctcagagct cacctgtgca cttctaaatt gaattggccc acggtgtcca 5847
 accaagaagg agcatctgca ctccgagaaa gatgtgttct gtaactgccc cagtgtgacc 5907
 ccgcagtggc tctcgggtgt agatatgcat gactaagatt gatgctgggc aaaatgtaga 5967
 tgatctttca ttatgttgtg ggcagcgtct ttctctgcct ttgctatatg cagtcagcag 6027
 taagcctttt gctaaaagag ttttgtttga cttctgagat ccaaggctga ttgttgtaa 6087
 aaaaaaaaaa a 6098

<210> 238
 <211> 2007
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1298) .. (1804)

<400> 238
 agattcggca cgaggaaatt tctttactat ctacactatt ctaccctaag atgccaatat 60
 ctactgagac tctccaaaac aggcacagat tatccagcat ttccccagct tagatgggtca 120
 tttttttgtg ggatgcctgt taacatctcc cctggatgtt aatgttctga ggagcatggt 180
 ttgggaaagg acctcgtggg acttacagga agtagaaaga tgtcacccat taaaggccac 240
 cacggtaaga acattcctct ccttttagca gttgcttaag ctgcacaagt tggagtaaga 300
 tgtcacccctt tttatccagg tcattgggtt agctgacagg gagccaagat tgaaatctaa 360
 gatctttgcc ctgcaggatt cagggttaat ggacatcctg agatgggagg aaggagcttt 420
 cattacagcc ttgtgggtct tgactacca gtccctgcag gagccagtgg agttcctgcc 480
 atgggtgtccc tgaggagggt tagctttctca cctaccctgc cgccaagccc ctcagtctgg 540
 gtcttctttt cccatgcagc ctccagccca ggctgcatac tatggctgtg gccagtgac 600
 acccaccag cctgccccca ggtggacatc ccagccacct agaccttcct gtgagtgacc 660
 cagccccttc cactctcaga ctggcctatt ggtgtggggc ccgtgaggca gtcataacac 720

agggatgaaa cctggctctg ccacttccca aggtgggtga cttcacttct ctgagcctca	780
gtttcctctt ctgagcatgg gcctgaatga gacgtgtgta aagtaccaag cacagtgggtg	840
agccaatgga agacacgcag ctagccacca gcagtcacat ccaaagatgc ctctgatttg	900
tgactctgaa aattcttgca aagctgagaa ggtgaaattc ctctggctat attgttgacc	960
aaaggccctc ctctgtaaga gtgaattgca cgctcacttg aaactatctt gagggactaa	1020
ggtgtacaat cctggtgctt atgcagtttg gggctctagg tagacacgag ctggctttga	1080
aattgtagat tcctacactc cccctttctg gagttctggg tctaagtga ttgactccta	1140
tttctgttgt gaatgttgta gtttcccttc ccattctott ggtggccctg gaagcttcta	1200
ggcacagtgt gccaccctga ttattccac cactccatcc aacttttctc tctctgtggt	1260
gtctgcacca caagctgcct accctccagg tgccctca atg gtc cgg cca cca gtt	1315
Met Val Arg Pro Pro Val	
1	
gtg cct cgg cgc ccc ccg gcc cac atc agc agt gtc agg cag gcc tcc	1363
Val Pro Arg Arg Pro Pro Ala His Ile Ser Ser Val Arg Gln Ala Ser	
7 12 17 22	
acc cag gtg cca cgc acg gtg cct cat acc cag aga gta gcc aac att	1411
Thr Gln Val Pro Arg Thr Val Pro His Thr Gln Arg Val Ala Asn Ile	
23 28 33 38	
ggt act cag acc aca gga ccc agt ggg gta gga tgc tgt aca cca ggc	1459
Gly Thr Gln Thr Thr Gly Pro Ser Gly Val Gly Cys Cys Thr Pro Gly	
39 44 49 54	
cgg ccg ctc ctg ccg tgc aaa tgt tcc tca gca gca cat agc acc tat	1507
Arg Pro Leu Leu Pro Cys Lys Cys Ser Ser Ala Ala His Ser Thr Tyr	
55 60 65 70	
cgg gtc cag gag ccg gct gtg cac atc cca gga cag gag ccc ctg acc	1555
Arg Val Gln Glu Pro Ala Val His Ile Pro Gly Gln Glu Pro Leu Thr	
71 76 81 86	
gcg tcc atg ctg gct gcg gcg ccc ctg cat gag caa aag cag atg att	1603
Ala Ser Met Leu Ala Ala Pro Leu His Glu Gln Lys Gln Met Ile	
87 92 97 102	
ggg gag cgt ctc tac ccc ctt atc cat gat gtc cac acc cag ctg gct	1651
Gly Glu Arg Leu Tyr Pro Leu Ile His Asp Val His Thr Gln Leu Ala	
103 108 113 118	
ggc aag atc acg ggc atg ctg ctg gag att gac aac tcg gag ctg ttg	1699
Gly Lys Ile Thr Gly Met Leu Leu Glu Ile Asp Asn Ser Glu Leu Leu	
119 124 129 134	
ctc atg ctg gag tct cca gaa tcc ctc cat gcc aag ata gac gag gca	1747
Leu Met Leu Glu Ser Pro Glu Ser Leu His Ala Lys Ile Asp Glu Ala	
135 140 145 150	

gtg gcc gtg ctg cag gca cac cag gct atg gag cag ccg aag gcg tac 1795
Val Ala Val Leu Gln Ala His Gln Ala Met Glu Gln Pro Lys Ala Tyr
151 156 161 166

atg cac tga aaccaga aaaggaaatc ctcgcttcca tggctgccaa aaggacagt 1851
Met His *
167

tttctggctc tcagccctaa ggccttgcaa actctaactt atttcccaat tagtctgtat 1911

ctataacttgg gctctgtatg tgaatgaagg ttggtcaccc atccagccta ttaccttttg 1971

ctttgtgtat taaaagtgtc gcaaaaaaaaa aaaaaa 2007

<210> 239
<211> 1408
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (401)..(1072)

<400> 239
tcgattacgc caagcttggc acgagggggc taatgaagcc tagaccccag ctggattgga 60
agcaaaggcc tttccttcac tgggaaagggt gctgctgcta cccatctcat tattctaaga 120
gtgattgaga atagaggggc tgaagggaaa cgaaagtagg agaatgttgg ccagagctag 180
tagagaaaga acgtaatat gagaaagcag acatcagtgc taggtgaggt gctttcttta 240
aagagctgtg tgtatagact ggggaggagt ctgtctgggg acaggaatgc tgattccttt 300
ttttccttgg gcagaatcct aatgtacctg gctagctggt ggtgagtagg ggctttgggg 360
ccaacttggt gggctcccca aggaaacccc tttgaaacca atg gat gca ttc acg 415
Met Asp Ala Phe Thr
1

ggc tcg ggt ctc aag agg aag ttt gat gat gtg gat gtg ggc tca tca 463
Gly Ser Gly Leu Lys Arg Lys Phe Asp Asp Val Asp Val Gly Ser Ser
6 11 16 21

gtt tcc aac tca gat gat gag atc tcc agc agt gat agt gct gac agc 511
Val Ser Asn Ser Asp Asp Glu Ile Ser Ser Ser Asp Ser Ala Asp Ser
22 27 32 37

tgc gac agc ctc aat cct cct acc act gcc agc ttc aca ccc aca tcc 559
Cys Asp Ser Leu Asn Pro Pro Thr Thr Ala Ser Phe Thr Pro Thr Ser
38 43 48 53

atc ctg aag cgg cag aag cag ctg cgg agg aag aat gta cgc ttt gac 607

Ile	Leu	Lys	Arg	Gln	Lys	Gln	Leu	Arg	Arg	Lys	Asn	Val	Arg	Phe	Asp		
54					59					64					69		
cag	gtg	act	gta	tac	tac	ttt	gcc	cgg	cgc	caa	ggg	ttt	acc	agt	gtg	655	
Gln	Val	Thr	Val	Tyr	Tyr	Phe	Ala	Arg	Arg	Gln	Gly	Phe	Thr	Ser	Val		
70					75					80					85		
ccc	agc	cag	ggg	ggg	agc	tct	ctg	ggc	atg	gcc	cag	cgc	cat	aac	tct	703	
Pro	Ser	Gln	Gly	Gly	Ser	Ser	Leu	Gly	Met	Ala	Gln	Arg	His	Asn	Ser		
86					91					96					101		
gta	cgg	agc	tat	aca	ctc	tgt	gag	ttt	gcc	cag	gaa	cag	gag	gtg	aac	751	
Val	Arg	Ser	Tyr	Thr	Leu	Cys	Glu	Phe	Ala	Gln	Glu	Gln	Glu	Val	Asn		
102					107					112					117		
cat	cga	gag	att	ctg	cgt	gag	cac	ctg	aag	gaa	gag	aaa	ctc	cat	gcc	799	
His	Arg	Glu	Ile	Leu	Arg	Glu	His	Leu	Lys	Glu	Glu	Lys	Leu	His	Ala		
118					123					128					133		
aag	aaa	atg	aag	ctg	acc	aag	aat	ggg	aca	gtg	gag	tcg	gtg	gag	gct	847	
Lys	Lys	Met	Lys	Leu	Thr	Lys	Asn	Gly	Thr	Val	Glu	Ser	Val	Glu	Ala		
134					139					144					149		
gat	ggc	ctg	acg	ctg	gat	gat	gtg	tca	gat	gaa	gat	att	gat	gtg	gaa	895	
Asp	Gly	Leu	Thr	Leu	Asp	Asp	Val	Ser	Asp	Glu	Asp	Ile	Asp	Val	Glu		
150					155					160					165		
aat	gtg	gag	gtg	gat	gat	tac	ttc	ttc	ctg	cag	cct	ctg	ccc	acc	aaa	943	
Asn	Val	Glu	Val	Asp	Asp	Tyr	Phe	Phe	Leu	Gln	Pro	Leu	Pro	Thr	Lys		
166					171					176					181		
cgg	cga	cgg	gcc	ctg	ctg	agg	gct	tct	ggg	gtc	cac	cgt	att	gat	gct	991	
Arg	Arg	Arg	Ala	Leu	Leu	Arg	Ala	Ser	Gly	Val	His	Arg	Ile	Asp	Ala		
182					187					192					197		
gaa	gag	aag	caa	gaa	ctt	cga	gcc	atc	cgc	ctg	tca	cgg	gaa	gaa	tgt	1039	
Glu	Glu	Lys	Gln	Glu	Leu	Arg	Ala	Ile	Arg	Leu	Ser	Arg	Glu	Glu	Cys		
198					203					208					213		
ggg	tgt	gac	tgc	cga	ctg	tat	tgt	gac	cca	taa	gcgtgtgc	ctgcagccag				1090	
Gly	Cys	Asp	Cys	Arg	Leu	Tyr	Cys	Asp	Pro	*							
214					219					224							
gctgggatta	aatgccaggt	ggatcgc	atg	tcctttccat	gtggctgctc	ccgggatggc										1150	
tgtgggaaca	tggcaggacg	cattgaattt	aatccaatcc	gggtccggac	tcattacctc											1210	
cacaccatta	tgaagctgga	gctggagagc	aagcggcagg	tgagccgccc	agcagcccca											1270	
gatgaggagc	cctccccgac	tgccagttgc	agcctgacag	gagcacaggg	ctctgagacc											1330	
caggacttcc	aggagttcat	tgctgagaat	gagacagcag	tgatgcacct	gcagagtgca											1390	
gaggaactgg	agcggctc															1408	

<210> 240
 <211> 4953
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(4953)

<400> 240

atg gcc tgt gct gtg gtt tca gag aag cac aag gca gga agc aag agg 48
 Met Ala Cys Ala Val Val Ser Glu Lys His Lys Ala Gly Ser Lys Arg
 1 5 10

cat tta gca cag gct cat ggt gag atg ctg tca ggt atc acc tac att 96
 His Leu Ala Gln Ala His Gly Glu Met Leu Ser Gly Ile Thr Tyr Ile
 17 22 27 32

aag ttt gtc aaa gtc cct ggg gaa ctg gtt act gca aag atg gct gaa 144
 Lys Phe Val Lys Val Pro Gly Glu Leu Val Thr Ala Lys Met Ala Glu
 33 38 43 48

ata aga gag cag tgt gtg gca ggc ccc cgt gga gga tca acg cag tgg 192
 Ile Arg Glu Gln Cys Val Ala Gly Pro Arg Gly Gly Ser Thr Gln Trp
 49 54 59 64

ctg aac acc ggg aag gaa ctg gca ctt gga gtc tgg aca ttt gaa act 240
 Leu Asn Thr Gly Lys Glu Leu Ala Leu Gly Val Trp Thr Phe Glu Thr
 65 70 75 80

tgg gag aga ggc tca cca ctt ttg agt cca cgg ggc ttg cac ctc cac 288
 Trp Glu Arg Gly Ser Pro Leu Leu Ser Pro Arg Gly Leu His Leu His
 81 86 91 96

aag aca aac atc cct agg cca ccc aga gta ggc aag aga gga ggt gaa 336
 Lys Thr Asn Ile Pro Arg Pro Pro Arg Val Gly Lys Arg Gly Gly Glu
 97 102 107 112

gcc tcg gga gaa acc cct ccc ttg gca gct ggt tta aga ccc aaa acg 384
 Ala Ser Gly Glu Thr Pro Pro Leu Ala Ala Gly Leu Arg Pro Lys Thr
 113 118 123 128

ggg ata caa atg ccc ctg aga gag cag tgg tat act gga ata gat gag 432
 Gly Ile Gln Met Pro Leu Arg Glu Gln Trp Tyr Thr Gly Ile Asp Glu
 129 134 139 144

gat ggg cac atg gtg gag agg cgt gtt ttt gtg tac cag ccc ttc ttc 480
 Asp Gly His Met Val Glu Arg Arg Val Phe Val Tyr Gln Pro Phe Phe
 145 150 155 160

tct gcc gac ctc ctc aac tgg aaa aac aat acc cca tcc tat act gaa 528
 Ser Ala Asp Leu Leu Asn Trp Lys Asn Asn Thr Pro Ser Tyr Thr Glu
 161 166 171 176

aag ccg caa gct cta att gat ttg ctc caa act att atc cag acc cat 576
 Lys Pro Gln Ala Leu Ile Asp Leu Leu Gln Thr Ile Ile Gln Thr His

177	182	187	192	
aac ccc act tgg gct gat tgc cac cag ttg ctc atg ttc ctc ttt aac				624
Asn Pro Thr Trp Ala Asp Cys His Gln Leu Leu Met Phe Leu Phe Asn				
193	198	203	208	
aca gat gaa agg cgg aga gtg ctc caa gca gca act aag tgg cta gag				672
Thr Asp Glu Arg Arg Arg Val Leu Gln Ala Ala Thr Lys Trp Leu Glu				
209	214	219	224	
gaa cat gca ccg gct gat tac caa aac ccc caa gag tat gta agg acc				720
Glu His Ala Pro Ala Asp Tyr Gln Asn Pro Gln Glu Tyr Val Arg Thr				
225	230	235	240	
cag tta ccg gga acc gac ccc cag tgg gac cca aat gaa aga gag gat				768
Gln Leu Pro Gly Thr Asp Pro Gln Trp Asp Pro Asn Glu Arg Glu Asp				
241	246	251	256	
atg caa agg cta aac cga tac agg gaa gct ctc ttg gaa gga tta aag				816
Met Gln Arg Leu Asn Arg Tyr Arg Glu Ala Leu Leu Glu Gly Leu Lys				
257	262	267	272	
agg gga gcc cag aag gcc aca aac gtg gcc att cag gga aaa gaa gaa				864
Arg Gly Ala Gln Lys Ala Thr Asn Val Ala Ile Gln Gly Lys Glu Glu				
273	278	283	288	
agt cca gca caa ttc tac gag agg ctg tgt gag gcc tat tgt atg tat				912
Ser Pro Ala Gln Phe Tyr Glu Arg Leu Cys Glu Ala Tyr Cys Met Tyr				
289	294	299	304	
act ccc ttt gat ccc aat agt cct gaa aat cag cgc atg att aac atg				960
Thr Pro Phe Asp Pro Asn Ser Pro Glu Asn Gln Arg Met Ile Asn Met				
305	310	315	320	
gct tta gtt agt caa agt gca gaa gac att aga aga aaa ctg cag aaa				1008
Ala Leu Val Ser Gln Ser Ala Glu Asp Ile Arg Arg Lys Leu Gln Lys				
321	326	331	336	
cag gct ggg ttt gca ggg atg aac aca tca cag tta tta gaa ata gct				1056
Gln Ala Gly Phe Ala Gly Met Asn Thr Ser Gln Leu Leu Glu Ile Ala				
337	342	347	352	
aac cag gtg ttt gta aac agg gat gca gta agc cct aag gaa aac cgc				1104
Asn Gln Val Phe Val Asn Arg Asp Ala Val Ser Pro Lys Glu Asn Arg				
353	358	363	368	
aga gag aat gaa cat cag gtc cgg cga aat gcc gac ctg tta gct gca				1152
Arg Glu Asn Glu His Gln Val Arg Arg Asn Ala Asp Leu Leu Ala Ala				
369	374	379	384	
gca atc aca ggg gtc ccc cca aag agg caa ggg aag ggg ggc ccc ggg				1200
Ala Ile Thr Gly Val Pro Pro Lys Arg Gln Gly Lys Gly Gly Pro Gly				
385	390	395	400	
aaa gaa att cag cct ggt tgt cag agc ttg cag cgt aat cag tgt gct				1248
Lys Glu Ile Gln Pro Gly Cys Gln Ser Leu Gln Arg Asn Gln Cys Ala				
401	406	411	416	

tat tgt aaa gaa ata gga cat tgg aag aac aaa tgc cct cag cta aaa	1296
Tyr Cys Lys Glu Ile Gly His Trp Lys Asn Lys Cys Pro Gln Leu Lys	
417 422 427 432	
gga aaa caa ggt gac tgc gag cag gag gat cca gac aag gag gaa ggg	1344
Gly Lys Gln Gly Asp Ser Glu Gln Glu Asp Pro Asp Lys Glu Glu Gly	
433 438 443 448	
gcc ctg ctc aac ctg gca gaa agg acc ccc aaa gag cct atg gtc agg	1392
Ala Leu Leu Asn Leu Ala Glu Arg Thr Pro Lys Glu Pro Met Val Arg	
449 454 459 464	
atg aca gtt ggg ggt aaa gac att gat ttt ctt gta ³ gat acc ggt gct	1440
Met Thr Val Gly Gly Lys Asp Ile Asp Phe Leu Val Asp Thr Gly Ala	
465 470 475 480	
gaa cat tgc gta gta acc acc ccg gtc agc ccc tta tcc aaa aag act	1488
Glu His Ser Val Val Thr Thr Pro Val Ser Pro Leu Ser Lys Lys Thr	
481 486 491 496	
att gac ata att gga gcc aca gga gtt tca gca aaa caa gct ttc tgc	1536
Ile Asp Ile Ile Gly Ala Thr Gly Val Ser Ala Lys Gln Ala Phe Cys	
497 502 507 512	
ttg ccc cgg act tgt act gta gga gga cat aaa gtg att cat cag ttt	1584
Leu Pro Arg Thr Cys Thr Val Gly Gly His Lys Val Ile His Gln Phe	
513 518 523 528	
ttg tac atg cct gat tgt ccc ttg ccc ttg ttg gga agg gac ttg ctt	1632
Leu Tyr Met Pro Asp Cys Pro Leu Pro Leu Leu Gly Arg Asp Leu Leu	
529 534 539 544	
agc aaa ctg aga gcc act atc tat ttt aca gag cat ggc tct ttg ctg	1680
Ser Lys Leu Arg Ala Thr Ile Tyr Phe Thr Glu His Gly Ser Leu Leu	
545 550 555 560	
cta aag tta ccc gga acg gga gtc att atg acc ctt atg gta ccc cga	1728
Leu Lys Leu Pro Gly Thr Gly Val Ile Met Thr Leu Met Val Pro Arg	
561 566 571 576	
gag gag gaa tgg aaa ctt ttc tta act gag tgc ggc caa gag ata aga	1776
Glu Glu Glu Trp Lys Leu Phe Leu Thr Glu Ser Gly Gln Glu Ile Arg	
577 582 587 592	
cca gct ctg gct aag tgg tgg cca aga gtg tgg gca gaa gac aac cct	1824
Pro Ala Leu Ala Lys Trp Trp Pro Arg Val Trp Ala Glu Asp Asn Pro	
593 598 603 608	
cca ggg ttg gca gtc aac caa gcc ccc gta ctt ata gaa gtt aag cct	1872
Pro Gly Leu Ala Val Asn Gln Ala Pro Val Leu Ile Glu Val Lys Pro	
609 614 619 624	
agg gcc cag ccg gtt agg caa aaa cag tac ccg gtc ccc aga gaa gct	1920
Arg Ala Gln Pro Val Arg Gln Lys Gln Tyr Pro Val Pro Arg Glu Ala	
625 630 635 640	

ctt caa ggt atc cag gtc cat ctc aag tgc cta aga acc ttt gga att Leu Gln Gly Ile Gln Val His Leu Lys Cys Leu Arg Thr Phe Gly Ile 641 646 651 656	1968
ata gtt cct tgt cag tct cca tgg aac act ccc ctc ctg cct gtt ccc Ile Val Pro Cys Gln Ser Pro Trp Asn Thr Pro Leu Leu Pro Val Pro 657 662 667 672	2016
aag cct ggg acc aag gac tac agg ccg gta cag gat ttg cgc ttg gtt Lys Pro Gly Thr Lys Asp Tyr Arg Pro Val Gln Asp Leu Arg Leu Val 673 678 683 688	2064
aat cag gct aca gtg act tta cac cca aca gta cct aac tgg tac aca Asn Gln Ala Thr Val Thr Leu His Pro Thr Val Pro Asn Trp Tyr Thr 689 694 699 704	2112
ttg ctg ggg ttg ctg cca gct gag gac agc tgg ttc acc tgc ttg gac Leu Leu Gly Leu Leu Pro Ala Glu Asp Ser Trp Phe Thr Cys Leu Asp 705 710 715 720	2160
ctg aaa gat gct ttc ttt agc atc aga tta gcc cct gag agc cag aag Leu Lys Asp Ala Phe Phe Ser Ile Arg Leu Ala Pro Glu Ser Gln Lys 721 726 731 736	2208
ctg ttt gcc ttt cag tgg gaa gat ccg gag tca ggt gtc act act cag Leu Phe Ala Phe Gln Trp Glu Asp Pro Glu Ser Gly Val Thr Thr Gln 737 742 747 752	2256
tac act tgg atc cgg ctt ccc aaa ggg ttc aag aac tcc ccc acc atc Tyr Thr Trp Ile Arg Leu Pro Lys Gly Phe Lys Asn Ser Pro Thr Ile 753 758 763 768	2304
ttc ggg gag gca ttg gct caa gac ctc cag aag ttt ccc acc aga gac Phe Gly Glu Ala Leu Ala Gln Asp Leu Gln Lys Phe Pro Thr Arg Asp 769 774 779 784	2352
cta ggc tgc atg ttg ctc cag tac gtt gat gac ctt ttt ctg gga cac Leu Gly Cys Met Leu Leu Gln Tyr Val Asp Asp Leu Phe Leu Gly His 785 790 795 800	2400
cct acg gca gtc agg tgc gcc aag gga aca gat gct cta ctc cgg cac Pro Thr Ala Val Arg Cys Ala Lys Gly Thr Asp Ala Leu Leu Arg His 801 806 811 816	2448
ctg gag gac tgt ggg tat aag gtg ttc aag aaa aaa gtt cag atc tgc Leu Glu Asp Cys Gly Tyr Lys Val Phe Lys Lys Lys Val Gln Ile Cys 817 822 827 832	2496
cga cag cag gta cgt tac ttg gga ttt act atc cgg cag ggg gag tgc Arg Gln Gln Val Arg Tyr Leu Gly Phe Thr Ile Arg Gln Gly Glu Cys 833 838 843 848	2544
agc ctg gga tca aaa aga aag caa gtc att tgt aat cta ccg gag cct Ser Leu Gly Ser Lys Arg Lys Gln Val Ile Cys Asn Leu Pro Glu Pro 849 854 859 864	2592
aag acc aga agg cag agc cct gtc aag cat gac tgt gta gaa gtg ttg	2640

Lys Thr Arg Arg Gln Ser Pro Val Lys His Asp Cys Val Glu Val Leu	
865 870 875 880	
gac tca gtt tac tct agc aga cct gac ctc cgg gac cag cct tgg gca	2688
Asp Ser Val Tyr Ser Ser Arg Pro Asp Leu Arg Asp Gln Pro Trp Ala	
881 886 891 896	
tca gta gac tgg gta cta tac gtg gat ggg agc agc ttc atc aac cca	2736
Ser Val Asp Trp Val Leu Tyr Val Asp Gly Ser Ser Phe Ile Asn Pro	
897 902 907 912	
caa gga gag aga tgt gca ggg tat gcg gtg gta act ctg gac act gtt	2784
Gln Gly Glu Arg Cys Ala Gly Tyr Ala Val Val Thr Leu Asp Thr Val	
913 918 923 928	
gtt gaa gcc cga tgc ttg ccc cag ggc act tca gct cag aaa act gaa	2832
Val Glu Ala Arg Ser Leu Pro Gln Gly Thr Ser Ala Gln Lys Thr Glu	
929 934 939 944	
ctc att gct tta att tgg gcc tta gaa ctc agt gaa gca cct gat ctt	2880
Leu Ile Ala Leu Ile Trp Ala Leu Glu Leu Ser Glu Ala Pro Asp Leu	
945 950 955 960	
gta cct act tat tct aaa gaa gaa aat gac ttt ctc cag gca gag gga	2928
Val Pro Thr Tyr Ser Lys Glu Glu Asn Asp Phe Leu Gln Ala Glu Gly	
961 966 971 976	
gga caa gtg atg gag gaa gga ttg att cgg tta cca gat ggg aga gta	2976
Gly Gln Val Met Glu Glu Gly Leu Ile Arg Leu Pro Asp Gly Arg Val	
977 982 987 992	
gct gtg cca cag ctg cta gga gct gca gtt gta ctg gct gtc cat gaa	3024
Ala Val Pro Gln Leu Leu Gly Ala Ala Val Val Leu Ala Val His Glu	
993 998 1003 1008	
acc acc cat cta ggt cag gaa tca ctt gaa aag ttg tta ggc tgg tat	3072
Thr Thr His Leu Gly Gln Glu Ser Leu Glu Lys Leu Leu Gly Trp Tyr	
1009 1014 1019 1024	
ttc tac atc tgc cat ttg tca gcc ctt gcc aaa acg gtg acc cag cgg	3120
Phe Tyr Ile Ser His Leu Ser Ala Leu Ala Lys Thr Val Thr Gln Arg	
1025 1030 1035 1040	
tgt gtt acc tgc cga cag cat aat gcg agg caa ggt cta gct gtt cca	3168
Cys Val Thr Cys Arg Gln His Asn Ala Arg Gln Gly Leu Ala Val Pro	
1041 1046 1051 1056	
cct ggc ata caa gct tat gga gaa gcc ccc ttt gaa gat ctg gat cca	3216
Pro Gly Ile Gln Ala Tyr Gly Glu Ala Pro Phe Glu Asp Leu Asp Pro	
1057 1062 1067 1072	
ggt gga ctt cac aga gat gcc aaa gtg tgg aga ttt gga ctg cct tta	3264
Gly Gly Leu His Arg Asp Ala Lys Val Trp Arg Phe Gly Leu Pro Leu	
1073 1078 1083 1088	
tggt atc ggc tca gat aac ggg ccg gca ttt gtg gct gac ttg gta cag	3312
Trp Ile Gly Ser Asp Asn Gly Pro Ala Phe Val Ala Asp Leu Val Gln	

1089	1094	1099	1104	
aag atg gca aag gta ttg ggg atc aca tgg aaa ctg cat gct gcc tac				3360
Lys Met Ala Lys Val Leu Gly Ile Thr Trp Lys Leu His Ala Ala Tyr				
1105	1110	1115	1120	
cgg cct cag agt tcc gga aag gtg gag cag atg aat cgg act atc aaa				3408
Arg Pro Gln Ser Ser Gly Lys Val Glu Gln Met Asn Arg Thr Ile Lys				
1121	1126	1131	1136	
aat agt tta ggg aaa aac aaa aag gac cca gtt tat ctt cag aag ggg				3456
Asn Ser Leu Gly Lys Asn Lys Lys Asp Pro Val Tyr Leu Gln Lys Gly				
1137	1142	1147	1152	
gaa gcc aac ccc tcc tgt gct gcc ggt cac tgt aac cca cta gaa cta				3504
Glu Ala Asn Pro Ser Cys Ala Ala Gly His Cys Asn Pro Leu Glu Leu				
1153	1158	1163	1168	
ata att acc aat ccc cta gat ccc cgt tgg aaa aac gga gaa cgt gta				3552
Ile Ile Thr Asn Pro Leu Asp Pro Arg Trp Lys Asn Gly Glu Arg Val				
1169	1174	1179	1184	
acc ctg ggg att gat ggg aca ggg tta aac ccc caa gtt gcc att tta				3600
Thr Leu Gly Ile Asp Gly Thr Gly Leu Asn Pro Gln Val Ala Ile Leu				
1185	1190	1195	1200	
att aga ggg gag gtc ccc aag cgc tct ccc aaa cca gta ttt caa acc				3648
Ile Arg Gly Glu Val Pro Lys Arg Ser Pro Lys Pro Val Phe Gln Thr				
1201	1206	1211	1216	
ttt tat gag gag ctg aat ctg cca gca cca gaa ctt cca aaa aag aca				3696
Phe Tyr Glu Glu Leu Asn Leu Pro Ala Pro Glu Leu Pro Lys Lys Thr				
1217	1222	1227	1232	
aaa aat ttg ttt ctg caa tta gca gaa aat gta gct cat tcc ctt aaa				3744
Lys Asn Leu Phe Leu Gln Leu Ala Glu Asn Val Ala His Ser Leu Lys				
1233	1238	1243	1248	
gtt act tct tgt tat gta tgc ggg gga acc act atc gga gac cga tgg				3792
Val Thr Ser Cys Tyr Val Cys Gly Gly Thr Thr Ile Gly Asp Arg Trp				
1249	1254	1259	1264	
cct tgg gaa gcc cga gag ttg gtg cct act gat cca gct cct gac ata				3840
Pro Trp Glu Ala Arg Glu Leu Val Pro Thr Asp Pro Ala Pro Asp Ile				
1265	1270	1275	1280	
att cca gtt cag aag gcc caa gct agc aac ttc tgg gtc tta aaa acc				3888
Ile Pro Val Gln Lys Ala Gln Ala Ser Asn Phe Trp Val Leu Lys Thr				
1281	1286	1291	1296	
tca att att gga caa tac tgt ata gct aga gaa ggg aaa gac ttt atc				3936
Ser Ile Ile Gly Gln Tyr Cys Ile Ala Arg Glu Gly Lys Asp Phe Ile				
1297	1302	1307	1312	
atc cct gta gga aag ctt aat tgt ata gga cag aag ttg tat aac agc				3984
Ile Pro Val Gly Lys Leu Asn Cys Ile Gly Gln Lys Leu Tyr Asn Ser				
1313	1318	1323	1328	

aca aca aag aca att act tgt tgg ggc cta aac cac act gaa aag aat	4032
Thr Thr Lys Thr Ile Thr Cys Trp Gly Leu Asn His Thr Glu Lys Asn	
1329 1334 1339 1344	
cca ttt agt aaa ttt tct aag tta aaa act gct tgg gct cat cca gaa	4080
Pro Phe Ser Lys Phe Ser Lys Leu Lys Thr Ala Trp Ala His Pro Glu	
1345 1350 1355 1360	
tct cat cag gac tgg atg gct ccc gct gga cta tac tgg ata tgt ggg	4128
Ser His Gln Asp Trp Met Ala Pro Ala Gly Leu Tyr Trp Ile Cys Gly	
1361 1366 1371 1376	
cac aga gcc tat att cgg tta cct gat aaa tgg gca ggc agt tgt gtt	4176
His Arg Ala Tyr Ile Arg Leu Pro Asp Lys Trp Ala Gly Ser Cys Val	
1377 1382 1387 1392	
att ggc act att aag ctg tgc ttt ttc tta tta ccc ata aaa acg ggt	4224
Ile Gly Thr Ile Lys Leu Cys Phe Phe Leu Leu Pro Ile Lys Thr Gly	
1393 1398 1403 1408	
gag ctc cta ggt ttc ccc atc tat gcc tcc caa gaa aag aga ggc ata	4272
Glu Leu Leu Gly Phe Pro Ile Tyr Ala Ser Gln Glu Lys Arg Gly Ile	
1409 1414 1419 1424	
gtt ata gga aac tgg aaa gat aat gag tgg ccc cct gaa agg atc ata	4320
Val Ile Gly Asn Trp Lys Asp Asn Glu Trp Pro Pro Glu Arg Ile Ile	
1425 1430 1435 1440	
cag tat tat ggg cct gcc aca tgg gca caa gac ggc tca tgg gga tac	4368
Gln Tyr Tyr Gly Pro Ala Thr Trp Ala Gln Asp Gly Ser Trp Gly Tyr	
1441 1446 1451 1456	
cga acc ccc atc tac atg ctc aat cgg atc ata cgg ttg cag gcc atc	4416
Arg Thr Pro Ile Tyr Met Leu Asn Arg Ile Ile Arg Leu Gln Ala Ile	
1457 1462 1467 1472	
tta aaa ata att act aat gaa act ggc aga gct ttg act gtt ttg gct	4464
Leu Lys Ile Ile Thr Asn Glu Thr Gly Arg Ala Leu Thr Val Leu Ala	
1473 1478 1483 1488	
tgg caa gaa acc caa atg agg aat gct atc tat cag aat aga ctg gcc	4512
Trp Gln Glu Thr Gln Met Arg Asn Ala Ile Tyr Gln Asn Arg Leu Ala	
1489 1494 1499 1504	
ttg gac tac ttg cta gca gct gaa gga gga gtt tgt gga aac ttt aac	4560
Leu Asp Tyr Leu Leu Ala Ala Glu Gly Gly Val Cys Gly Asn Phe Asn	
1505 1510 1515 1520	
tta acc aat tgc tgc cta caa ata gat gat caa gga cag gtg gtt gaa	4608
Leu Thr Asn Cys Cys Leu Gln Ile Asp Asp Gln Gly Gln Val Val Glu	
1521 1526 1531 1536	
aac ata gtc agg gac atg aca aag gtg gca cat gtg cct gta cag att	4656
Asn Ile Val Arg Asp Met Thr Lys Val Ala His Val Pro Val Gln Ile	
1537 1542 1547 1552	

aaa ctg tac acg agt tta atc ctg agt ctt tat ttg gaa aat ggt ttc 4704
 Lys Leu Tyr Thr Ser Leu Ile Leu Ser Leu Tyr Leu Glu Asn Gly Phe
 1553 1558 1563 1568

 cag cta tgg gag gat tta aaa ccc tca tta agt aca tct aac tgt cct 4752
 Gln Leu Trp Glu Asp Leu Lys Pro Ser Leu Ser Thr Ser Asn Cys Pro
 1569 1574 1579 1584

 aag aat aaa gat aag gat gaa gac caa tct gaa ctg ctt act gct gac 4800
 Lys Asn Lys Asp Lys Asp Glu Asp Gln Ser Glu Leu Leu Thr Ala Asp
 1585 1590 1595 1600

 aga ggg ggc tgt ttt ggg gaa atg gca gtc aga act ccc tca gag gcc 4848
 Arg Gly Gly Cys Phe Gly Glu Met Ala Val Arg Thr Pro Ser Glu Ala
 1601 1606 1611 1616

 tat cta aag gtt ccc agc aga aga agc cat cgt cca aag ctc cgg ttg 4896
 Tyr Leu Lys Val Pro Ser Arg Arg Ser His Arg Pro Lys Leu Arg Leu
 1617 1622 1627 1632

 aat gac tgt ttg gag ttt gat ggc ctg aag gca aga aca gac aaa ctg 4944
 Asn Asp Cys Leu Glu Phe Asp Gly Leu Lys Ala Arg Thr Asp Lys Leu
 1633 1638 1643 1648

 ggc tat tag 4953
 Gly Tyr *
 1649

<210> 241
 <211> 844
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (10)..(705)

<400> 241
 atctattcgc atg atg aag ata ccc cac caa acc caa aaa aag aga tct 48
 Met Met Lys Ile Pro His Gln Thr Gln Lys Lys Arg Ser
 1 5 10

 ctc gag gat ccg aat tcg cgg ccg cgt cga cct atg agc tgc acc atc 96
 Leu Glu Asp Pro Asn Ser Arg Pro Arg Arg Pro Met Ser Cys Thr Ile
 14 19 24 29

 gag aag atc ctg aca gac gcc aag acg ctg ctg gag agg cta cgg gag 144
 Glu Lys Ile Leu Thr Asp Ala Lys Thr Leu Leu Glu Arg Leu Arg Glu
 30 35 40 45

 cac gat gcg gcc gcc gag tcg ctg gtg gat cag tcg gcg gcg ctg cac 192
 His Asp Ala Ala Ala Glu Ser Leu Val Asp Gln Ser Ala Ala Leu His
 46 51 56 61

cgg cgg gta gca gct atg cgg gag gcg ggg aca gcg ctt ccg gac cag	240
Arg Arg Val Ala Ala Met Arg Glu Ala Gly Thr Ala Leu Pro Asp Gln	
62 67 72 77	
tat caa gag gat gca tcc gat atg aag gac atg tcc aaa tac aaa cct	288
Tyr Gln Glu Asp Ala Ser Asp Met Lys Asp Met Ser Lys Tyr Lys Pro	
78 83 88 93	
cac att ctg ctg tcc caa gag aac aca cag att aga gac ttg caa cag	336
His Ile Leu Leu Ser Gln Glu Asn Thr Gln Ile Arg Asp Leu Gln Gln	
94 99 104 109	
gaa aac aga gag cta tgg att tcc ttg gag gaa cac cag gat gct ttg	384
Glu Asn Arg Glu Leu Trp Ile Ser Leu Glu Glu His Gln Asp Ala Leu	
110 115 120 125	
gaa ctt atc atg agc aaa tat cgg aaa cag atg tta cag tta atg gtt	432
Glu Leu Ile Met Ser Lys Tyr Arg Lys Gln Met Leu Gln Leu Met Val	
126 131 136 141	
gct aaa aaa gcg gtg gat gct gaa cca gtc ctg aaa gct cac cag tct	480
Ala Lys Lys Ala Val Asp Ala Glu Pro Val Leu Lys Ala His Gln Ser	
142 147 152 157	
cac tct gca gaa att gag agt cag att gac aga atc tgt gaa atg gga	528
His Ser Ala Glu Ile Glu Ser Gln Ile Asp Arg Ile Cys Glu Met Gly	
158 163 168 173	
gaa gtg atg agg aaa gca gtt cag gtg gat gat gac cag ttt tgt aag	576
Glu Val Met Arg Lys Ala Val Gln Val Asp Asp Asp Gln Phe Cys Lys	
174 179 184 189	
att cag gaa aaa tta gcc caa tta gag ctt gaa aat aag gaa ctt cga	624
Ile Gln Glu Lys Leu Ala Gln Leu Glu Leu Glu Asn Lys Glu Leu Arg	
190 195 200 205	
gaa tta ttg tcc atc agc agt gag tct ctt caa gcc aga aag gaa aac	672
Glu Leu Leu Ser Ile Ser Ser Glu Ser Leu Gln Ala Arg Lys Glu Asn	
206 211 216 221	
tca atg gac act gct tcc caa gcc atc aaa taa ctgaactc tgaatgatgg	723
Ser Met Asp Thr Ala Ser Gln Ala Ile Lys *	
222 227 232	
ctggagattg tctatcaagg aaggaagtta ctgtcttccc attcaagtac tgtccattaa	783
gtgtcttgcc tcagatttga tttaatctta attaaaggta tcaggtggca aaaaaaaaaa	843
a	844

<210> 242
 <211> 2753
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (416)..(2353)

<220>

<221> misc_feature

<222> (1)...(2753)

<223> n = a,t,c or g

<400> 242

```
ccgagccgag cgccgaggac cgtgctaccc caggcccggg ctgccccagc gcaggctcct      60
ctctggcagc agcggcggcg cggngacccc ngccctcgg cctccnnttc ccatcccacc      120
tcccagacct tcctcttccc gcagcacgcc cggcccggcc cggccgtggc cctcctcagt      180
gcgggccgcc atggcagagg cgtccggcgc ggggaaaatc tagcccgggg atttcatgcg      240
gcctagctcg gttccgctc ctctcgcgc ggcccagcg gctgcccgca cccagcccc      300
actccgggcc tccgtgtctc tcctgtgatc gactgacac ggccgggggg ttagaatgga      360
acaaactgaa ggcccgatga gagaaaggga aagttaagga tgctggagca gaaca atg      418
                                         Met
                                         1

gat ttc tct ttc tct ttc atg caa ggg atc atg gga aac aca att cag      466
Asp Phe Ser Phe Ser Phe Met Gln Gly Ile Met Gly Asn Thr Ile Gln
   2                               7               12           17

caa cca cct caa ctc att gac tcc gcc aac atc cgt cag gag gat gcc      514
Gln Pro Pro Gln Leu Ile Asp Ser Ala Asn Ile Arg Gln Glu Asp Ala
   18                          23               28           33

ttt gat aac aac agt gac att gct gaa gat ggt ggc cag aca cca tat      562
Phe Asp Asn Asn Ser Asp Ile Ala Glu Asp Gly Gly Gln Thr Pro Tyr
   34                          39               44           49

gaa gct act ttg cag caa ggc ttt cag tac cca gct aca aca gaa gat      610
Glu Ala Thr Leu Gln Gln Gly Phe Gln Tyr Pro Ala Thr Thr Glu Asp
   50                          55               60           65

ctt cct cca ctc aca aat ggg tat cca tca tca atc agt gtg tat gaa      658
Leu Pro Pro Leu Thr Asn Gly Tyr Pro Ser Ser Ile Ser Val Tyr Glu
   66                          71               76           81

act caa acc aaa tac cag tca tat aat cag tat cct aat ggg tca gcc      706
Thr Gln Thr Lys Tyr Gln Ser Tyr Asn Gln Tyr Pro Asn Gly Ser Ala
   82                          87               92           97

aat ggc ttt ggt gca gtt aga aac ttt agc ccc act gac tat tat cat      754
Asn Gly Phe Gly Ala Val Arg Asn Phe Ser Pro Thr Asp Tyr Tyr His
   98                          103              108           113

tca gaa att cca aac aca aga cca cat gaa att ctg gaa aaa cct tcc      802
```


Ser Glu Ile Pro Asn Thr Arg Pro His Glu Ile Leu Glu Lys Pro Ser	
114 119 124 129	
cct cca cag cca cca cct cct cct tcg gta cca caa act gtg att cca	850
Pro Pro Gln Pro Pro Pro Pro Pro Ser Val Pro Gln Thr Val Ile Pro	
130 135 140 145	
aag aag act ggc tca cct gaa att aaa cta aaa ata acc aaa act atc	898
Lys Lys Thr Gly Ser Pro Glu Ile Lys Leu Lys Ile Thr Lys Thr Ile	
146 151 156 161	
cag aat ggc agg gaa ttg ttt gag tct tcc ctt tgt gga gac ctt tta	946
Gln Asn Gly Arg Glu Leu Phe Glu Ser Ser Leu Cys Gly Asp Leu Leu	
162 167 172 177	
aat gaa gta cag gca agt gag cac acg aaa tca aag cat gaa agc aga	994
Asn Glu Val Gln Ala Ser Glu His Thr Lys Ser Lys His Glu Ser Arg	
178 183 188 193	
aaa gaa aag agg aaa aaa agc aac aag cat gac tca tca aga tct gaa	1042
Lys Glu Lys Arg Lys Lys Ser Asn Lys His Asp Ser Ser Arg Ser Glu	
194 199 204 209	
gag cgc aag tca cac aaa atc ccc aaa tta gaa cca gag gaa caa aat	1090
Glu Arg Lys Ser His Lys Ile Pro Lys Leu Glu Pro Glu Glu Gln Asn	
210 215 220 225	
aga cca aat gag agg gtt gac act gta tca gaa aaa cca agg gaa gaa	1138
Arg Pro Asn Glu Arg Val Asp Thr Val Ser Glu Lys Pro Arg Glu Glu	
226 231 236 241	
cca gta cta aaa gag gaa gcc cca gtt cag cca ata cta tct tct gtt	1186
Pro Val Leu Lys Glu Glu Ala Pro Val Gln Pro Ile Leu Ser Ser Val	
242 247 252 257	
cca aca acg gaa gtg tcc act ggt gtt aag ttt cag gtt ggc gat ctt	1234
Pro Thr Thr Glu Val Ser Thr Gly Val Lys Phe Gln Val Gly Asp Leu	
258 263 268 273	
gtg tgg tcc aag gtg gga acc tat cct tgg tgg cct tgt atg gtt tca	1282
Val Trp Ser Lys Val Gly Thr Tyr Pro Trp Trp Pro Cys Met Val Ser	
274 279 284 289	
agt gat ccc cag ctt gag gtt cat act aaa att aac aca aga ggt gcc	1330
Ser Asp Pro Gln Leu Glu Val His Thr Lys Ile Asn Thr Arg Gly Ala	
290 295 300 305	
cga gaa tat cat gtc cag ttt ttt agc aac cag cca gag agg gcg tgg	1378
Arg Glu Tyr His Val Gln Phe Phe Ser Asn Gln Pro Glu Arg Ala Trp	
306 311 316 321	
gtt cat gaa aaa cgg gta cga gag tat aaa ggt cat aaa cag tat gaa	1426
Val His Glu Lys Arg Val Arg Glu Tyr Lys Gly His Lys Gln Tyr Glu	
322 327 332 337	
gaa tta ctg gct gag gca acc aaa caa gcc agc aat cac tct gag aaa	1474
Glu Leu Leu Ala Glu Ala Thr Lys Gln Ala Ser Asn His Ser Glu Lys	

338	343	348	353	
caa aag att cgg aaa ccc cga cct cag aga gaa cgt gct cag tgg gat				1522
Gln Lys Ile Arg Lys Pro Arg Pro Gln Arg Glu Arg Ala Gln Trp Asp				
354	359	364	369	
att ggc att gcc cat gca gag aaa gca ttg aaa atg act cga gaa gaa				1570
Ile Gly Ile Ala His Ala Glu Lys Ala Leu Lys Met Thr Arg Glu Glu				
370	375	380	385	
aga ata gaa cag tat act ttt att tac att gat aaa cag cct gaa gag				1618
Arg Ile Glu Gln Tyr Thr Phe Ile Tyr Ile Asp Lys Gln Pro Glu Glu				
386	391	396	401	
gct tta tcc caa gca aaa aag agt gtt gcc tcc aaa acc gaa gtt aaa				1666
Ala Leu Ser Gln Ala Lys Lys Ser Val Ala Ser Lys Thr Glu Val Lys				
402	407	412	417	
aaa acc cga cga cca aga tct gtg ctg aat act cag cca gaa cag acc				1714
Lys Thr Arg Arg Pro Arg Ser Val Leu Asn Thr Gln Pro Glu Gln Thr				
418	423	428	433	
aat gca ggg gag gtg gcc tcc tca ctc tca agt act gaa att cgg aga				1762
Asn Ala Gly Glu Val Ala Ser Ser Leu Ser Ser Thr Glu Ile Arg Arg				
434	439	444	449	
cat agc cag agg cgg cac aca agt gcg gaa gag gaa gag cca ccg cct				1810
His Ser Gln Arg Arg His Thr Ser Ala Glu Glu Glu Glu Pro Pro Pro				
450	455	460	465	
gtt aaa ata gcc tgg aaa act gcg gca gca agg aaa tcc tta cca gct				1858
Val Lys Ile Ala Trp Lys Thr Ala Ala Ala Arg Lys Ser Leu Pro Ala				
466	471	476	481	
tcc att acg atg cac aaa ggg agc ctg gat ttg cag aag tgt aac atg				1906
Ser Ile Thr Met His Lys Gly Ser Leu Asp Leu Gln Lys Cys Asn Met				
482	487	492	497	
tct cca gtt gtg aaa att gaa caa gtg ttt gct ctt cag aat gct aca				1954
Ser Pro Val Val Lys Ile Glu Gln Val Phe Ala Leu Gln Asn Ala Thr				
498	503	508	513	
ggg gat ggg aaa ttt atc gat caa ttt gtt tat tca aca aag gga att				2002
Gly Asp Gly Lys Phe Ile Asp Gln Phe Val Tyr Ser Thr Lys Gly Ile				
514	519	524	529	
ggg aac aaa aca gaa ata agt gtc agg ggg caa gac agg ctt ata att				2050
Gly Asn Lys Thr Glu Ile Ser Val Arg Gly Gln Asp Arg Leu Ile Ile				
530	535	540	545	
tct aca cca aac cag aga aat gaa aag cca acg cag agt gta tca tct				2098
Ser Thr Pro Asn Gln Arg Asn Glu Lys Pro Thr Gln Ser Val Ser Ser				
546	551	556	561	
cct gaa gca aca tct ggt tct aca ggc tca gta gaa aag aag caa cag				2146
Pro Glu Ala Thr Ser Gly Ser Thr Gly Ser Val Glu Lys Lys Gln Gln				
562	567	572	577	

aga aga tca att aga act cgt tct gaa tca gag aaa tcc act gag gtt	2194
Arg Arg Ser Ile Arg Thr Arg Ser Glu Ser Glu Lys Ser Thr Glu Val	
578 583 588 593	

gtg cca aag aag aag atc aaa aag gag cag gtt gaa aca gtt cct cag	2242
Val Pro Lys Lys Lys Ile Lys Lys Glu Gln Val Glu Thr Val Pro Gln	
594 599 604 609	

gct aca gtg aag act gga tta cag aaa ggg tcc gcg gac cgg gga gtg	2290
Ala Thr Val Lys Thr Gly Leu Gln Lys Gly Ser Ala Asp Arg Gly Val	
610 615 620 625	

cag ggc tot gtc aga ttc agt gac agc tcc gtc tcc gca gcg att gag	2338
Gln Gly Ser Val Arg Phe Ser Asp Ser Ser Val Ser Ala Ala Ile Glu	
626 631 636 641	

gaa act gtg gac tga gattcctgta caatttcac ccagaaaactc cagacttgta	2393
Glu Thr Val Asp *	
642	

gtctccatgc aagattttctt tgtcggcggc ttgataaaca gtttctttgt tttcgatttt	2453
--	------

gatttcgcca atcatcatta ttggcatttt cctgcctggt ttcttcttca agactctgaa	2513
---	------

caattgcttt aacagtcaaa tgattttttt ttttcggttt gagctggatg ggtacagctt	2573
---	------

aaatcatggg tccagcctaa aaaccacat ttaacttaca ctgatcaatt tcaacatgga	2633
--	------

ctgttttttg ttttttggtt ttaaataaag catcattaat gcacatctgc agggggttgc	2693
---	------

caaacagccc aaactgtata cattacaatc attaaaagtt cttatttttt ttaaaaaaaa	2753
---	------

<210> 243

<211> 4468

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (249)..(1940)

<400> 243

atttggccct cgaggccaag aattcggcac gagctcattg tgtctgtgtc gaggcgtcgg	60
---	----

gagggcctaa gtccgtgtgc ggtgcccttc ggccggcctg agccccagag tcagctcccc	120
---	-----

tttctcgccc agcgccccca ggccgctccc ggggctcacg gaatagtaaa gaaacacatc	180
---	-----

ataaaacctc ccaggacata aaggtagca cagaccctgt ttggatcaag tcagttcctg	240
--	-----

gagcctga atg atg act gct gaa tca cgg gaa gcc acg ggt ctg tcc cca	290
Met Met Thr Ala Glu Ser Arg Glu Ala Thr Gly Leu Ser Pro	

1

5

10

cag gct gca cag gag aag gat ggt atc gta ata gtg aag gtg gaa gag	338
Gln Ala Ala Gln Glu Lys Asp Gly Ile Val Ile Val Lys Val Glu Glu	
15 20 25 30	
gaa gat gag gaa gac cac atg tgg ggg cag gat tcc acc cta cag gac	386
Glu Asp Glu Glu Asp His Met Trp Gly Gln Asp Ser Thr Leu Gln Asp	
31 36 41 46	
acg cct cct cca gac cca gag ata ttc cgc caa cgc ttc agg cgc ttc	434
Thr Pro Pro Pro Asp Pro Glu Ile Phe Arg Gln Arg Phe Arg Arg Phe	
47 52 57 62	
tgt tac cag aac act ttt ggg ccc cga gag gct ctc agt cgg ctg aag	482
Cys Tyr Gln Asn Thr Phe Gly Pro Arg Glu Ala Leu Ser Arg Leu Lys	
63 68 73 78	
gaa ctt tgt cat cag tgg ctg cgg cca gaa ata aac acc aag gaa cag	530
Glu Leu Cys His Gln Trp Leu Arg Pro Glu Ile Asn Thr Lys Glu Gln	
79 84 89 94	
atc ctg gag ctt ctg gtg cta gag cag ttt ctt tcc atc ctg ccc aag	578
Ile Leu Glu Leu Leu Val Leu Glu Gln Phe Leu Ser Ile Leu Pro Lys	
95 100 105 110	
gag ctc cag gtc tgg ctg cag gaa tac cgc ccc gat agt gga gag gag	626
Glu Leu Gln Val Trp Leu Gln Glu Tyr Arg Pro Asp Ser Gly Glu Glu	
111 116 121 126	
gcc gtg acc ctt cta gaa gac ttg gag ctt gat tta tca gga caa cag	674
Ala Val Thr Leu Leu Glu Asp Leu Glu Leu Asp Leu Ser Gly Gln Gln	
127 132 137 142	
gtc cca ggt caa gtt cat gga cct gag atg ctc gca agg ggg atg gtg	722
Val Pro Gly Gln Val His Gly Pro Glu Met Leu Ala Arg Gly Met Val	
143 148 153 158	
cct ctg gat cca gtt cag gag tcc tcg agc ttt gac ctt cat cac gag	770
Pro Leu Asp Pro Val Gln Glu Ser Ser Ser Phe Asp Leu His His Glu	
159 164 169 174	
gcc acc cag tcc cac ttc aaa cat tcg tct cgg aaa ccc cgc ctc tta	818
Ala Thr Gln Ser His Phe Lys His Ser Ser Arg Lys Pro Arg Leu Leu	
175 180 185 190	
cag tca cga gct ctt cct gct gcc cac att cct gca ccc cct cat gag	866
Gln Ser Arg Ala Leu Pro Ala Ala His Ile Pro Ala Pro Pro His Glu	
191 196 201 206	
ggt agt ccc aga gac cag gcg atg gca tct gca cta ttc aca gcg gat	914
Gly Ser Pro Arg Asp Gln Ala Met Ala Ser Ala Leu Phe Thr Ala Asp	
207 212 217 222	
tcc cag gca atg gtg aag atc gag gac atg gct gtg tcc ctc att ctg	962
Ser Gln Ala Met Val Lys Ile Glu Asp Met Ala Val Ser Leu Ile Leu	
223 228 233 238	

gag gaa tgg gga tgt cag aat ctg gct cgg agg aat ctc agt agg gac	1010
Glu Glu Trp Gly Cys Gln Asn Leu Ala Arg Arg Asn Leu Ser Arg Asp	
239 244 249 254	
aac agg cag gag aat tat ggg agc gca ttt ccc cag ggt ggt gaa aac	1058
Asn Arg Gln Glu Asn Tyr Gly Ser Ala Phe Pro Gln Gly Gly Glu Asn	
255 260 265 270	
agg aat gag aac gag gag tca acc tca aag gct gaa acc tcg gaa gat	1106
Arg Asn Glu Asn Glu Glu Ser Thr Ser Lys Ala Glu Thr Ser Glu Asp	
271 276 281 286	
tca gca tca cgc ggg gag aca aca gga aga tcc cag aaa gag ttt gga	1154
Ser Ala Ser Arg Gly Glu Thr Thr Gly Arg Ser Gln Lys Glu Phe Gly	
287 292 297 302	
gag aaa cgt gac cag gag ggc aaa aca gga gaa aga cag cag aaa aac	1202
Glu Lys Arg Asp Gln Glu Gly Lys Thr Gly Glu Arg Gln Gln Lys Asn	
303 308 313 318	
cct gag gag aaa acc agg aaa gag aaa aga gat tca ggg cca gct ata	1250
Pro Glu Glu Lys Thr Arg Lys Glu Lys Arg Asp Ser Gly Pro Ala Ile	
319 324 329 334	
gga aag gac aaa aaa acc atc aca gga gag aga ggt cca agg gag aag	1298
Gly Lys Asp Lys Lys Thr Ile Thr Gly Glu Arg Gly Pro Arg Glu Lys	
335 340 345 350	
ggg aaa gga ttg gga aga agc ttc agt ctg agc tcc aac ttc acc acc	1346
Gly Lys Gly Leu Gly Arg Ser Phe Ser Leu Ser Ser Asn Phe Thr Thr	
351 356 361 366	
cct gaa gaa gtt ccc acg gga aca aag tct cac aga tgt gat gaa tgt	1394
Pro Glu Glu Val Pro Thr Gly Thr Lys Ser His Arg Cys Asp Glu Cys	
367 372 377 382	
ggt aaa tgc ttc acg aga agt tca agc ctt atc cgc cat aaa ata atc	1442
Gly Lys Cys Phe Thr Arg Ser Ser Ser Leu Ile Arg His Lys Ile Ile	
383 388 393 398	
cac act gga gaa aag ccc tat gaa tgt agt gag tgt ggg aaa gcc ttc	1490
His Thr Gly Glu Lys Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ala Phe	
399 404 409 414	
agt ctt aac tcc aac ctt gtc ctg cat cag agg atc cac aca gga gag	1538
Ser Leu Asn Ser Asn Leu Val Leu His Gln Arg Ile His Thr Gly Glu	
415 420 425 430	
aaa cct cat gaa tgt aac gag tgt ggc aag gcc ttc agc cac agt tcc	1586
Lys Pro His Glu Cys Asn Glu Cys Gly Lys Ala Phe Ser His Ser Ser	
431 436 441 446	
aat ctc atc ctc cat cag cgc atc cac tct gga gag aaa cct tat gaa	1634
Asn Leu Ile Leu His Gln Arg Ile His Ser Gly Glu Lys Pro Tyr Glu	
447 452 457 462	
tgt aat gag tgc ggg aag gcc ttc agc cag agc tcg gac ctc acc aag	1682

ctcattcaga ctgacttcta caggacttct acgtgtgtga taaaagcctg tgaatcgtga	2936
gtccctgaaa tatggtagcc tggcccagct tctaaagagg accttcgtag ccacaaggca	2996
tgtataacct ctagggtctg atgtgtgttt tgttccaaat ataaacgaaa ggcactagtc	3056
agccgcctgc atagactttc taaacagtga gtaaatacca tggaatgtca gaaatgactt	3116
tatcatcgtc atcttgaaga aaaatatgaa cactgatgaa ggtcattttt tttttttgac	3176
atctttctgt ggcaaagctc ttagaattct ttgcagttag ctgctgaaca gtatgatgat	3236
ttggggattt tctgaatcat ttgtacttag atactggagt tcagaagatg tgatttttgt	3296
tgtttttcag aaaaaggaac gtggtaggga gtgttttttc ccacgctttt ccagtaactt	3356
tgcaaaagca ttaattgttc actggcaatt actaaatgta ttttgttgct ctgagaaact	3416
cagcagtgtg ctgagatgtg gctggctgtg ccacgtcat agtgcacagt gaactttctg	3476
tttcttatca ctaaagactg aggtgaggtt atgaaacttt cattgggtccc atcgttgtgc	3536
gcaggggtgca actggctacc tagaagctga tggcaggaga ctgtttcaca cacaggagat	3596
tgtgagctgt gtaagtagtc atcgccactc aagtaggaca agggtcctac ccaaggctag	3656
gaccgccctg cggaaacaga aacatagact gagaacaaac ctcaagacta tcagtgtgac	3716
ctccccataa caagagaacc ccataatatag tttgagactt tcccttgaga aacttatact	3776
aaaactatta ctcatcagtc attcactgat cagcagctaa agtccatgag accaaatggg	3836
tttatatgga accaacaaaag tgggagctaa aactgcacag tggtcattct ttggcctctc	3896
cttggcttta tgacttaaac caactacaac ttcctatag cttctaagca gtttcatcag	3956
cattacttgg gaaaacgtgt tgcaagtcaa ccagtcacta ggatatttct acccatgcaa	4016
cggagaaaaa acccattact ccagaagagt atatctaagt aactaaaatg gaggcagaaa	4076
atgttttaag gattttcttc aaagaataag ccacagcaat ggttttgtag aaaactcctg	4136
tgtttttgag caaggacttt tgccctctag aaagcaactg aggccagggt cggtggctca	4196
cgctgtaat ccagcactt tgggaggccg aggtgagcgg atcacctgag gtcaggagtt	4256
ttgagaccag cctggccaac atggtaaaat ccgtctctc ctaaaattat aaaaattagc	4316
cgggcatgat ggtgggcacc tgtaatccca gctacttggg aggctgaggc aggagaatca	4376
cttgaaccca ggaggcagag gttgcagtga gccaaagattg cacactgcac tccagcctgg	4436
gtgactagca aaactccatc tcaaaaaaaaa aa	4468

<210> 244
 <211> 461
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (47)..(274)

<400> 244

```

atttggccct cgaggccaag aattcggcac gagggacaga tgcctc   atg ttg aag   55
                                     Met Leu Lys
                                     1

cag ggg tct caa cct ggc tca cct cca gca aca ttg agc ctc cag cac   103
Gln Gly Ser Gln Pro Gly Ser Pro Pro Ala Thr Leu Ser Leu Gln His
  4              9              14              19

ctc ctg tct acc aag ccc cgt gcc agt cct gcc cag aac ccc cag gag   151
Leu Leu Ser Thr Lys Pro Arg Ala Ser Pro Ala Gln Asn Pro Gln Glu
  20              25              30              35

ccc atg agc cct ctg act ctc cac acc ata ccc cag tcc atc ctc ctc   199
Pro Met Ser Pro Leu Thr Leu His Thr Ile Pro Gln Ser Ile Leu Leu
  36              41              46              51

cag agc act cgg ccg cct gtc ctg ccc cag cca cgt gct gtc cgc ccc   247
Gln Ser Thr Arg Pro Pro Val Leu Pro Gln Pro Arg Ala Val Arg Pro
  52              57              62              67

cga gaa gct cta tgt cat aaa tct taa ctcag atgggagagg gagcctcaga   299
Arg Glu Ala Leu Cys His Lys Ser *
  68              73

gtcacatagc cctggggccca aacccagct cctccacca agtactgatg gtcaggttct   359

tcagcctcag tttctgtagc tgtaagatgg ggagaatgat ctctgggagg gttaaattgt   419

cggcaaaatg gccaaagatt gggctctggg actaggacca tg   461

```

<210> 245
 <211> 5532
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (534)..(4262)

<400> 245

```

cattcgctcc aggggttttg gaccctaggt tgcggagtcc ttaccctacc ctggcctctc   60

gagcagttgt ccccataact cggaatctag agccgctggt gcgaggcagg agcacgtggc   120

```


Thr Cys Ile Gly Thr Pro Tyr Tyr Leu Ser Pro Glu Ile Cys Glu Asn	
162 167 172 177	
aaa cct tac aat aat aaa agt gac att tgg gct ctg ggg tgt gtc ctt	1112
Lys Pro Tyr Asn Asn Lys Ser Asp Ile Trp Ala Leu Gly Cys Val Leu	
178 183 188 193	
tat gag ctg tgt aca ctt aaa cat gct ttt gaa gct ggc agt atg aaa	1160
Tyr Glu Leu Cys Thr Leu Lys His Ala Phe Glu Ala Gly Ser Met Lys	
194 199 204 209	
aac ctg gta ctg aag ata ata tct gga tct ttt cca cct gtg tct ttg	1208
Asn Leu Val Leu Lys Ile Ile Ser Gly Ser Phe Pro Pro Val Ser Leu	
210 215 220 225	
cat tat tcc tat gat ctc cgc agt ttg gtg tct cag tta ttt aaa aga	1256
His Tyr Ser Tyr Asp Leu Arg Ser Leu Val Ser Gln Leu Phe Lys Arg	
226 231 236 241	
aat cct agg gat aga cca tca gtc aac tcc ata ttg gag aaa ggt ttt	1304
Asn Pro Arg Asp Arg Pro Ser Val Asn Ser Ile Leu Glu Lys Gly Phe	
242 247 252 257	
ata gcc aaa cgc att gaa aag ttt ctc tct cct cag ctt att gca gaa	1352
Ile Ala Lys Arg Ile Glu Lys Phe Leu Ser Pro Gln Leu Ile Ala Glu	
258 263 268 273	
gaa ttt tgt cta aaa aca ttt tcg aag ttt gga tca cag cct ata cca	1400
Glu Phe Cys Leu Lys Thr Phe Ser Lys Phe Gly Ser Gln Pro Ile Pro	
274 279 284 289	
gct aaa aga cca gct tca gga caa aac tcg att tct gtt atg cct gct	1448
Ala Lys Arg Pro Ala Ser Gly Gln Asn Ser Ile Ser Val Met Pro Ala	
290 295 300 305	
cag aaa att aca aag cct gcc gct aaa tat gga ata cct tta gca tat	1496
Gln Lys Ile Thr Lys Pro Ala Ala Lys Tyr Gly Ile Pro Leu Ala Tyr	
306 311 316 321	
aag aaa tat gga gat aaa aaa tta cac gaa aag aaa cca ctg caa aaa	1544
Lys Lys Tyr Gly Asp Lys Lys Leu His Glu Lys Lys Pro Leu Gln Lys	
322 327 332 337	
cat aaa cag gcc cat caa act cca gag aag aga gtg aat act ggg gaa	1592
His Lys Gln Ala His Gln Thr Pro Glu Lys Arg Val Asn Thr Gly Glu	
338 343 348 353	
gaa agg agg aaa ata tct gag gaa gca gca aga aag aga agg ctg gaa	1640
Glu Arg Arg Lys Ile Ser Glu Glu Ala Ala Arg Lys Arg Arg Leu Glu	
354 359 364 369	
ttt att gaa aaa gaa aag aaa caa aag gat cag att att agt tta atg	1688
Phe Ile Glu Lys Glu Lys Lys Gln Lys Asp Gln Ile Ile Ser Leu Met	
370 375 380 385	
aag gct gaa caa atg aaa agg caa gaa aag gaa agg ttg gaa aga ata	1736
Lys Ala Glu Gln Met Lys Arg Gln Glu Lys Glu Arg Leu Glu Arg Ile	

386	391	396	401	
aat agg gcc agg gaa caa gga tgg aga aat gtg cta agt gct ggt gga				1784
Asn Arg Ala Arg Glu Gln Gly Trp Arg Asn Val Leu Ser Ala Gly Gly				
402	407	412	417	
agt ggt gaa gta aag gct cct ttt ctg ggc agt gga ggg act ata gct				1832
Ser Gly Glu Val Lys Ala Pro Phe Leu Gly Ser Gly Gly Thr Ile Ala				
418	423	428	433	
cca tca tct ttt tct tct cga gga cag tat gaa cat tac cat gcc att				1880
Pro Ser Ser Phe Ser Ser Arg Gly Gln Tyr Glu His Tyr His Ala Ile				
434	439	444	449	
ttt gac caa atg cag caa caa aga gca gaa gat aat gaa gct aaa tgg				1928
Phe Asp Gln Met Gln Gln Gln Arg Ala Glu Asp Asn Glu Ala Lys Trp				
450	455	460	465	
aaa aga gaa ata tat ggt cga ggt ctt cca gaa agg caa aaa ggg cag				1976
Lys Arg Glu Ile Tyr Gly Arg Gly Leu Pro Glu Arg Gln Lys Gly Gln				
466	471	476	481	
cta gct gta gaa aga gct aaa caa gta gaa gag ttc ctg cag cga aaa				2024
Leu Ala Val Glu Arg Ala Lys Gln Val Glu Glu Phe Leu Gln Arg Lys				
482	487	492	497	
cgg gaa gct atg cag aat aaa gct cga gcc gaa gga cat atg gga atc				2072
Arg Glu Ala Met Gln Asn Lys Ala Arg Ala Glu Gly His Met Gly Ile				
498	503	508	513	
ctg caa aac ctg gca gct atg tat gga ggc agg ccc agc tct tca aga				2120
Leu Gln Asn Leu Ala Ala Met Tyr Gly Gly Arg Pro Ser Ser Ser Arg				
514	519	524	529	
gga ggg aag cca aga aac aaa gag gaa gag gtt tat ctg gca aga ctg				2168
Gly Gly Lys Pro Arg Asn Lys Glu Glu Glu Val Tyr Leu Ala Arg Leu				
530	535	540	545	
agg caa ata aga cta cag aat ttc aat gag cgc caa cag att aaa gcc				2216
Arg Gln Ile Arg Leu Gln Asn Phe Asn Glu Arg Gln Gln Ile Lys Ala				
546	551	556	561	
aaa ctt cgt ggt gaa aag aaa gaa gct aat cat tct gaa gga caa gaa				2264
Lys Leu Arg Gly Glu Lys Lys Glu Ala Asn His Ser Glu Gly Gln Glu				
562	567	572	577	
gga agt gaa gag gct gac atg agg cgc aaa aaa atc gaa tca ctg aag				2312
Gly Ser Glu Glu Ala Asp Met Arg Arg Lys Lys Ile Glu Ser Leu Lys				
578	583	588	593	
gcc cat gca aat gca cgt gct gct gta cta aaa gaa caa cta gaa cga				2360
Ala His Ala Asn Ala Arg Ala Ala Val Leu Lys Glu Gln Leu Glu Arg				
594	599	604	609	
aag aga aag gag gct tat gag aga gaa aaa aaa gtg tgg gaa gag cat				2408
Lys Arg Lys Glu Ala Tyr Glu Arg Glu Lys Lys Val Trp Glu Glu His				
610	615	620	625	

ttg gtg gct aaa gga gtt aag agt tct gat gtt tct cca cct ttg gga	2456
Leu Val Ala Lys Gly Val Lys Ser Ser Asp Val Ser Pro Pro Leu Gly	
626 631 636 641	
cag cat gaa aca ggt ggc tct cca tca aag caa cag atg aga tct gtt	2504
Gln His Glu Thr Gly Gly Ser Pro Ser Lys Gln Gln Met Arg Ser Val	
642 647 652 657	
att tct gta act tca gct ttg aaa gaa gtt ggc gtg gac agt agt tta	2552
Ile Ser Val Thr Ser Ala Leu Lys Glu Val Gly Val Asp Ser Ser Leu	
658 663 668 673	
act gat acc cgg gaa act tca gaa gag atg caa aag acc aac aat gct	2600
Thr Asp Thr Arg Glu Thr Ser Glu Glu Met Gln Lys Thr Asn Asn Ala	
674 679 684 689	
att tca agt aag cga gaa ata ctt cgt aga tta aat gaa aat ctt aaa	2648
Ile Ser Ser Lys Arg Glu Ile Leu Arg Arg Leu Asn Glu Asn Leu Lys	
690 695 700 705	
gct caa gaa gat gaa aaa gga aag cag aat ctc tct gat act ttt gag	2696
Ala Gln Glu Asp Glu Lys Gly Lys Gln Asn Leu Ser Asp Thr Phe Glu	
706 711 716 721	
ata aat gtt cat gaa gat gcc aaa gag cat gaa aaa gaa aaa tca gtt	2744
Ile Asn Val His Glu Asp Ala Lys Glu His Glu Lys Glu Lys Ser Val	
722 727 732 737	
tca tct gat cgc aag aag tgg gag gca gga ggt caa ctt gtg att cct	2792
Ser Ser Asp Arg Lys Lys Trp Glu Ala Gly Gly Gln Leu Val Ile Pro	
738 743 748 753	
ctg gat gag tta aca cta gat aca tcc ttc tct aca act gaa aga cat	2840
Leu Asp Glu Leu Thr Leu Asp Thr Ser Phe Ser Thr Thr Glu Arg His	
754 759 764 769	
aca gtg gga gaa gtt att aaa tta ggt cct aat gga tct cca aga aga	2888
Thr Val Gly Glu Val Ile Lys Leu Gly Pro Asn Gly Ser Pro Arg Arg	
770 775 780 785	
gcc tgg ggg aaa agt ccg aca gat tct gtt cta aag ata ctt gga gaa	2936
Ala Trp Gly Lys Ser Pro Thr Asp Ser Val Leu Lys Ile Leu Gly Glu	
786 791 796 801	
gct gaa cta caa ctt cag aca gaa cta tta gaa aat aca act att aga	2984
Ala Glu Leu Gln Leu Gln Thr Glu Leu Leu Glu Asn Thr Thr Ile Arg	
802 807 812 817	
agt gag att tct ccc gaa ggg gaa aag tac aaa ccc tta att act gga	3032
Ser Glu Ile Ser Pro Glu Gly Glu Lys Tyr Lys Pro Leu Ile Thr Gly	
818 823 828 833	
gaa aaa aaa gta caa tgt att tca cat gaa ata aac cca tca gct att	3080
Glu Lys Lys Val Gln Cys Ile Ser His Glu Ile Asn Pro Ser Ala Ile	
834 839 844 849	

gtt gat tct cct gtt gag aca aaa agt ccc gag ttc agt gag gca tct	3128
Val Asp Ser Pro Val Glu Thr Lys Ser Pro Glu Phe Ser Glu Ala Ser	
850 855 860 865	
cca cag atg tca ttg aaa ctg gaa gga aat tta gaa gaa cct gat gat	3176
Pro Gln Met Ser Leu Lys Leu Glu Gly Asn Leu Glu Glu Pro Asp Asp	
866 871 876 881	
ttg gaa aca gaa att cta caa gag cca agt gga aca aac aaa gat gag	3224
Leu Glu Thr Glu Ile Leu Gln Glu Pro Ser Gly Thr Asn Lys Asp Glu	
882 887 892 897	
agc ttg cca tgc act att act gat gtg tgg att agt gag gaa aaa gaa	3272
Ser Leu Pro Cys Thr Ile Thr Asp Val Trp Ile Ser Glu Glu Lys Glu	
898 903 908 913	
aca aag gaa act cag tcg gca gat agg atc acc att cag gaa aat gaa	3320
Thr Lys Glu Thr Gln Ser Ala Asp Arg Ile Thr Ile Gln Glu Asn Glu	
914 919 924 929	
gtt tct gaa gat gga gtc tcg agt act gtg gac caa ctt agt gac att	3368
Val Ser Glu Asp Gly Val Ser Ser Thr Val Asp Gln Leu Ser Asp Ile	
930 935 940 945	
cat ata gag cct gga acc aat gat tct cag cac tct aaa tgt gat gta	3416
His Ile Glu Pro Gly Thr Asn Asp Ser Gln His Ser Lys Cys Asp Val	
946 951 956 961	
gat aag tct gtg caa ccg gaa cca ttt ttc cat aag gtg gtt cat tct	3464
Asp Lys Ser Val Gln Pro Glu Pro Phe Phe His Lys Val Val His Ser	
962 967 972 977	
gaa cac ttg aac tta gtc cct caa gtt caa tca gtt cag tgt tca cca	3512
Glu His Leu Asn Leu Val Pro Gln Val Gln Ser Val Gln Cys Ser Pro	
978 983 988 993	
gaa gaa tcc ttt gca ttt cga tct cac tcg cat tta cca cca aaa aat	3560
Glu Glu Ser Phe Ala Phe Arg Ser His Ser His Leu Pro Pro Lys Asn	
994 999 1004 1009	
aaa aac aag aat tcc ttg ctg att gga ctt tca act ggt ctg ttt gat	3608
Lys Asn Lys Asn Ser Leu Leu Ile Gly Leu Ser Thr Gly Leu Phe Asp	
1010 1015 1020 1025	
gca aac aac cca aag atg tta agg aca tgt tca ctt cca gat ctc tca	3656
Ala Asn Asn Pro Lys Met Leu Arg Thr Cys Ser Leu Pro Asp Leu Ser	
1026 1031 1036 1041	
aag ctg ttc aga acc ctt atg gat gtt ccc acc gta gga gat gtt cgt	3704
Lys Leu Phe Arg Thr Leu Met Asp Val Pro Thr Val Gly Asp Val Arg	
1042 1047 1052 1057	
caa gac aat ctt gaa ata gat gaa att aaa gat gaa aac att aaa gaa	3752
Gln Asp Asn Leu Glu Ile Asp Glu Ile Lys Asp Glu Asn Ile Lys Glu	
1058 1063 1068 1073	
gga cct tct gat tct gaa gac att gtg ttt gaa gaa act gac aca gat	3800

Gly Pro Ser Asp Ser Glu Asp Ile Val Phe Glu Glu Thr Asp Thr Asp	
1074	1079 1084 1089
tta caa gag ctg cag gcc tcg atg gaa cag tta ctt agg gaa caa cct	3848
Leu Gln Glu Leu Gln Ala Ser Met Glu Gln Leu Leu Arg Glu Gln Pro	
1090	1095 1100 1105
ggt gaa gaa tac agt gaa gaa gaa gag tca gtc ttg aag aac agt gat	3896
Gly Glu Glu Tyr Ser Glu Glu Glu Glu Ser Val Leu Lys Asn Ser Asp	
1106	1111 1116 1121
gtg gag cca act gca aat ggg aca gat gtg gca gat gaa gat gac aat	3944
Val Glu Pro Thr Ala Asn Gly Thr Asp Val Ala Asp Glu Asp Asp Asn	
1122	1127 1132 1137
ccc agc agt gaa agt gcc ctg aac gaa gaa tgg cac tca gat aac agt	3992
Pro Ser Ser Glu Ser Ala Leu Asn Glu Glu Trp His Ser Asp Asn Ser	
1138	1143 1148 1153
gat ggt gaa att gct agt gaa tgt gaa tgc gat agt gtc ttt aac cat	4040
Asp Gly Glu Ile Ala Ser Glu Cys Glu Cys Asp Ser Val Phe Asn His	
1154	1159 1164 1169
tta gag gaa ctg aga ctt cat ctg gag cag gaa atg ggc ttt gaa aaa	4088
Leu Glu Glu Leu Arg Leu His Leu Glu Gln Glu Met Gly Phe Glu Lys	
1170	1175 1180 1185
ttc ttt gag gtt tat gag aaa ata aag gct att cat gaa gat gaa gat	4136
Phe Phe Glu Val Tyr Glu Lys Ile Lys Ala Ile His Glu Asp Glu Asp	
1186	1191 1196 1201
gaa aat att gaa att tgt tca aaa ata gtt caa aat att ttg gga aat	4184
Glu Asn Ile Glu Ile Cys Ser Lys Ile Val Gln Asn Ile Leu Gly Asn	
1202	1207 1212 1217
gaa cat cag cat ctt tat gcc aag att ctt cat tta gtc atg gca gat	4232
Glu His Gln His Leu Tyr Ala Lys Ile Leu His Leu Val Met Ala Asp	
1218	1223 1228 1233
gga gcc tac caa gaa gat aat gat gaa taa t cctcaaaatg ttttttaatc	4283
Gly Ala Tyr Gln Glu Asp Asn Asp Glu *	
1234	1239
ctcaactata tgaaagcatt tgaatttggc ttatcagaat aacaagcttc agtgggaaat	4343
acagcaatta tttattttaaa aaatcagatt taagatggac tttcttattg catgaaaaag	4403
atggagaaac atgocatttt tcaatgaaga ttctaataatt ttatctatatt tgttcattga	4463
attccatggt taaatctcat aaaatatata ctttattaaa tcatccaacc aaagcatagg	4523
aaacattgac ccagaacctg acttaatggt tttgaagatt tactatgcaa tagggtaact	4583
ttgagtttca gcaaatgtct ttaggttgaa ggaattacct atgtcatgaa ggacctgtct	4643
gtggtttttc aatggagtct ttaagcatga tcttttttct gtctagtact tgttttcatt	4703

ctggccagca gttctacatt aaatcacctt gtcaagggct ctgtttacat ctacacattt	4763
tgaagatgaa attttttagcc ttaaagttta tattctcaag tccttttaca atcagtggtg	4823
cacctgaact agcacacagg ctgtagaaac agtcttagaa atcattgaaa gatttgatta	4883
tgaaagaata gcaaaattat atttcttgac atataaaaag ttggtttaat gcctttat	4943
ctctttaagg accagaacca ggaatactgt atcgaaaaat tagtctgtgg atttaacact	5003
gacttagcat atagcttaaa gttgctcttt tggtttttaa cttoctccat acataagctt	5063
caaggacaat aagatgttaa aaaggaggaa ataattattt ttattttgac actgtgacag	5123
ttttggtaac taggatccta gggagggaaa tggttgctg ttgaacttct ttctgttatg	5183
agaggattta gttaggatcat taagatgttg atcacacagc ttcaatcaca atatgccaag	5243
tataacctgg tttcgtaga ggtgtctaca gtccagatgt tcttcgtaat aaaagcaaag	5303
ttttgaacc tctgagtcca aagcaggctg gttggcataa tatgtaattt gaaaaataaa	5363
atcttatctt gcagcactat cagtatgttg aatttattat gtatattatt tctaatatcc	5423
gaaactaaat acttgatttt ttaatatgtg tggttatttt atgatattgc tattaaattt	5483
ttattatcta aaaaaaaaaa aaaaaaaaaa aactgcggcc gcaagctta	5532

<210> 246
 <211> 5448
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (534) .. (4178)

<400> 246	
cattcgctcc agggttttgg gaccctaggt tgcgaggtcc ttaccctacc ctggcctctc	60
gagcagttgt ccccataact cggaatctag agcgcgtgtt gcgaggcagg agcacgtggc	120
agtcaagtag cttcccagtc ccgaacgccg ccggtcccca ccccgccgtg gccactagca	180
acgacctctg tgaagttgga gaggcggtaa cggaggcact cccctgctg cccccgccg	240
tttctacggg gtcagaaac cagtttgttt gtttcgtcgg ggtagtgtcg acctgtctta	300
cgggcgtcgc ccgagacagg acggagtcaa acccgtggta tcaactgaag acgagtgtca	360
ggatgtcatt ttcaaatgc gggatggtac ctctgcttta ttaagccccg taggaagact	420
gccacaccta gactgatgct tattagtcac caccgttatt cctactaacg tcctgtgtca	480

ctgagttttt taaatgtcta gcatatctgt aaagatgcct tagaaaaaga atc	atg	536
	Met	
	1	
gag aag tat gtt aga cta cag aag att gga gaa ggt tca ttt gga aaa		584
Glu Lys Tyr Val Arg Leu Gln Lys Ile Gly Glu Gly Ser Phe Gly Lys		
2 7 12 17		
gcc att ctt gtt aaa tct aca gaa gat ggc aga cag tat gtt atc aag		632
Ala Ile Leu Val Lys Ser Thr Glu Asp Gly Arg Gln Tyr Val Ile Lys		
18 23 28 33		
gaa att aac atc tca aga atg tcc agt aaa gaa aga gaa gaa tca agg		680
Glu Ile Asn Ile Ser Arg Met Ser Ser Lys Glu Arg Glu Glu Ser Arg		
34 39 44 49		
aga gaa gtt gca gta ttg gca aac atg aag cat cca aat att gtc cag		728
Arg Glu Val Ala Val Leu Ala Asn Met Lys His Pro Asn Ile Val Gln		
50 55 60 65		
tat aga gaa tca ttt gaa gaa aat ggc tct ctc tac ata gta atg gat		776
Tyr Arg Glu Ser Phe Glu Glu Asn Gly Ser Leu Tyr Ile Val Met Asp		
66 71 76 81		
tac tgt gag gga ggg gat ctg ttt aag cga ata aat gct cag aaa ggc		824
Tyr Cys Glu Gly Gly Asp Leu Phe Lys Arg Ile Asn Ala Gln Lys Gly		
82 87 92 97		
gtt ttg ttt caa gag gat cag att ttg gac tgg ttt gta cag ata tgt		872
Val Leu Phe Gln Glu Asp Gln Ile Leu Asp Trp Phe Val Gln Ile Cys		
98 103 108 113		
ttg gcc ctg aaa cat gta cat gat aga aaa att ctt cat cga gac att		920
Leu Ala Leu Lys His Val His Asp Arg Lys Ile Leu His Arg Asp Ile		
114 119 124 129		
aaa tct cag aac ata ttt tta act aaa gat gga aca gta caa ctt gga		968
Lys Ser Gln Asn Ile Phe Leu Thr Lys Asp Gly Thr Val Gln Leu Gly		
130 135 140 145		
gat ttt gga att gct aga gtt ctt aat agt act gta gag ctg gct cga		1016
Asp Phe Gly Ile Ala Arg Val Leu Asn Ser Thr Val Glu Leu Ala Arg		
146 151 156 161		
act tgc ata ggg acc cca tac tac ttg tca cct gaa atc tgt gaa aac		1064
Thr Cys Ile Gly Thr Pro Tyr Tyr Leu Ser Pro Glu Ile Cys Glu Asn		
162 167 172 177		
aaa cct tac aat aat aaa agt gac att tgg gct ctg ggg tgt gtc ctt		1112
Lys Pro Tyr Asn Asn Lys Ser Asp Ile Trp Ala Leu Gly Cys Val Leu		
178 183 188 193		
tat gag ctg tgt aca ctt aaa cat gct ttt gaa gct ggc agt atg aaa		1160
Tyr Glu Leu Cys Thr Leu Lys His Ala Phe Glu Ala Gly Ser Met Lys		
194 199 204 209		
aac ctg gta ctg aag ata ata tct gga tct ttt cca cct gtg tct ttg		1208

Asn	Leu	Val	Leu	Lys	Ile	Ile	Ser	Gly	Ser	Phe	Pro	Pro	Val	Ser	Leu	
210					215					220					225	
cat	tat	tcc	tat	gat	ctc	cgc	agt	ttg	gtg	tct	cag	tta	ttt	aaa	aga	1256
His	Tyr	Ser	Tyr	Asp	Leu	Arg	Ser	Leu	Val	Ser	Gln	Leu	Phe	Lys	Arg	
226					231					236					241	
aat	cct	agg	gat	aga	cca	tca	gtc	aac	tcc	ata	ttg	gag	aaa	ggg	ttt	1304
Asn	Pro	Arg	Asp	Arg	Pro	Ser	Val	Asn	Ser	Ile	Leu	Glu	Lys	Gly	Phe	
242					247					252					257	
ata	gcc	aaa	cgc	att	gaa	aag	ttt	ctc	tct	cct	cag	ctt	att	gca	gaa	1352
Ile	Ala	Lys	Arg	Ile	Glu	Lys	Phe	Leu	Ser	Pro	Gln	Leu	Ile	Ala	Glu	
258					263					268					273	
gaa	ttt	tgt	cta	aaa	aca	ttt	tcg	aag	ttt	gga	tca	cag	cct	ata	cca	1400
Glu	Phe	Cys	Leu	Lys	Thr	Phe	Ser	Lys	Phe	Gly	Ser	Gln	Pro	Ile	Pro	
274					279					284					289	
gct	aaa	aga	cca	gct	tca	gga	caa	aac	tcg	att	tct	gtt	atg	cct	gct	1448
Ala	Lys	Arg	Pro	Ala	Ser	Gly	Gln	Asn	Ser	Ile	Ser	Val	Met	Pro	Ala	
290					295					300					305	
cag	aaa	att	aca	aag	cct	gcc	gct	aaa	tat	gga	ata	cct	tta	gca	tat	1496
Gln	Lys	Ile	Thr	Lys	Pro	Ala	Ala	Lys	Tyr	Gly	Ile	Pro	Leu	Ala	Tyr	
306					311					316					321	
aag	aaa	tat	gga	gat	aaa	aaa	tta	cac	gaa	aag	aaa	cca	ctg	caa	aaa	1544
Lys	Lys	Tyr	Gly	Asp	Lys	Lys	Leu	His	Glu	Lys	Lys	Pro	Leu	Gln	Lys	
322					327					332					337	
cat	aaa	cag	gcc	cat	caa	act	cca	gag	aag	aga	gtg	aat	act	ggg	gaa	1592
His	Lys	Gln	Ala	His	Gln	Thr	Pro	Glu	Lys	Arg	Val	Asn	Thr	Gly	Glu	
338					343					348					353	
gaa	agg	agg	aaa	ata	tct	gag	gaa	gca	gca	aga	aag	aga	agg	ctg	gaa	1640
Glu	Arg	Arg	Lys	Ile	Ser	Glu	Glu	Ala	Ala	Arg	Lys	Arg	Arg	Leu	Glu	
354					359					364					369	
ttt	att	gaa	aaa	gaa	aag	aaa	caa	aag	gat	cag	att	att	agt	tta	atg	1688
Phe	Ile	Glu	Lys	Glu	Lys	Lys	Gln	Lys	Asp	Gln	Ile	Ile	Ser	Leu	Met	
370					375					380					385	
aag	gct	gaa	caa	atg	aaa	agg	caa	gaa	aag	gaa	agg	ttg	gaa	aga	ata	1736
Lys	Ala	Glu	Gln	Met	Lys	Arg	Gln	Glu	Lys	Glu	Arg	Leu	Glu	Arg	Ile	
386					391					396					401	
aat	agg	gcc	agg	gaa	caa	gga	tgg	aga	aat	gtg	cta	agt	gct	ggg	gga	1784
Asn	Arg	Ala	Arg	Glu	Gln	Gly	Trp	Arg	Asn	Val	Leu	Ser	Ala	Gly	Gly	
402					407					412					417	
agt	ggg	gaa	gta	aag	gct	cct	ttt	ctg	ggc	agt	gga	ggg	act	ata	gct	1832
Ser	Gly	Glu	Val	Lys	Ala	Pro	Phe	Leu	Gly	Ser	Gly	Gly	Thr	Ile	Ala	
418					423					428					433	
cca	tca	tct	ttt	tct	tct	cga	gga	cag	tat	gaa	cat	tac	cat	gcc	att	1880
Pro	Ser	Ser	Phe	Ser	Ser	Arg	Gly	Gln	Tyr	Glu	His	Tyr	His	Ala	Ile	

434	439	444	449	
ttt gac caa atg cag	caa caa aga gca gaa gat aat gaa gct aaa tgg			1928
Phe Asp Gln Met Gln	Gln Gln Arg Ala Glu Asp Asn Glu Ala Lys Trp			
450	455	460	465	
aaa aga gaa ata tat ggt cga ggt ctt cca gaa agg caa aaa ggg cag				1976
Lys Arg Glu Ile Tyr Gly Arg Gly Leu Pro Glu Arg Gln Lys Gly Gln				
466	471	476	481	
cta gct gta gaa aga gct aaa caa gta gaa gag ttc ctg cag cga aaa				2024
Leu Ala Val Glu Arg Ala Lys Gln Val Glu Glu Phe Leu Gln Arg Lys				
482	487	492	497	
cgg gaa gct atg cag aat aaa gct cga gcc gaa gga cat atg gtt tat				2072
Arg Glu Ala Met Gln Asn Lys Ala Arg Ala Glu Gly His Met Val Tyr				
498	503	508	513	
ctg gca aga ctg agg caa ata aga cta cag aat ttc aat gag cgc caa				2120
Leu Ala Arg Leu Arg Gln Ile Arg Leu Gln Asn Phe Asn Glu Arg Gln				
514	519	524	529	
cag att aaa gcc aaa ctt cgt ggt gaa aag aaa gaa gct aat cat tct				2168
Gln Ile Lys Ala Lys Leu Arg Gly Glu Lys Lys Glu Ala Asn His Ser				
530	535	540	545	
gaa gga caa gaa gga agt gaa gag gct gac atg agg cgc aaa aaa atc				2216
Glu Gly Gln Glu Gly Ser Glu Glu Ala Asp Met Arg Arg Lys Lys Ile				
546	551	556	561	
gaa tca ctg aag gcc cat gca aat gca cgt gct gct gta cta aaa gaa				2264
Glu Ser Leu Lys Ala His Ala Asn Ala Arg Ala Ala Val Leu Lys Glu				
562	567	572	577	
caa cta gaa cga aag aga aag gag gct tat gag aga gaa aaa aaa gtg				2312
Gln Leu Glu Arg Lys Arg Lys Glu Ala Tyr Glu Arg Glu Lys Lys Val				
578	583	588	593	
tgg gaa gag cat ttg gtg gct aaa gga gtt aag agt tct gat gtt tct				2360
Trp Glu Glu His Leu Val Ala Lys Gly Val Lys Ser Ser Asp Val Ser				
594	599	604	609	
cca cct ttg gga cag cat gaa aca ggt ggc tct cca tca aag caa cag				2408
Pro Pro Leu Gly Gln His Glu Thr Gly Gly Ser Pro Ser Lys Gln Gln				
610	615	620	625	
atg aga tct gtt att tct gta act tca gct ttg aaa gaa gtt ggc gtg				2456
Met Arg Ser Val Ile Ser Val Thr Ser Ala Leu Lys Glu Val Gly Val				
626	631	636	641	
gac agt agt tta act gat acc cgg gaa act tca gaa gag atg caa aag				2504
Asp Ser Ser Leu Thr Asp Thr Arg Glu Thr Ser Glu Glu Met Gln Lys				
642	647	652	657	
acc aac aat gct att tca agt aag cga gaa ata ctt cgt aga tta aat				2552
Thr Asn Asn Ala Ile Ser Ser Lys Arg Glu Ile Leu Arg Arg Leu Asn				
658	663	668	673	

gaa aat ctt aaa gct caa gaa gat gaa aaa gga aag cag aat ctc tct	2600
Glu Asn Leu Lys Ala Gln Glu Asp Glu Lys Gly Lys Gln Asn Leu Ser	
674 679 684 689	
gat act ttt gag ata aat gtt cat gaa gat gcc aaa gag cat gaa aaa	2648
Asp Thr Phe Glu Ile Asn Val His Glu Asp Ala Lys Glu His Glu Lys	
690 695 700 705	
gaa aaa tca gtt tca tct gat cgc aag aag tgg gag gca gga ggt caa	2696
Glu Lys Ser Val Ser Ser Asp Arg Lys Lys Trp Glu Ala Gly Gly Gln	
706 711 716 721	
ctt gtg att cct ctg gat gag tta aca cta gat aca tcc ttc tct aca	2744
Leu Val Ile Pro Leu Asp Glu Leu Thr Leu Asp Thr Ser Phe Ser Thr	
722 727 732 737	
act gaa aga cat aca gtg gga gaa gtt att aaa tta ggt cct aat gga	2792
Thr Glu Arg His Thr Val Gly Glu Val Ile Lys Leu Gly Pro Asn Gly	
738 743 748 753	
tct cca aga aga gcc tgg ggg aaa agt ccg aca gat tct gtt cta aag	2840
Ser Pro Arg Arg Ala Trp Gly Lys Ser Pro Thr Asp Ser Val Leu Lys	
754 759 764 769	
ata ctt gga gaa gct gaa cta caa ctt cag aca gaa cta tta gaa aat	2888
Ile Leu Gly Glu Ala Glu Leu Gln Leu Gln Thr Glu Leu Leu Glu Asn	
770 775 780 785	
aca act att aga agt gag att tct ccc gaa ggg gaa aag tac aaa ccc	2936
Thr Thr Ile Arg Ser Glu Ile Ser Pro Glu Gly Glu Lys Tyr Lys Pro	
786 791 796 801	
tta att act gga gaa aaa aaa gta caa tgt att tca cat gaa ata aac	2984
Leu Ile Thr Gly Glu Lys Lys Val Gln Cys Ile Ser His Glu Ile Asn	
802 807 812 817	
cca tca gct att gtt gat tct cct gtt gag aca aaa agt ccc gag ttc	3032
Pro Ser Ala Ile Val Asp Ser Pro Val Glu Thr Lys Ser Pro Glu Phe	
818 823 828 833	
agt gag gca tct cca cag atg tca ttg aaa ctg gaa gga aat tta gaa	3080
Ser Glu Ala Ser Pro Gln Met Ser Leu Lys Leu Glu Gly Asn Leu Glu	
834 839 844 849	
gaa cct gat gat ttg gaa aca gaa att cta caa gag cca agt gga aca	3128
Glu Pro Asp Asp Leu Glu Thr Glu Ile Leu Gln Glu Pro Ser Gly Thr	
850 855 860 865	
aac aaa gat gag agc ttg cca tgc act att act gat gtg tgg att agt	3176
Asn Lys Asp Glu Ser Leu Pro Cys Thr Ile Thr Asp Val Trp Ile Ser	
866 871 876 881	
gag gaa aaa gaa aca aag gaa act cag tgc gca gat agg atc acc att	3224
Glu Glu Lys Glu Thr Lys Glu Thr Gln Ser Ala Asp Arg Ile Thr Ile	
882 887 892 897	

cag gaa aat gaa gtt tct gaa gat gga gtc tcg agt act gtg gac caa	3272
Gln Glu Asn Glu Val Ser Glu Asp Gly Val Ser Ser Thr Val Asp Gln	
898 903 908 913	
ctt agt gac att cat ata gag cct gga acc aat gat tct cag cac tct	3320
Leu Ser Asp Ile His Ile Glu Pro Gly Thr Asn Asp Ser Gln His Ser	
914 919 924 929	
aaa tgt gat gta gat aag tct gtg caa ccg gaa cca ttt ttc cat aag	3368
Lys Cys Asp Val Asp Lys Ser Val Gln Pro Glu Pro Phe Phe His Lys	
930 935 940 945	
gtg gtt cat tct gaa cac ttg aac tta gtc cct caa gtt caa tca gtt	3416
Val Val His Ser Glu His Leu Asn Leu Val Pro Gln Val Gln Ser Val	
946 951 956 961	
cag tgt tca cca gaa gaa tcc ttt gca ttt cga tct cac tcg cat tta	3464
Gln Cys Ser Pro Glu Glu Ser Phe Ala Phe Arg Ser His Ser His Leu	
962 967 972 977	
cca cca aaa aat aaa aac aag aat tcc ttg ctg att gga ctt tca act	3512
Pro Pro Lys Asn Lys Asn Lys Asn Ser Leu Leu Ile Gly Leu Ser Thr	
978 983 988 993	
ggg ctg ttt gat gca aac aac cca aag atg tta agg aca tgt tca ctt	3560
Gly Leu Phe Asp Ala Asn Asn Pro Lys Met Leu Arg Thr Cys Ser Leu	
994 999 1004 1009	
cca gat ctc tca aag ctg ttc aga acc ctt atg gat gtt ccc acc gta	3608
Pro Asp Leu Ser Lys Leu Phe Arg Thr Leu Met Asp Val Pro Thr Val	
1010 1015 1020 1025	
gga gat gtt cgt caa gac aat ctt gaa ata gat gaa att aaa gat gaa	3656
Gly Asp Val Arg Gln Asp Asn Leu Glu Ile Asp Glu Ile Lys Asp Glu	
1026 1031 1036 1041	
aac att aaa gaa gga cct tct gat tct gaa gac att gtg ttt gaa gaa	3704
Asn Ile Lys Glu Gly Pro Ser Asp Ser Glu Asp Ile Val Phe Glu Glu	
1042 1047 1052 1057	
act gac aca gat tta caa gag ctg cag gcc tcg atg gaa cag tta ctt	3752
Thr Asp Thr Asp Leu Gln Glu Leu Gln Ala Ser Met Glu Gln Leu Leu	
1058 1063 1068 1073	
agg gaa caa cct ggt gaa gaa tac agt gaa gaa gaa gag tca gtc ttg	3800
Arg Glu Gln Pro Gly Glu Glu Tyr Ser Glu Glu Glu Glu Ser Val Leu	
1074 1079 1084 1089	
aag aac agt gat gtg gag cca act gca aat ggg aca gat gtg gca gat	3848
Lys Asn Ser Asp Val Glu Pro Thr Ala Asn Gly Thr Asp Val Ala Asp	
1090 1095 1100 1105	
gaa gat gac aat ccc agc agt gaa agt gcc ctg aac gaa gaa tgg cac	3896
Glu Asp Asp Asn Pro Ser Ser Glu Ser Ala Leu Asn Glu Glu Trp His	
1106 1111 1116 1121	
tca gat aac agt gat ggt gaa att gct agt gaa tgt gaa tgc gat agt	3944

taataaaagc aaagtttttg aacctctgag tccaaagcag gctggttggc ataatatgta 5265
 atttgaaaaa taaaatctta tcttgcagca ctatcagtat gttgaattta ttatgtatat 5325
 tatttcta atccgaaact aaatacttga ttttttaata tgtgtgttta ttttatgata 5385
 ttgctattaa atttttatta tctaaaaaaa aaaaaaaaaa aaaaaactgc ggccgcaagc 5445
 tta 5448

<210> 247
 <211> 1767
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1767)

<400> 247

atg act act cag ttg cca gct tac gtg gca att ttg ctt ttc tat gtc 48
 Met Thr Thr Gln Leu Pro Ala Tyr Val Ala Ile Leu Leu Phe Tyr Val
 1 5 10

tca aga gcc agc tgc cag gac act ttc act gca gct gtt tat gag cat 96
 Ser Arg Ala Ser Cys Gln Asp Thr Phe Thr Ala Ala Val Tyr Glu His
 17 22 27 32

gca gcg ata ttg ccc aat gcc acc cta aca cca gtg tct cgt gag gag 144
 Ala Ala Ile Leu Pro Asn Ala Thr Leu Thr Pro Val Ser Arg Glu Glu
 33 38 43 48

gct ttg gca tta atg aat cgg aat ctg gac att ttg gaa gga gcg atc 192
 Ala Leu Ala Leu Met Asn Arg Asn Leu Asp Ile Leu Glu Gly Ala Ile
 49 54 59 64

aca tca gca gca gat cag ggt gcg cat att att gtg act cca gaa gat 240
 Thr Ser Ala Ala Asp Gln Gly Ala His Ile Ile Val Thr Pro Glu Asp
 65 70 75 80

gct att tat ggc tgg aac ttc aac agg gac tct ctc tac cca tat ttg 288
 Ala Ile Tyr Gly Trp Asn Phe Asn Arg Asp Ser Leu Tyr Pro Tyr Leu
 81 86 91 96

gag gac atc cca gac cct gaa gta aac tgg atc ccc tgt aat aat cgt 336
 Glu Asp Ile Pro Asp Pro Glu Val Asn Trp Ile Pro Cys Asn Asn Arg
 97 102 107 112

aac agg gac atg gat aaa gct gga aac cat cat tct cag caa act aac 384
 Asn Arg Asp Met Asp Lys Ala Gly Asn His His Ser Gln Gln Thr Asn
 113 118 123 128

aca gga aca gaa aac aaa aca ctg cat gtt ctc gct cat aag tgg gag 432
 Thr Gly Thr Glu Asn Lys Thr Leu His Val Leu Ala His Lys Trp Glu

129	134	139	144	
ttg aac aac gag aat aca tgg aca caa gga ggg gaa cat cac aca ccg				480
Leu Asn Asn Glu Asn Thr Trp Thr Gln Gly Gly Glu His His Thr Pro				
145	150	155	160	
ggg cct gtc ggg gag tcg ggg gct aag gga ggg atg gca tta gga gaa				528
Gly Pro Val Gly Glu Ser Gly Ala Lys Gly Gly Met Ala Leu Gly Glu				
161	166	171	176	
ata cct aat gta gat gat ggg ttg atc tta gag aaa agc ttt cag ttt				576
Ile Pro Asn Val Asp Asp Gly Leu Ile Leu Glu Lys Ser Phe Gln Phe				
177	182	187	192	
tcc ctc att cag tat gat acc agc cat ggg tct gtc ata aat ggc tat				624
Ser Leu Ile Gln Tyr Asp Thr Ser His Gly Ser Val Ile Asn Gly Tyr				
193	198	203	208	
tat tgt gtt gag acc cca gta caa gaa aga ctc agc tgc ctg gcc aag				672
Tyr Cys Val Glu Thr Pro Val Gln Glu Arg Leu Ser Cys Leu Ala Lys				
209	214	219	224	
aac aac tct atc tat gtt gtg gca aat att ggg gac aag aag cca tgc				720
Asn Asn Ser Ile Tyr Val Val Ala Asn Ile Gly Asp Lys Lys Pro Cys				
225	230	235	240	
gat acc agt gat cct cag tgt ccc cct gat ggc cgt tac caa tac aac				768
Asp Thr Ser Asp Pro Gln Cys Pro Pro Asp Gly Arg Tyr Gln Tyr Asn				
241	246	251	256	
act gat gtg gta ttt gat tct caa gga aaa ctg gtg gca cgc tac cat				816
Thr Asp Val Val Phe Asp Ser Gln Gly Lys Leu Val Ala Arg Tyr His				
257	262	267	272	
aag caa aac ctt ttc atg ggt gaa aat caa ttc aat gta ccc aag gag				864
Lys Gln Asn Leu Phe Met Gly Glu Asn Gln Phe Asn Val Pro Lys Glu				
273	278	283	288	
cct gag att gtg act ttc aat acc acc ttt gga agt ttt ggc att ttc				912
Pro Glu Ile Val Thr Phe Asn Thr Thr Phe Gly Ser Phe Gly Ile Phe				
289	294	299	304	
aca tgc ttt gat ata ctc ttc cat gat cct gct gtt acc ttg gtg aaa				960
Thr Cys Phe Asp Ile Leu Phe His Asp Pro Ala Val Thr Leu Val Lys				
305	310	315	320	
gat ttc cac gtg gac acc ata gta ttc cca aca gct tgg atg aat gtt				1008
Asp Phe His Val Asp Thr Ile Val Phe Pro Thr Ala Trp Met Asn Val				
321	326	331	336	
ttg cca cat ttg tca gct gtt gaa ttc cac tca gct tgg gct atg ggc				1056
Leu Pro His Leu Ser Ala Val Glu Phe His Ser Ala Trp Ala Met Gly				
337	342	347	352	
atg agg gtc aat ttc ctt gca tcc aac ata cat tac ccc tca aag aaa				1104
Met Arg Val Asn Phe Leu Ala Ser Asn Ile His Tyr Pro Ser Lys Lys				
353	358	363	368	

atg aca gga agt ggc atc tat gca ccc aat tct tca aga gca ttt cat	1152
Met Thr Gly Ser Gly Ile Tyr Ala Pro Asn Ser Ser Arg Ala Phe His	
369 374 379 384	
tat gat atg aag aca gaa gag gga aaa ctc ctc ctc tcg caa ctg gat	1200
Tyr Asp Met Lys Thr Glu Glu Gly Lys Leu Leu Leu Ser Gln Leu Asp	
385 390 395 400	
tcc cac cca tcc cat tct gca gtg gtg aac tgg act tcc tat gcc agc	1248
Ser His Pro Ser His Ser Ala Val Val Asn Trp Thr Ser Tyr Ala Ser	
401 406 411 416	
agt ata gaa gcg ctc tca tca gga aac aag gaa ttt aaa ggc act gtc	1296
Ser Ile Glu Ala Leu Ser Ser Gly Asn Lys Glu Phe Lys Gly Thr Val	
417 422 427 432	
ttt ttc gat gaa ttc act ttt gtg aag ctc aca gga gtt gca gga aat	1344
Phe Phe Asp Glu Phe Thr Phe Val Lys Leu Thr Gly Val Ala Gly Asn	
433 438 443 448	
tat aca gtt tgt cag aaa gat ctc tgc tgt cat tta agc tac aaa atg	1392
Tyr Thr Val Cys Gln Lys Asp Leu Cys Cys His Leu Ser Tyr Lys Met	
449 454 459 464	
tct gag aac ata cca aat gaa gtg tac gct cta ggg gca ttt gac gga	1440
Ser Glu Asn Ile Pro Asn Glu Val Tyr Ala Leu Gly Ala Phe Asp Gly	
465 470 475 480	
ctg cac act gtg gaa ggg cgc tat tat cta cag att tgt acc ctg ttg	1488
Leu His Thr Val Glu Gly Arg Tyr Tyr Leu Gln Ile Cys Thr Leu Leu	
481 486 491 496	
aaa tgt aaa acg act aat tta aac act tgc ggt gac tca gct gaa aca	1536
Lys Cys Lys Thr Thr Asn Leu Asn Thr Cys Gly Asp Ser Ala Glu Thr	
497 502 507 512	
gct tct acc agg ttt gaa atg ttc tcc ctc agt ggc act ttc gga acc	1584
Ala Ser Thr Arg Phe Glu Met Phe Ser Leu Ser Gly Thr Phe Gly Thr	
513 518 523 528	
cag tat gtc ttt cct gag gtg ttg ctg agt gaa aat cag ctt gca cct	1632
Gln Tyr Val Phe Pro Glu Val Leu Leu Ser Glu Asn Gln Leu Ala Pro	
529 534 539 544	
gga gaa ttt cag tgc tgt gat gat gga caa tta cat agt acc gat aac	1680
Gly Glu Phe Gln Cys Cys Asp Asp Gly Gln Leu His Ser Thr Asp Asn	
545 550 555 560	
agc cat gca ctg tgc aaa gca tgc cct tct gca cag gag agc aag gca	1728
Ser His Ala Leu Cys Lys Ala Cys Pro Ser Ala Gln Glu Ser Lys Ala	
561 566 571 576	
ctt gca gta gtg atc tat gcc agc aaa aca tca ttt tga	1767
Leu Ala Val Val Ile Tyr Ala Ser Lys Thr Ser Phe *	
577 582 587	

<210> 248
 <211> 7453
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(4362)

<400> 248

atg gcg cag aga act gga ctc gag gat cca gag agg tat ctc ttt gtg	48
Met Ala Gln Arg Thr Gly Leu Glu Asp Pro Glu Arg Tyr Leu Phe Val	
1 5 10	
gac agg gct gtc atc tac aac cct gcc act caa gct gat tgg aca gct	96
Asp Arg Ala Val Ile Tyr Asn Pro Ala Thr Gln Ala Asp Trp Thr Ala	
17 22 27 32	
aaa aag cta gtg tgg att cca tca gaa cgc cat ggt ttt gag gca gct	144
Lys Lys Leu Val Trp Ile Pro Ser Glu Arg His Gly Phe Glu Ala Ala	
33 38 43 48	
agt atc aaa gaa gaa cgg gga gat gaa gtt atg gtg gag ttg gca gag	192
Ser Ile Lys Glu Glu Arg Gly Asp Glu Val Met Val Glu Leu Ala Glu	
49 54 59 64	
aat gga aag aaa gca atg gtc aac aaa gat gat att cag aag atg aac	240
Asn Gly Lys Lys Ala Met Val Asn Lys Asp Asp Ile Gln Lys Met Asn	
65 70 75 80	
cca cct aag ttt tcc aag gtg gag gat atg gca gaa ttg aca tgc ttg	288
Pro Pro Lys Phe Ser Lys Val Glu Asp Met Ala Glu Leu Thr Cys Leu	
81 86 91 96	
aat gaa gct tcc gtt tta cat aat ctg aag gat cgc tac tat tca gga	336
Asn Glu Ala Ser Val Leu His Asn Leu Lys Asp Arg Tyr Tyr Ser Gly	
97 102 107 112	
cta atc tat act tat tct gga ctc ttc tgt gta gtt ata aac cct tac	384
Leu Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Val Ile Asn Pro Tyr	
113 118 123 128	
aag aat ctt cca att tac tct gag aat att att gaa atg tac aga ggg	432
Lys Asn Leu Pro Ile Tyr Ser Glu Asn Ile Ile Glu Met Tyr Arg Gly	
129 134 139 144	
aag aag cgt cat gag atg cct cca cac atc tat gct ata tct gaa tct	480
Lys Lys Arg His Glu Met Pro Pro His Ile Tyr Ala Ile Ser Glu Ser	
145 150 155 160	
gct tac aga tgc atg ctt caa gat cgt gag gac cag tca att ctt tgc	528
Ala Tyr Arg Cys Met Leu Gln Asp Arg Glu Asp Gln Ser Ile Leu Cys	
161 166 171 176	

acg ggt gag tca ggt gct ggg aag aca gaa aat aca aag aaa gtt att	576
Thr Gly Glu Ser Gly Ala Gly Lys Thr Glu Asn Thr Lys Lys Val Ile	
177 182 187 192	
cag tac ctt gcc cat gtt gct tct tca cat aaa gga aga aag gac cat	624
Gln Tyr Leu Ala His Val Ala Ser Ser His Lys Gly Arg Lys Asp His	
193 198 203 208	
aat att cct ggg gaa ctt gaa cgg cag ctt ttg caa gca aat cca att	672
Asn Ile Pro Gly Glu Leu Glu Arg Gln Leu Leu Gln Ala Asn Pro Ile	
209 214 219 224	
ctg gaa tca ttt gga aat gcg aag act gtg aaa aat gat aac tca tct	720
Leu Glu Ser Phe Gly Asn Ala Lys Thr Val Lys Asn Asp Asn Ser Ser	
225 230 235 240	
cgt ttt ggc aaa ttt att cgg atc aac ttt gat gta act ggc tat atc	768
Arg Phe Gly Lys Phe Ile Arg Ile Asn Phe Asp Val Thr Gly Tyr Ile	
241 246 251 256	
gtt ggg gcc aac att gaa aca tac ctt ctg gaa aag tct cgt gct gtt	816
Val Gly Ala Asn Ile Glu Thr Tyr Leu Leu Glu Lys Ser Arg Ala Val	
257 262 267 272	
cgt caa gca aaa gat gaa cgt act ttt cat atc ttt tac cag ttg tta	864
Arg Gln Ala Lys Asp Glu Arg Thr Phe His Ile Phe Tyr Gln Leu Leu	
273 278 283 288	
tct gga gca gga gaa cac cta aag tct gat ttg ctt ctt gaa gga ttt	912
Ser Gly Ala Gly Glu His Leu Lys Ser Asp Leu Leu Leu Glu Gly Phe	
289 294 299 304	
aat aac tac agg ttt ctc tcc aat ggc tat att cct att ccg gga cag	960
Asn Asn Tyr Arg Phe Leu Ser Asn Gly Tyr Ile Pro Ile Pro Gly Gln	
305 310 315 320	
caa gac aaa gat aat ttc cag gag acc atg gaa gca atg cac ata atg	1008
Gln Asp Lys Asp Asn Phe Gln Glu Thr Met Glu Ala Met His Ile Met	
321 326 331 336	
ggc ttc tcc cat gaa gag att ctg tca atg ctt aaa gta gta tct tca	1056
Gly Phe Ser His Glu Glu Ile Leu Ser Met Leu Lys Val Val Ser Ser	
337 342 347 352	
gtg cta cag ttt gga aat att tct ttc aaa aag gag aga aat act gat	1104
Val Leu Gln Phe Gly Asn Ile Ser Phe Lys Lys Glu Arg Asn Thr Asp	
353 358 363 368	
caa gct tcc atg cca gaa aat aca gtt gcg cag aag ctc tgc cat ctt	1152
Gln Ala Ser Met Pro Glu Asn Thr Val Ala Gln Lys Leu Cys His Leu	
369 374 379 384	
ctt ggg atg aat gtg atg gag ttt act cgg gcc atc ctg act ccc cgg	1200
Leu Gly Met Asn Val Met Glu Phe Thr Arg Ala Ile Leu Thr Pro Arg	
385 390 395 400	

atc aag gtc ggc cga gac tat gtg caa aaa gcc cag acc aaa gaa cag Ile Lys Val Gly Arg Asp Tyr Val Gln Lys Ala Gln Thr Lys Glu Gln 401 406 411 416	1248
gca gat ttt gca gta gaa gca ttg gca aaa gct acc tat gag cgg ctc Ala Asp Phe Ala Val Glu Ala Leu Ala Lys Ala Thr Tyr Glu Arg Leu 417 422 427 432	1296
ttt cgc tgg ctc gtt cat cgc atc aat aaa gct ctg gat agg acc aaa Phe Arg Trp Leu Val His Arg Ile Asn Lys Ala Leu Asp Arg Thr Lys 433 438 443 448	1344
cgt cag gga gca tct ttc att gga atc ctg gat att gct gga ttt gaa Arg Gln Gly Ala Ser Phe Ile Gly Ile Leu Asp Ile Ala Gly Phe Glu 449 454 459 464	1392
att ttt gag ctg aac tcc ttt gaa caa ctt tgc atc aac tac acc aat Ile Phe Glu Leu Asn Ser Phe Glu Gln Leu Cys Ile Asn Tyr Thr Asn 465 470 475 480	1440
gag aag ctg cag cag ctg ttc aac cac acc atg ttt atc cta gaa caa Glu Lys Leu Gln Gln Leu Phe Asn His Thr Met Phe Ile Leu Glu Gln 481 486 491 496	1488
gag gaa tac cag cgc gaa ggc atc gag tgg aac ttc atc gat ttc ggg Glu Glu Tyr Gln Arg Glu Gly Ile Glu Trp Asn Phe Ile Asp Phe Gly 497 502 507 512	1536
ctg gat ctg cag cca tgc atc gac cta ata gag aga cct gcg aac cct Leu Asp Leu Gln Pro Cys Ile Asp Leu Ile Glu Arg Pro Ala Asn Pro 513 518 523 528	1584
cct ggt gta ctg gcc ctt ttg gat gaa gaa tgc tgg ttc cct aaa gcc Pro Gly Val Leu Ala Leu Leu Asp Glu Glu Cys Trp Phe Pro Lys Ala 529 534 539 544	1632
aca gat aaa acc ttt gtt gaa aaa ctg gtt caa gag caa ggt tcc cac Thr Asp Lys Thr Phe Val Glu Lys Leu Val Gln Glu Gln Gly Ser His 545 550 555 560	1680
tcc aag ttt cag aaa cct cga caa tta aaa gac aaa gct gat ttt tgc Ser Lys Phe Gln Lys Pro Arg Gln Leu Lys Asp Lys Ala Asp Phe Cys 561 566 571 576	1728
att ata cat tat gca ggg aag gtg gac tat aag gca gat gag tgg ctg Ile Ile His Tyr Ala Gly Lys Val Asp Tyr Lys Ala Asp Glu Trp Leu 577 582 587 592	1776
atg aag aat atg gac ccc ctg aat gac aac gtg gcc acc ctt ttg cac Met Lys Asn Met Asp Pro Leu Asn Asp Asn Val Ala Thr Leu Leu His 593 598 603 608	1824
cag tca tca gac aga ttt gtg gca gag ctt tgg aaa gat gtg gac cgt Gln Ser Ser Asp Arg Phe Val Ala Glu Leu Trp Lys Asp Val Asp Arg 609 614 619 624	1872
atc gtg ggt ctg gat caa gtc act ggt atg act gag aca gct ttt ggc	1920

Ile Val Gly Leu Asp Gln Val Thr Gly Met Thr Glu Thr Ala Phe Gly	625	630	635	640	
tcc gca tat aaa acc aag aag ggc atg ttt cgt acc gtt ggg caa ctc	1968				
Ser Ala Tyr Lys Thr Lys Lys Gly Met Phe Arg Thr Val Gly Gln Leu	641	646	651	656	
tac aaa gaa tct ctc acc aag ctg atg gca act ctc cga aac acc aac	2016				
Tyr Lys Glu Ser Leu Thr Lys Leu Met Ala Thr Leu Arg Asn Thr Asn	657	662	667	672	
cct aac ttt gtt cgt tgt atc att cca aat cac gag aag agg gct gga	2064				
Pro Asn Phe Val Arg Cys Ile Ile Pro Asn His Glu Lys Arg Ala Gly	673	678	683	688	
aaa ttg gat cca cac cta gtc cta gat cag ctt cgc tgt aat ggt gtc	2112				
Lys Leu Asp Pro His Leu Val Leu Asp Gln Leu Arg Cys Asn Gly Val	689	694	699	704	
ctg gaa ggg atc cga atc tgt cgc cag ggc ttc cct aac cga ata gtt	2160				
Leu Glu Gly Ile Arg Ile Cys Arg Gln Gly Phe Pro Asn Arg Ile Val	705	710	715	720	
ttc caa gaa ttc aga cag aga tat gag atc cta act cca aat gct att	2208				
Phe Gln Glu Phe Arg Gln Arg Tyr Glu Ile Leu Thr Pro Asn Ala Ile	721	726	731	736	
cct aaa ggt ttt atg gat ggt aaa cag gcc tgt gaa cga atg atc cgg	2256				
Pro Lys Gly Phe Met Asp Gly Lys Gln Ala Cys Glu Arg Met Ile Arg	737	742	747	752	
gct tta gaa ttg gac cca aac ttg tac aga att gga cag agc aag ata	2304				
Ala Leu Glu Leu Asp Pro Asn Leu Tyr Arg Ile Gly Gln Ser Lys Ile	753	758	763	768	
ttt ttc aga gct gga gtt ctg gca cac tta gag gaa gaa aga gat tta	2352				
Phe Phe Arg Ala Gly Val Leu Ala His Leu Glu Glu Glu Arg Asp Leu	769	774	779	784	
aaa atc acc gat atc att atc ttc ttc cag gcc gtt tgc aga ggt tac	2400				
Lys Ile Thr Asp Ile Ile Ile Phe Phe Gln Ala Val Cys Arg Gly Tyr	785	790	795	800	
ctg gcc aga aag gcc ttt gcc aag aag cag cag caa cta agt gcc tta	2448				
Leu Ala Arg Lys Ala Phe Ala Lys Lys Gln Gln Gln Leu Ser Ala Leu	801	806	811	816	
aag gtc ttg cag cgg aac tgt gcc gcg tac ctg aaa tta cgg cac tgg	2496				
Lys Val Leu Gln Arg Asn Cys Ala Ala Tyr Leu Lys Leu Arg His Trp	817	822	827	832	
cag tgg tgg cga gtc ttc aca aag gtg aag ccg ctt cta caa gtg act	2544				
Gln Trp Trp Arg Val Phe Thr Lys Val Lys Pro Leu Leu Gln Val Thr	833	838	843	848	
cgc cag gag gaa gaa ctt cag gcc aaa gat gaa gag ctg ttg aag gtg	2592				
Arg Gln Glu Glu Glu Leu Gln Ala Lys Asp Glu Glu Leu Leu Lys Val					

849	854	859	864	
aag gag aag cag aca aag gtg gaa gga gag ctg gag gag atg gag cgg				2640
Lys Glu Lys Gln Thr Lys Val Glu Gly Glu Leu Glu Glu Met Glu Arg				
865	870	875	880	
aag cac cag cag ctt tta gaa gag aag aat atc ctt gca gaa caa cta				2688
Lys His Gln Gln Leu Leu Glu Glu Lys Asn Ile Leu Ala Glu Gln Leu				
881	886	891	896	
caa gca gag act gag ctc ttt gct gaa gca gaa gag atg agg gca aga				2736
Gln Ala Glu Thr Glu Leu Phe Ala Glu Ala Glu Glu Met Arg Ala Arg				
897	902	907	912	
ctt gct gct aaa aag cag gaa tta gaa gag att cta cat gac ttg gag				2784
Leu Ala Ala Lys Lys Gln Glu Leu Glu Glu Ile Leu His Asp Leu Glu				
913	918	923	928	
tct agg gtt gaa gaa gaa gaa gaa aga aac caa atc ctc caa aat gaa				2832
Ser Arg Val Glu Glu Glu Glu Glu Arg Asn Gln Ile Leu Gln Asn Glu				
929	934	939	944	
aag aaa aaa atg caa gca cat att cag gac ctg gaa gaa cag cta gac				2880
Lys Lys Lys Met Gln Ala His Ile Gln Asp Leu Glu Glu Gln Leu Asp				
945	950	955	960	
gag gag gaa ggg gct cgg caa aag ctg cag ctg gaa aag gtg aca gca				2928
Glu Glu Glu Gly Ala Arg Gln Lys Leu Gln Leu Glu Lys Val Thr Ala				
961	966	971	976	
gag gcc aag atc aag aag atg gaa gag gag att ctg ctt ctc gag gac				2976
Glu Ala Lys Ile Lys Lys Met Glu Glu Glu Ile Leu Leu Leu Glu Asp				
977	982	987	992	
caa aat tcc aag ttc atc aaa gaa aag aaa ctc atg gaa gat cgc att				3024
Gln Asn Ser Lys Phe Ile Lys Glu Lys Lys Leu Met Glu Asp Arg Ile				
993	998	1003	1008	
gct gag tgt tcc tct cag ctg gct gaa gag gaa gaa aag gcg aaa aac				3072
Ala Glu Cys Ser Ser Gln Leu Ala Glu Glu Glu Glu Lys Ala Lys Asn				
1009	1014	1019	1024	
ttg gcc aaa atc agg aat aag caa gaa gtg atg atc tca gat tta gaa				3120
Leu Ala Lys Ile Arg Asn Lys Gln Glu Val Met Ile Ser Asp Leu Glu				
1025	1030	1035	1040	
gaa cgc tta aag aag gaa gaa aag act cgt cag gaa ctg gaa aag gcc				3168
Glu Arg Leu Lys Lys Glu Glu Lys Thr Arg Gln Glu Leu Glu Lys Ala				
1041	1046	1051	1056	
aaa aga aaa ctc gac ggg gag acg acc gac ctg cag gac cag atc gca				3216
Lys Arg Lys Leu Asp Gly Glu Thr Thr Asp Leu Gln Asp Gln Ile Ala				
1057	1062	1067	1072	
gag ctg cag gcg cag att gat gag ctc aag ctg cag ctg gcc aag aag				3264
Glu Leu Gln Ala Gln Ile Asp Glu Leu Lys Leu Gln Leu Ala Lys Lys				
1073	1078	1083	1088	

gag gag gag ctg cag ggc gca ctg gcc aga ggt gat gat gaa aca ctc Glu Glu Glu Leu Gln Gly Ala Leu Ala Arg Gly Asp Asp Glu Thr Leu 1089 1094 1099 1104	3312
cat aag aac aat gcc ctt aaa gtt gtg cga gag cta caa gcc caa att His Lys Asn Asn Ala Leu Lys Val Val Arg Glu Leu Gln Ala Gln Ile 1105 1110 1115 1120	3360
gct gaa ctt cag gaa gac ttt gaa tcc gag aag gct tca cgg aac aag Ala Glu Leu Gln Glu Asp Phe Glu Ser Glu Lys Ala Ser Arg Asn Lys 1121 1126 1131 1136	3408
gcc gaa aag cag aaa agg gac ttg agt gag gaa ctg gaa gct ctg aaa Ala Glu Lys Gln Lys Arg Asp Leu Ser Glu Glu Leu Glu Ala Leu Lys 1137 1142 1147 1152	3456
aca gag ctg gag gac acg ctg gac acc acg gca gcc cag cag gaa cta Thr Glu Leu Glu Asp Thr Leu Asp Thr Thr Ala Ala Gln Gln Glu Leu 1153 1158 1163 1168	3504
cgt aca aaa cgt gaa caa gaa gtg gca gag ctg aag aaa gct ctt gag Arg Thr Lys Arg Glu Gln Glu Val Ala Glu Leu Lys Lys Ala Leu Glu 1169 1174 1179 1184	3552
gag gaa act aag aac cat gaa gct caa atc cag gac atg aga caa aga Glu Glu Thr Lys Asn His Glu Ala Gln Ile Gln Asp Met Arg Gln Arg 1185 1190 1195 1200	3600
cac gca aca gcc ctg gag gag ctc tca gag cag ctg gaa cag gcc aag His Ala Thr Ala Leu Glu Glu Leu Ser Glu Gln Leu Glu Gln Ala Lys 1201 1206 1211 1216	3648
cgg ttc aaa gca aat cta gag aag aac aag cag ggc ctg gag aca gat Arg Phe Lys Ala Asn Leu Glu Lys Asn Lys Gln Gly Leu Glu Thr Asp 1217 1222 1227 1232	3696
aac aag gag ctg gcg tgt gag gtg aag gtc ctg cag cag gtc aag gct Asn Lys Glu Leu Ala Cys Glu Val Lys Val Leu Gln Gln Val Lys Ala 1233 1238 1243 1248	3744
gag tct gag cac aag agg aag aag ctc gac gcg cag gtc cag gag ctc Glu Ser Glu His Lys Arg Lys Lys Leu Asp Ala Gln Val Gln Glu Leu 1249 1254 1259 1264	3792
cat gcc aag gtc tct gaa ggc gac agg ctc agg gtg gag ctg gcg gag His Ala Lys Val Ser Glu Gly Asp Arg Leu Arg Val Glu Leu Ala Glu 1265 1270 1275 1280	3840
aaa gca agt aag ctg cag aat gag cta gat aat gtc tcc acc ctt ctg Lys Ala Ser Lys Leu Gln Asn Glu Leu Asp Asn Val Ser Thr Leu Leu 1281 1286 1291 1296	3888
gaa gaa gca gag aag aag ggt att aaa ttt gct aag gat gca gct agt Glu Glu Ala Glu Lys Lys Gly Ile Lys Phe Ala Lys Asp Ala Ala Ser 1297 1302 1307 1312	3936

ctt gag tct caa cta cag gat aca cag gag ctt ctt cag gag gag aca Leu Glu Ser Gln Leu Gln Asp Thr Gln Glu Leu Leu Gln Glu Glu Thr 1313 1318 1323 1328	3984
cgc cag aaa cta aac ctg agc agt cgg atc cgg cag ctg gaa gag gag Arg Gln Lys Leu Asn Leu Ser Ser Arg Ile Arg Gln Leu Glu Glu Glu 1329 1334 1339 1344	4032
aag aac agt ctt cag gag cag cag gag gag gag gag gag gcc agg aag Lys Asn Ser Leu Gln Glu Gln Gln Glu Glu Glu Glu Glu Ala Arg Lys 1345 1350 1355 1360	4080
aac ctg gag aag caa gtg ctg gcc ctg cag tcc cag ttg gct gat acc Asn Leu Glu Lys Gln Val Leu Ala Leu Gln Ser Gln Leu Ala Asp Thr 1361 1366 1371 1376	4128
aag aag aaa gta gat gac gac ctg gga aca att gaa agt ctg gaa gaa Lys Lys Lys Val Asp Asp Asp Leu Gly Thr Ile Glu Ser Leu Glu Glu 1377 1382 1387 1392	4176
gcc aag aag aag ctt ctg aag gac gcg gag gcc ctg agc cag cgc ctg Ala Lys Lys Lys Leu Leu Lys Asp Ala Glu Ala Leu Ser Gln Arg Leu 1393 1398 1403 1408	4224
gag gag aag gca ctg gcg tat gac aaa ctg gag aag acc aag aac cgc Glu Glu Lys Ala Leu Ala Tyr Asp Lys Leu Glu Lys Thr Lys Asn Arg 1409 1414 1419 1424	4272
ctg cag cag gag ctg gac gac ctc acg gtg gac ctg gac cac cag cgc Leu Gln Gln Glu Leu Asp Asp Leu Thr Val Asp Leu Asp His Gln Arg 1425 1430 1435 1440	4320
cag gtc gcc tcc aac ttg gag aag aag caa gaa gaa gtt tga ccagctg Gln Val Ala Ser Asn Leu Glu Lys Lys Gln Glu Glu Val * 1441 1446 1451	4369
ttagcagaag agaagagcat ctctgctcgc tatgccgaag agcgggaccg ggccgaagcc	4429
gaggccagag agaaagaaac caaagccctg tcaactggccc gggccctcga ggaagccctg	4489
gaggccaagg aggagtttga gaggcagaac aagcagctcc gagcagacat ggaagacctc	4549
atgagctcca aagatgatgt gggaaaaaac gttcacgaac ttgaaaaatc caaacggggc	4609
ctagagcagc aggtggagga aatgaggacc cagctggagg agctggaaga cgaactccag	4669
gccacggaag atgccaagct tcgtctggag gtcaacatgc aggccatgaa ggcgcagttc	4729
gagagagacc tgcaaaccag ggatgagcag aatgaagaga agaagcggct gctgatcaaa	4789
caggtgcggg agctcgaggc ggagctggag gatgagagga aacagcgggc gcttgctgta	4849
gcttcaaaga aaaagatgga gatagacctg aaggacctcg aagcccaa at cgaggctgcg	4909
aacaaagctc gggatgaggt gattaagcag ctccgcaagc tccaggctca gatgaaggat	4969
taccaacgtg aattagaaga agctcgtgca tccagagatg agatttttgc tcaatccaaa	5029

gagagtgaaa agaaattgaa gagtctggaa gcagaaatcc ttcaattgca ggaggaactt	5089
gcctcatctg agcgagcccg ccgacacgcc gagcaggaga gagatgagct ggcggaacgag	5149
atcaccaaca gcgcctctgg caagtccgcg ctgctggatg agaagcggcg tctggaagct	5209
cggatcgcac agctggagga ggagctggaa gaggagcaga gcaacatgga gctgctcaac	5269
gaccgcttcc gcaagaccac tctacagggtg gacacactga acgccgagct agcagccgag	5329
cgcagcgccg ccgagaagag tgacaatgca cgccagcaac tggagcggca gaacaaggag	5389
ctgaaggcca agctgcagga actcgagggt gctgtcaagt ctaagttaa ggccaccatc	5449
tcagccctgg aggccaaagat tgggcagctg gaggagcagc ttgagcagga agccaaggaa	5509
cgagcagccg ccaacaaatt agtccgtcgc actgagaaga agctgaaaga aatcttcatg	5569
caggttgagg atgagcgtcg acacgcggac cagtataaag agcagatgga gaaggccaac	5629
gctcggatga agcagcttaa acgccagctg gaggaagcag aagaagaagc gacgcgtgcc	5689
aacgcattct ggcgtaaaact ccagcgggaa ctggatgatg ccaccgaggc caacgagggc	5749
ctgagccgcg aggtcagcac cctgaagaac cggctgaggc ggggtggccc catcagcttc	5809
tcttccagcc gatctggcgg gcgccagctg caccttgaag gagcttccct ggagctctcc	5869
gacgatgaca cagaaagtaa gaccagtgat gtcaacgaga cgcagccacc ccagtcagag	5929
taaagttgca ggaagccaga ggaggcaata cagtgggaca gttaggaatg caccgggggc	5989
ctcctgcaga tttcgaaaat tggcaagcta cgggattcct tctgaaaga tcaactgtgt	6049
cttaaggctc tccagcctat gcatactgta tctgtctca gacttaggta caattgctcc	6109
cctttttata tatagacaca cacaggacac atatattaaa cagattgttt catcattgca	6169
tctattttcc atatagtcac caagagacca ttttataaaa catggtaaga ccctttttaa	6229
aacaaactcc aggccttgg ttgcgggtcg ctgggttatt ggggcagcgc cgtggctcgtc	6289
actcagtcgc tctgcatgct ctctgtcata cagacaggta acctagttct gtgttcacgt	6349
ggcccccgac gactcagcca catcaagtct cctagaccac tgtggactct aaactgcact	6409
tgtctctctc atttccttca aataatgatc aatgctatct cagtgaagaa actgtgaaag	6469
gggctttgga aagagtagga ggggtgggct ggatcggaag caacacccat ttggggttac	6529
catgtccatc cccaagggg ggccctgcc ctcgagtcga tgggtgtccg catctactca	6589
tgtgaactgg ccttggcgag ggctgggtctg tgcatagaag ggatagtggc cacactgcag	6649
ctgaggcccc aggtggcagc catggatcat gtagacttcc agatgggtctc ccgaaccgcc	6709

tggtctgtgcc ggcgccctcc tcacgtcagg agcaagcagc cgtggacccc taagccgagc	6769
tggtggaagg cccctccctg tcgccagccg ggccctcatg ctgaccttgc aaattcagcc	6829
gctgctttga gcccaaaatg ggaatattgg ttttgtgtcc gaggcttggt ccaagtttgt	6889
caatgaggtt tatggagcct ccagaacaga tgccatcttc ctgaatgttg acatgccagt	6949
gggtgtgact ccttcatttt tcctttctccc ttccctttgg acagtgttac agtgaacact	7009
tagcatcctg tttttggttg gtagttaagc aaactgacat tacggaaagt gccttagaca	7069
ctacagtact aagacaatgt tgaatatatc attcgctctc ataacaattt aatgtattca	7129
gttttgactg tgcttcatat catgtacctc tctagtcaaa gtggtattac agacattcag	7189
tgacaatgaa tcagtgttaa ttctaaatcc ttgatcctct gcaatgtgct tgaaaacaca	7249
aaccttttgg gttaaaagct ttaacatcta ttaggaagaa tttgtcctgt gggtttggaa	7309
tcttggtattt tcccccttta tgaactgtac tggctgttga ccaccagaca cctgaccgca	7369
aatatctttt cttgtattcc catatttcta gacaatgatt tttgtaagac aataaattta	7429
ttcattatag ataaaaaaaa aaaa	7453

<210> 249
 <211> 7501
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (4410)

<400> 249

atg gcg cag aga act gga ctc gag gat cca gag agg tat ctc ttt gtg	48
Met Ala Gln Arg Thr Gly Leu Glu Asp Pro Glu Arg Tyr Leu Phe Val	
1 5 10	
gac agg gct gtc atc tac aac cct gcc act caa gct gat tgg aca gct	96
Asp Arg Ala Val Ile Tyr Asn Pro Ala Thr Gln Ala Asp Trp Thr Ala	
17 22 27 32	
aaa aag cta gtg tgg att cca tca gaa cgc cat ggt ttt gag gca gct	144
Lys Lys Leu Val Trp Ile Pro Ser Glu Arg His Gly Phe Glu Ala Ala	
33 38 43 48	
agt atc aaa gaa gaa cgg gga gat gaa gtt atg gtg gag ttg gca gag	192
Ser Ile Lys Glu Glu Arg Gly Asp Glu Val Met Val Glu Leu Ala Glu	
49 54 59 64	
aat gga aag aaa gca atg gtc aac aaa gat gat att cag aag atg aac	240
Asn Gly Lys Lys Ala Met Val Asn Lys Asp Asp Ile Gln Lys Met Asn	

65	70	75	80	
cca cct aag ttt tcc aag gtg gag gat atg gca gaa ttg aca tgc ttg				288
Pro Pro Lys Phe Ser Lys Val Glu Asp Met Ala Glu Leu Thr Cys Leu				
81	86	91	96	
aat gaa gct tcc gtt tta cat aat ctg aag gat cgc tac tat tca gga				336
Asn Glu Ala Ser Val Leu His Asn Leu Lys Asp Arg Tyr Tyr Ser Gly				
97	102	107	112	
cta atc tat act tat tct gga ctc ttc tgt gta gtt ata aac cct tac				384
Leu Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Val Ile Asn Pro Tyr				
113	118	123	128	
aag aat ctt cca att tac tct gag aat att att gaa atg tac aga ggg				432
Lys Asn Leu Pro Ile Tyr Ser Glu Asn Ile Ile Glu Met Tyr Arg Gly				
129	134	139	144	
aag aag cgt cat gag atg cct cca cac atc tat gct ata tct gaa tct				480
Lys Lys Arg His Glu Met Pro Pro His Ile Tyr Ala Ile Ser Glu Ser				
145	150	155	160	
gct tac aga tgc atg ctt caa gat cgt gag gac cag tca att ctt tgc				528
Ala Tyr Arg Cys Met Leu Gln Asp Arg Glu Asp Gln Ser Ile Leu Cys				
161	166	171	176	
acg ggt gag tca ggt gct ggg aag aca gaa aat aca aag aaa gtt att				576
Thr Gly Glu Ser Gly Ala Gly Lys Thr Glu Asn Thr Lys Lys Val Ile				
177	182	187	192	
cag tac ctt gcc cat gtt gct tct tca cat aaa gga aga aag gac cat				624
Gln Tyr Leu Ala His Val Ala Ser Ser His Lys Gly Arg Lys Asp His				
193	198	203	208	
aat att cct cag gaa tgc cct aaa cca gtg aaa cac cag agt gga tcc				672
Asn Ile Pro Gln Glu Ser Pro Lys Pro Val Lys His Gln Ser Gly Ser				
209	214	219	224	
ctg ttg tat ggg gaa ctt gaa cgg cag ctt ttg caa gca aat cca att				720
Leu Leu Tyr Gly Glu Leu Glu Arg Gln Leu Leu Gln Ala Asn Pro Ile				
225	230	235	240	
ctg gaa tca ttt gga aat gcg aag act gtg aaa aat gat aac tca tct				768
Leu Glu Ser Phe Gly Asn Ala Lys Thr Val Lys Asn Asp Asn Ser Ser				
241	246	251	256	
cgt ttt ggc aaa ttt att cgg atc aac ttt gat gta act ggc tat atc				816
Arg Phe Gly Lys Phe Ile Arg Ile Asn Phe Asp Val Thr Gly Tyr Ile				
257	262	267	272	
gtt ggg gcc aac att gaa aca tac ctt ctg gaa aag tct cgt gct gtt				864
Val Gly Ala Asn Ile Glu Thr Tyr Leu Leu Glu Lys Ser Arg Ala Val				
273	278	283	288	
cgt caa gca aaa gat gaa cgt act ttt cat atc ttt tac cag ttg tta				912
Arg Gln Ala Lys Asp Glu Arg Thr Phe His Ile Phe Tyr Gln Leu Leu				
289	294	299	304	

tct gga gca gga gaa cac cta aag tct gat ttg ctt ctt gaa gga ttt	960
Ser Gly Ala Gly Glu His Leu Lys Ser Asp Leu Leu Leu Glu Gly Phe	
305 310 315 320	
aat aac tac agg ttt ctc tcc aat ggc tat att cct att ccg gga cag	1008
Asn Asn Tyr Arg Phe Leu Ser Asn Gly Tyr Ile Pro Ile Pro Gly Gln	
321 326 331 336	
caa gac aaa gat aat ttc cag gag acc atg gaa gca atg cac ata atg	1056
Gln Asp Lys Asp Asn Phe Gln Glu Thr Met Glu Ala Met His Ile Met	
337 342 347 352	
ggc ttc tcc cat gaa gag att ctg tca atg ctt aaa gta gta tct tca	1104
Gly Phe Ser His Glu Glu Ile Leu Ser Met Leu Lys Val Val Ser Ser	
353 358 363 368	
gtg cta cag ttt gga aat att tct ttc aaa aag gag aga aat act gat	1152
Val Leu Gln Phe Gly Asn Ile Ser Phe Lys Lys Glu Arg Asn Thr Asp	
369 374 379 384	
caa gct tcc atg cca gaa aat aca gtt gcg cag aag ctc tgc cat ctt	1200
Gln Ala Ser Met Pro Glu Asn Thr Val Ala Gln Lys Leu Cys His Leu	
385 390 395 400	
ctt ggg atg aat gtg atg gag ttt act cgg gcc atc ctg act ccc cgg	1248
Leu Gly Met Asn Val Met Glu Phe Thr Arg Ala Ile Leu Thr Pro Arg	
401 406 411 416	
atc aag gtc ggc cga gac tat gtg caa aaa gcc cag acc aaa gaa cag	1296
Ile Lys Val Gly Arg Asp Tyr Val Gln Lys Ala Gln Thr Lys Glu Gln	
417 422 427 432	
gca gat ttt gca gta gaa gca ttg gca aaa gct acc tat gag cgg ctc	1344
Ala Asp Phe Ala Val Glu Ala Leu Ala Lys Ala Thr Tyr Glu Arg Leu	
433 438 443 448	
ttt cgc tgg ctc gtt cat cgc atc aat aaa gct ctg gat agg acc aaa	1392
Phe Arg Trp Leu Val His Arg Ile Asn Lys Ala Leu Asp Arg Thr Lys	
449 454 459 464	
cgt cag gga gca tct ttc att gga atc ctg gat att gct gga ttt gaa	1440
Arg Gln Gly Ala Ser Phe Ile Gly Ile Leu Asp Ile Ala Gly Phe Glu	
465 470 475 480	
att ttt gag ctg aac tcc ttt gaa caa ctt tgc atc aac tac acc aat	1488
Ile Phe Glu Leu Asn Ser Phe Glu Gln Leu Cys Ile Asn Tyr Thr Asn	
481 486 491 496	
gag aag ctg cag cag ctg ttc aac cac acc atg ttt atc cta gaa caa	1536
Glu Lys Leu Gln Gln Leu Phe Asn His Thr Met Phe Ile Leu Glu Gln	
497 502 507 512	
gag gaa tac cag cgc gaa ggc atc gag tgg aac ttc atc gat ttc ggg	1584
Glu Glu Tyr Gln Arg Glu Gly Ile Glu Trp Asn Phe Ile Asp Phe Gly	
513 518 523 528	

ctg gat ctg cag cca tgc atc gac cta ata gag aga cct gcg aac cct	1632
Leu Asp Leu Gln Pro Cys Ile Asp Leu Ile Glu Arg Pro Ala Asn Pro	
529 534 539 544	
cct ggt gta ctg gcc ctt ttg gat gaa gaa tgc tgg ttc cct aaa gcc	1680
Pro Gly Val Leu Ala Leu Leu Asp Glu Glu Cys Trp Phe Pro Lys Ala	
545 550 555 560	
aca gat aaa acc ttt gtt gaa aaa ctg gtt caa gag caa ggt tcc cac	1728
Thr Asp Lys Thr Phe Val Glu Lys Leu Val Gln Glu Gln Gly Ser His	
561 566 571 576	
tcc aag ttt cag aaa cct cga caa tta aaa gac aaa gct gat ttt tgc	1776
Ser Lys Phe Gln Lys Pro Arg Gln Leu Lys Asp Lys Ala Asp Phe Cys	
577 582 587 592	
att ata cat tat gca ggg aag gtg gac tat aag gca gat gag tgg ctg	1824
Ile Ile His Tyr Ala Gly Lys Val Asp Tyr Lys Ala Asp Glu Trp Leu	
593 598 603 608	
atg aag aat atg gac ccc ctg aat gac aac gtg gcc acc ctt ttg cac	1872
Met Lys Asn Met Asp Pro Leu Asn Asp Asn Val Ala Thr Leu Leu His	
609 614 619 624	
cag tca tca gac aga ttt gtg gca gag ctt tgg aaa gat gtg gac cgt	1920
Gln Ser Ser Asp Arg Phe Val Ala Glu Leu Trp Lys Asp Val Asp Arg	
625 630 635 640	
atc gtg ggt ctg gat caa gtc act ggt atg act gag aca gct ttt ggc	1968
Ile Val Gly Leu Asp Gln Val Thr Gly Met Thr Glu Thr Ala Phe Gly	
641 646 651 656	
tcc gca tat aaa acc aag aag ggc atg ttt cgt acc gtt ggg caa ctc	2016
Ser Ala Tyr Lys Thr Lys Lys Gly Met Phe Arg Thr Val Gly Gln Leu	
657 662 667 672	
tac aaa gaa tct ctc acc aag ctg atg gca act ctc cga aac acc aac	2064
Tyr Lys Glu Ser Leu Thr Lys Leu Met Ala Thr Leu Arg Asn Thr Asn	
673 678 683 688	
cct aac ttt gtt cgt tgt atc att cca aat cac gag aag agg gct gga	2112
Pro Asn Phe Val Arg Cys Ile Ile Pro Asn His Glu Lys Arg Ala Gly	
689 694 699 704	
aaa ttg gat cca cac cta gtc cta gat cag ctt cgc tgt aat ggt gtc	2160
Lys Leu Asp Pro His Leu Val Leu Asp Gln Leu Arg Cys Asn Gly Val	
705 710 715 720	
ctg gaa ggg atc cga atc tgt cgc cag ggc ttc cct aac cga ata gtt	2208
Leu Glu Gly Ile Arg Ile Cys Arg Gln Gly Phe Pro Asn Arg Ile Val	
721 726 731 736	
ttc caa gaa ttc aga cag aga tat gag atc cta act cca aat gct att	2256
Phe Gln Glu Phe Arg Gln Arg Tyr Glu Ile Leu Thr Pro Asn Ala Ile	
737 742 747 752	
cct aaa ggt ttt atg gat ggt aaa cag gcc tgt gaa cga atg atc cgg	2304

Pro Lys Gly Phe Met Asp Gly Lys Gln Ala Cys Glu Arg Met Ile Arg	
753 758 763 768	
gct tta gaa ttg gac cca aac ttg tac aga att gga cag agc aag ata	2352
Ala Leu Glu Leu Asp Pro Asn Leu Tyr Arg Ile Gly Gln Ser Lys Ile	
769 774 779 784	
ttt ttc aga gct gga gtt ctg gca cac tta gag gaa gaa aga gat tta	2400
Phe Phe Arg Ala Gly Val Leu Ala His Leu Glu Glu Glu Arg Asp Leu	
785 790 795 800	
aaa atc acc gat atc att atc ttc ttc cag gcc gtt tgc aga ggt tac	2448
Lys Ile Thr Asp Ile Ile Ile Phe Phe Gln Ala Val Cys Arg Gly Tyr	
801 806 811 816	
ctg gcc aga aag gcc ttt gcc aag aag cag cag caa cta agt gcc tta	2496
Leu Ala Arg Lys Ala Phe Ala Lys Lys Gln Gln Gln Leu Ser Ala Leu	
817 822 827 832	
aag gtc ttg cag cgg aac tgt gcc gcg tac ctg aaa tta cgg cac tgg	2544
Lys Val Leu Gln Arg Asn Cys Ala Ala Tyr Leu Lys Leu Arg His Trp	
833 838 843 848	
cag tgg tgg cga gtc ttc aca aag gtg aag ccg ctt cta caa gtg act	2592
Gln Trp Trp Arg Val Phe Thr Lys Val Lys Pro Leu Leu Gln Val Thr	
849 854 859 864	
cgc cag gag gaa gaa ctt cag gcc aaa gat gaa gag ctg ttg aag gtg	2640
Arg Gln Glu Glu Glu Leu Gln Ala Lys Asp Glu Glu Leu Leu Lys Val	
865 870 875 880	
aag gag aag cag aca aag gtg gaa gga gag ctg gag gag atg gag cgg	2688
Lys Glu Lys Gln Thr Lys Val Glu Gly Glu Leu Glu Glu Met Glu Arg	
881 886 891 896	
aag cac cag cag ctt tta gaa gag aag aat atc ctt gca gaa caa cta	2736
Lys His Gln Gln Leu Leu Glu Glu Lys Asn Ile Leu Ala Glu Gln Leu	
897 902 907 912	
caa gca gag act gag ctc ttt gct gaa gca gaa gag atg agg gca aga	2784
Gln Ala Glu Thr Glu Leu Phe Ala Glu Ala Glu Glu Met Arg Ala Arg	
913 918 923 928	
ctt gct gct aaa aag cag gaa tta gaa gag att cta cat gac ttg gag	2832
Leu Ala Ala Lys Lys Gln Glu Leu Glu Glu Ile Leu His Asp Leu Glu	
929 934 939 944	
tct agg gtt gaa gaa gaa gaa gaa aga aac caa atc ctc caa aat gaa	2880
Ser Arg Val Glu Glu Glu Glu Glu Arg Asn Gln Ile Leu Gln Asn Glu	
945 950 955 960	
aag aaa aaa atg caa gca cat att cag gac ctg gaa gaa cag cta gac	2928
Lys Lys Lys Met Gln Ala His Ile Gln Asp Leu Glu Glu Gln Leu Asp	
961 966 971 976	
gag gag gaa ggg gct cgg caa aag ctg cag ctg gaa aag gtg aca gca	2976
Glu Glu Glu Gly Ala Arg Gln Lys Leu Gln Leu Glu Lys Val Thr Ala	

977	982	987	992	
gag gcc aag atc aag aag atg gaa gag gag att ctg ctt ctc gag gac				3024
Glu Ala Lys Ile Lys Lys Met Glu Glu Glu Ile Leu Leu Leu Glu Asp				
993	998	1003	1008	
caa aat tcc aag ttc atc aaa gaa aag aaa ctc atg gaa gat cgc att				3072
Gln Asn Ser Lys Phe Ile Lys Glu Lys Lys Leu Met Glu Asp Arg Ile				
1009	1014	1019	1024	
gct gag tgt tcc tct cag ctg gct gaa gag gaa gaa aag gcg aaa aac				3120
Ala Glu Cys Ser Ser Gln Leu Ala Glu Glu Glu Glu Lys Ala Lys Asn				
1025	1030	1035	1040	
ttg gcc aaa atc agg aat aag caa gaa gtg atg atc tca gat tta gaa				3168
Leu Ala Lys Ile Arg Asn Lys Gln Glu Val Met Ile Ser Asp Leu Glu				
1041	1046	1051	1056	
gaa cgc tta aag aag gaa gaa aag act cgt cag gaa ctg gaa aag gcc				3216
Glu Arg Leu Lys Lys Glu Glu Lys Thr Arg Gln Glu Leu Glu Lys Ala				
1057	1062	1067	1072	
aaa aga aaa ctc gac ggg gag acg acc gac ctg cag gac cag atc gca				3264
Lys Arg Lys Leu Asp Gly Glu Thr Thr Asp Leu Gln Asp Gln Ile Ala				
1073	1078	1083	1088	
gag ctg cag gcg cag att gat gag ctc aag ctg cag ctg gcc aag aag				3312
Glu Leu Gln Ala Gln Ile Asp Glu Leu Lys Leu Gln Leu Ala Lys Lys				
1089	1094	1099	1104	
gag gag gag ctg cag ggc gca ctg gcc aga ggt gat gat gaa aca ctc				3360
Glu Glu Glu Leu Gln Gly Ala Leu Ala Arg Gly Asp Asp Glu Thr Leu				
1105	1110	1115	1120	
cat aag aac aat gcc ctt aaa gtt gtg cga gag cta caa gcc caa att				3408
His Lys Asn Asn Ala Leu Lys Val Val Arg Glu Leu Gln Ala Gln Ile				
1121	1126	1131	1136	
gct gaa ctt cag gaa gac ttt gaa tcc gag aag gct tca cgg aac aag				3456
Ala Glu Leu Gln Glu Asp Phe Glu Ser Glu Lys Ala Ser Arg Asn Lys				
1137	1142	1147	1152	
gcc gaa aag cag aaa agg gac ttg agt gag gaa ctg gaa gct ctg aaa				3504
Ala Glu Lys Gln Lys Arg Asp Leu Ser Glu Glu Leu Glu Ala Leu Lys				
1153	1158	1163	1168	
aca gag ctg gag gac acg ctg gac acc acg gca gcc cag cag gaa cta				3552
Thr Glu Leu Glu Asp Thr Leu Asp Thr Thr Ala Ala Gln Gln Glu Leu				
1169	1174	1179	1184	
cgt aca aaa cgt gaa caa gaa gtg gca gag ctg aag aaa gct ctt gag				3600
Arg Thr Lys Arg Glu Gln Glu Val Ala Glu Leu Lys Lys Ala Leu Glu				
1185	1190	1195	1200	
gag gaa act aag aac cat gaa gct caa atc cag gac atg aga caa aga				3648
Glu Glu Thr Lys Asn His Glu Ala Gln Ile Gln Asp Met Arg Gln Arg				
1201	1206	1211	1216	

cac gca aca gcc ctg gag gag ctc tca gag cag ctg gaa cag gcc aag	3696
His Ala Thr Ala Leu Glu Glu Leu Ser Glu Gln Leu Glu Gln Ala Lys	
1217 1222 1227 1232	
cgg ttc aaa gca aat cta gag aag aac aag cag ggc ctg gag aca gat	3744
Arg Phe Lys Ala Asn Leu Glu Lys Asn Lys Gln Gly Leu Glu Thr Asp	
1233 1238 1243 1248	
aac aag gag ctg gcg tgt gag gtg aag gtc ctg cag cag gtc aag gct	3792
Asn Lys Glu Leu Ala Cys Glu Val Lys Val Leu Gln Gln Val Lys Ala	
1249 1254 1259 1264	
gag tct gag cac aag agg aag aag ctc gac gcg cag gtc cag gag ctc	3840
Glu Ser Glu His Lys Arg Lys Lys Leu Asp Ala Gln Val Gln Glu Leu	
1265 1270 1275 1280	
cat gcc aag gtc tct gaa ggc gac agg ctc agg gtg gag ctg gcg gag	3888
His Ala Lys Val Ser Glu Gly Asp Arg Leu Arg Val Glu Leu Ala Glu	
1281 1286 1291 1296	
aaa gca agt aag ctg cag aat gag cta gat aat gtc tcc acc ctt ctg	3936
Lys Ala Ser Lys Leu Gln Asn Glu Leu Asp Asn Val Ser Thr Leu Leu	
1297 1302 1307 1312	
gaa gaa gca gag aag aag ggt att aaa ttt gct aag gat gca gct agt	3984
Glu Glu Ala Glu Lys Lys Gly Ile Lys Phe Ala Lys Asp Ala Ala Ser	
1313 1318 1323 1328	
ctt gag tct caa cta cag gat aca cag gag ctt ctt cag gag gag aca	4032
Leu Glu Ser Gln Leu Gln Asp Thr Gln Glu Leu Leu Gln Glu Glu Thr	
1329 1334 1339 1344	
cgc cag aaa cta aac ctg agc agt cgg atc cgg cag ctg gaa gag gag	4080
Arg Gln Lys Leu Asn Leu Ser Ser Arg Ile Arg Gln Leu Glu Glu Glu	
1345 1350 1355 1360	
aag aac agt ctt cag gag cag cag gag gag gag gag gag gcc agg aag	4128
Lys Asn Ser Leu Gln Glu Gln Gln Glu Glu Glu Glu Glu Ala Arg Lys	
1361 1366 1371 1376	
aac ctg gag aag caa gtg ctg gcc ctg cag tcc cag ttg gct gat acc	4176
Asn Leu Glu Lys Gln Val Leu Ala Leu Gln Ser Gln Leu Ala Asp Thr	
1377 1382 1387 1392	
aag aag aaa gta gat gac gac ctg gga aca att gaa agt ctg gaa gaa	4224
Lys Lys Lys Val Asp Asp Asp Leu Gly Thr Ile Glu Ser Leu Glu Glu	
1393 1398 1403 1408	
gcc aag aag aag ctt ctg aag gac gcg gag gcc ctg agc cag cgc ctg	4272
Ala Lys Lys Lys Leu Leu Lys Asp Ala Glu Ala Leu Ser Gln Arg Leu	
1409 1414 1419 1424	
gag gag aag gca ctg gcg tat gac aaa ctg gag aag acc aag aac cgc	4320
Glu Glu Lys Ala Leu Ala Tyr Asp Lys Leu Glu Lys Thr Lys Asn Arg	
1425 1430 1435 1440	

ctg cag cag gag ctg gac gac ctc acg gtg gac ctg gac cac cag cgc	4368
Leu Gln Gln Glu Leu Asp Asp Leu Thr Val Asp Leu Asp His Gln Arg	
1441 1446 1451 1456	
cag gtc gcc tcc aac ttg gag aag aag caa gaa gaa gtt tga ccagctg	4417
Gln Val Ala Ser Asn Leu Glu Lys Lys Gln Glu Glu Val *	
1457 1462 1467	
ttagcagaag agaagagcat ctctgctcgc tatgccgaag agcgggaccg ggccgaagcc	4477
gaggccagag agaaagaaac caaagccctg tcaactggccc gggccctcga ggaagccctg	4537
gaggccaagg aggagtttga gaggcagaac aagcagctcc gagcagacat ggaagacctc	4597
atgagctcca aagatgatgt gggaaaaaac gttcacgaac ttgaaaaatc caaacgggccc	4657
ctagagcagc aggtggagga aatgaggacc cagctggagg agctggaaga cgaactccag	4717
gccacggaag atgccaaagct tcgtctggag gtcaacatgc aggccatgaa ggcgcagttc	4777
gagagagacc tgcaaaccag ggatgagcag aatgaagaga agaagcggct gctgatcaaa	4837
caggtgcggg agctcgaggc ggagctggag gatgagagga aacagcgggc gcttgctgta	4897
gcttcaaaga aaaagatgga gatagacctg aaggacctcg aagcccaaat cgaggctgcg	4957
aacaaagctc gggatgaggt gattaagcag ctccgcaagc tccaggctca gatgaaggat	5017
taccaacgtg aattagaaga agctcgtgca tccagagatg agatttttgc tcaatccaaa	5077
gagagtgaaa agaaattgaa gagtctggaa gcagaaatcc ttcaattgca ggaggaactt	5137
gcctcatctg agcgagcccc cgcacacgcc gagcaggaga gagatgagct ggcggacgag	5197
atcaccaaca gcgcctctgg caagtccgcg ctgctggatg agaagcggcg tctggaagct	5257
cggatcgcac agctggagga ggagctggaa gaggagcaga gcaacatgga gctgctcaac	5317
gaccgcttcc gcaagaccac tctacagggtg gacacactga acgccgagct agcagccgag	5377
cgcagcggcg ccagagaagag tgacaatgca cgccagcaac tggagcggca gaacaaggag	5437
ctgaaggcca agctgcagga actcgaggggt gctgtcaagt ctaagttcaa ggccaccatc	5497
tcagccctgg aggccaaagat tgggcagctg gaggagcagc ttgagcagga agccaaggaa	5557
cgagcagccg ccaacaaatt agtccgtcgc actgagaaga agctgaaaga aatcttcatg	5617
caggttgagg atgagcgtcg acacgcggac cagtataaag agcagatgga gaaggccaac	5677
gctcggatga agcagcttaa acgccagctg gaggaagcag aagaagaagc gacgcgtgcc	5737
aacgcattct ggcgtaaact ccagcgggaa ctggatgatg ccaccgaggc caacgagggc	5797
ctgagccgcg aggtcagcac cctgaagaac cggctgaggc ggggtggccc catcagcttc	5857
tcttcagcc gatctggccg gcgccagctg caccttgaag gagcttcctt ggagctctcc	5917

gacgatgaca cagaaagtaa gaccagtgat gtcaacgaga cgcagccacc ccagtcagag	5977
taaagttgca ggaagccaga ggaggcaata cagtgggaca gtaggaatg cccccggggc	6037
ctcctgcaga tttcggaaat tggcaagcta cgggattcct tcttgaaaga tcaactgtgt	6097
cttaaggctc tccagcctat gcatactgta tcttgcttca gacttaggta caattgctcc	6157
cotTTTTata tatagacaca cacaggacac atatattaaa cagattgttt catcattgca	6217
tctattttcc atatagtcac caagagacca ttttataaaa catggtaaga ccttttttaa	6277
aacaaactcc aggccttgg ttgcgggtcg ctgggttatt ggggcagcgc cgtggctcgc	6337
actcagtcgc tctgcatgct ctctgtcata cagacaggta acctagttct gtgttcacgt	6397
ggccccgcac gactcagcca catcaagtct cctagaccac tgtggactct aaactgcact	6457
tgtctctctc atttccttca aataatgac aatgctatct cagtgcagca actgtgaaag	6517
gggctttgga aagagtagga ggggtgggct ggatcggaag caacacccat ttggggttac	6577
catgtccatc ccccaagggg ggccctgccc ctgcagtcga tgggtgtccg catctactca	6637
tgtgaactgg ccttggcgag ggctgggtctg tgcataaga ggatagtggc cacactgcag	6697
ctgaggcccc aggtggcagc catggatcat gtagacttcc agatgggtctc ccgaaccgcc	6757
tggctctgcc ggcccccctc tcacgtcagg agcaagcagc cgtggacccc taagccgagc	6817
tggtggaagg cccctccctg tgcagcccg ggccctcatg ctgaccttgc aaattcagcc	6877
gctgctttga gccc aaaatg ggaatattgg ttttgtgtcc gaggttgtt ccaagtttgt	6937
caatgagggt tatggagcct ccagaacaga tgccatctc ctgaatgttg acatgccagt	6997
gggtgtgact ccttcatttt tcttctccc tccctttgg acagtgttac agtgaacact	7057
tagcatcctg tttttggttg gtagttaagc aaactgacat tacggaaagt gccttagaca	7117
ctacagtact aagacaatgt tgaatatatc attcgctctc ataacaattt aatgtattca	7177
gttttgactg tgcttcatat catgtacctc tctagtcaaa gtggtattac agacattcag	7237
tgacaatgaa tcagtgttaa ttctaaatcc ttgatcctct gcaatgtgct tgaaaacaca	7297
aacotTTTTgg gttaaaagct ttaacatcta ttaggaagaa tttgtcctgt gggtttgga	7357
tcttggtatt tcccccttta tgaactgtac tggtgttgga ccaccagaca cctgaccgca	7417
aatatctttt cttgtattcc catatttcta gacaatgatt tttgtaagac aataaattta	7477
ttcattatag ataaaaaaaaaaaa	7501

<210> 250
 <211> 1163
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (258) .. (671)

<400> 250

```

gaggatgatg tatataacta tctattcgat gatgaagata cccacacaaa cccaaaaaaa      60

gagatctctc gaggatccga attcgcggcc gcgtcgaccg gggcttcgcg tctgtgcttc      120

ctgtggctga cgtcatctgg aggagatttg ctttcttttt ctccaaaagg ggaggaaatt      180

gaaactgagt ggcccacgat gggaagaggg gaaagcccag gggtagagga ggcctctggg      240

tgaaggcaga ggctaac  atg ggg ttc gga gcg acc ttg gcc gtt ggc ctg      290
                    Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu
                      1             5

acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc ttc acc tgc      338
Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys
 12             17             22             27

tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt ccg gtt gtc      386
Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val
 28             33             38             43

acc acc acc aca tcc acc act gtg gtg cat gcc cct tat cct cag cct      434
Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro
 44             49             54             59

cca agt gtg ccg ccc agc tac cct gga cca agc tac cag ggc tac cac      482
Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His
 60             65             70             75

acc atg ccg cct cag cca ggg atg cca gca gca ccc tac cca atg cag      530
Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln
 76             81             86             91

tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg gcc tac cac      578
Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His
 92             97             102            107

gag acc ctg gct gga gga gca gcc gcg ccc tac ccc gcc agc cag cct      626
Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro
108            113            118            123

cct tac aac ccg gcc tac atg gat gcc ccg aag gcg gcc ctg tga gca      674
Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu *
124            129            134

ttccctggcc tctctggctg ccacttggtt atgttgtgtg tgtgcgtgag tgggtgtgcag      734

```

gcgcgggttcc ttacgccccca tgtgtgctgt gtgtgtccag gcacgggttcc ttacgccccca 794
 tgtgtgctgt gtgtgtcctg cctgtatatg tggcttcctc tgatgctgac aaggtgggga 854
 acaatccttg ccagagtggg ctgggaccag actttgttct cttcctcacc tgaaattatg 914
 cttcctaaaaa tctcaagcca aactcaaaga atgggggtggt gggggggcacc ctgtgaggtg 974
 gcccctgaga ggtggggggc tctccagggc acatctggag ttcttctcca gcttacccta 1034
 ggggtgaccaa gtagggcctg tcacaccagg gtggcgcagc tttctgtgtg atgcaaattgt 1094
 gtcttggttt cggcagcgta accagctgct gcttgaggcc atggcttcgt cccggagttg 1154
 gcggtaccg 1163

<210> 251
 <211> 7269
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (73)..(3162)

<400> 251
 aagctggtac gcctgcaggt accgggtccgg aattcccggg tcgacgattt cgtaggaggg 60
 gcaaagctca ag atg gcg gac aaa acg cca ggc gga tct cag aag gcc 108
 Met Ala Asp Lys Thr Pro Gly Gly Ser Gln Lys Ala
 1 5 10
 agt tca aag acg aga tca tca gat gtt cat tca tct gga tct tca gat 156
 Ser Ser Lys Thr Arg Ser Ser Asp Val His Ser Ser Gly Ser Ser Asp
 13 18 23 28
 gca cat atg gat gca tct gga ccc tca gat agt gat atg cca agt cgg 204
 Ala His Met Asp Ala Ser Gly Pro Ser Asp Ser Asp Met Pro Ser Arg
 29 34 39 44
 aca cga cct aag agc cca aga aaa cat aat tat agg aat gaa agt gcc 252
 Thr Arg Pro Lys Ser Pro Arg Lys His Asn Tyr Arg Asn Glu Ser Ala
 45 50 55 60
 cgt gaa agc ctt tgt gat tct cct cat cag aat ctc tca aga cct ctt 300
 Arg Glu Ser Leu Cys Asp Ser Pro His Gln Asn Leu Ser Arg Pro Leu
 61 66 71 76
 ctg gaa aac aaa ctt aaa gca ttc agt att gga aaa atg agt aca gct 348
 Leu Glu Asn Lys Leu Lys Ala Phe Ser Ile Gly Lys Met Ser Thr Ala
 77 82 87 92
 aag cga act tta agt aaa aag gaa cag gaa gaa tta aag aaa aag gag 396
 Lys Arg Thr Leu Ser Lys Lys Glu Gln Glu Glu Leu Lys Lys Lys Glu

93	98	103	108	
gat gaa aag gca gct gct gag att tat gag gag ttt ctt gct gct ttt				444
Asp Glu Lys Ala Ala Ala Glu Ile Tyr Glu Glu Phe Leu Ala Ala Phe				
109	114	119	124	
gaa gga agt gat ggt aat aaa gtg aaa aca ttt gtg cga ggg ggt gtt				492
Glu Gly Ser Asp Gly Asn Lys Val Lys Thr Phe Val Arg Gly Gly Val				
125	130	135	140	
gtt aat gca gct aaa gaa gaa cat gaa aca gat gaa aaa aga ggt aaa				540
Val Asn Ala Ala Lys Glu Glu His Glu Thr Asp Glu Lys Arg Gly Lys				
141	146	151	156	
atc tat aag cca tct tca aga ttt gca gat caa aaa aat cct cca aat				588
Ile Tyr Lys Pro Ser Ser Arg Phe Ala Asp Gln Lys Asn Pro Pro Asn				
157	162	167	172	
cag tct tcc aat gaa aga cca cca tct ctt ctt gtg ata gaa acc aaa				636
Gln Ser Ser Asn Glu Arg Pro Pro Ser Leu Leu Val Ile Glu Thr Lys				
173	178	183	188	
aaa cct cca ctt aaa aaa gga gag aaa gaa aag aaa aaa agc aat ttg				684
Lys Pro Pro Leu Lys Lys Gly Glu Lys Glu Lys Lys Lys Ser Asn Leu				
189	194	199	204	
gaa ctc ttc aaa gaa gaa tta aag caa att caa gag gaa cgt gat gag				732
Glu Leu Phe Lys Glu Glu Leu Lys Gln Ile Gln Glu Glu Arg Asp Glu				
205	210	215	220	
aga cat aaa aca aaa ggc aga tta agt cga ttt gaa cct cct cag tca				780
Arg His Lys Thr Lys Gly Arg Leu Ser Arg Phe Glu Pro Pro Gln Ser				
221	226	231	236	
gat tct gat ggt cag cgt cgt tct atg gac gcg cct tca aga aga aat				828
Asp Ser Asp Gly Gln Arg Arg Ser Met Asp Ala Pro Ser Arg Arg Asn				
237	242	247	252	
aga tca tct ggt gtt ctt gat gat tac gca cct ggc tca cat gat gta				876
Arg Ser Ser Gly Val Leu Asp Asp Tyr Ala Pro Gly Ser His Asp Val				
253	258	263	268	
gga gat cca agc act act aat tta tac ctt gga aac att aat cca cag				924
Gly Asp Pro Ser Thr Thr Asn Leu Tyr Leu Gly Asn Ile Asn Pro Gln				
269	274	279	284	
atg aat gaa gaa atg ctg tgc caa gaa ttt gga aga ttt gga ccg tta				972
Met Asn Glu Glu Met Leu Cys Gln Glu Phe Gly Arg Phe Gly Pro Leu				
285	290	295	300	
gcc agt gtg aaa atc atg tgg cct aga act gat gaa gaa aga gcc aga				1020
Ala Ser Val Lys Ile Met Trp Pro Arg Thr Asp Glu Glu Arg Ala Arg				
301	306	311	316	
gag aga aat tgc ggc ttt gtg gcc ttt atg aat aga aga gat gct gaa				1068
Glu Arg Asn Cys Gly Phe Val Ala Phe Met Asn Arg Arg Asp Ala Glu				
317	322	327	332	

aga gct tta aaa aat ttg aat gga aaa atg att atg tct ttt gaa atg	1116
Arg Ala Leu Lys Asn Leu Asn Gly Lys Met Ile Met Ser Phe Glu Met	
333 338 343 348	
aag tta ggt tgg ggt aaa gct gta cct att cct cca cat cca ata tac	1164
Lys Leu Gly Trp Gly Lys Ala Val Pro Ile Pro Pro His Pro Ile Tyr	
349 354 359 364	
att ccg cct tct atg atg gaa cat acg ctt ccc cca cct cca tcc gga	1212
Ile Pro Pro Ser Met Met Glu His Thr Leu Pro Pro Pro Ser Gly	
365 370 375 380	
ctg cct ttt aat gcg cag cct aga gag cgg tta aaa aac cct aat gct	1260
Leu Pro Phe Asn Ala Gln Pro Arg Glu Arg Leu Lys Asn Pro Asn Ala	
381 386 391 396	
cct atg tta ccg cca cct aaa aac aaa gag gat ttt gag aag act ctg	1308
Pro Met Leu Pro Pro Pro Lys Asn Lys Glu Asp Phe Glu Lys Thr Leu	
397 402 407 412	
tcg caa gcc ata gtc aaa gtg gtt atc cca aca gaa agg aat ttg ctc	1356
Ser Gln Ala Ile Val Lys Val Val Ile Pro Thr Glu Arg Asn Leu Leu	
413 418 423 428	
gcc ctg ata cat cga atg ata gag ttt gtt gta cgt gaa ggg cca atg	1404
Ala Leu Ile His Arg Met Ile Glu Phe Val Val Arg Glu Gly Pro Met	
429 434 439 444	
ttt gaa gct atg att atg aac aga gaa atc aac aat cct atg ttc agg	1452
Phe Glu Ala Met Ile Met Asn Arg Glu Ile Asn Asn Pro Met Phe Arg	
445 450 455 460	
ttc tta ttt gaa aac cag aca cca gcc cat gtt tac tat agg tgg aag	1500
Phe Leu Phe Glu Asn Gln Thr Pro Ala His Val Tyr Tyr Arg Trp Lys	
461 466 471 476	
ctt tat tct att ctg cag gga gat tct cca act aaa tgg cgg acg gaa	1548
Leu Tyr Ser Ile Leu Gln Gly Asp Ser Pro Thr Lys Trp Arg Thr Glu	
477 482 487 492	
gat ttt cgt atg ttc aaa aat gga tct ttt tgg agg cca cca cca tta	1596
Asp Phe Arg Met Phe Lys Asn Gly Ser Phe Trp Arg Pro Pro Pro Leu	
493 498 503 508	
aat ccg tac ttg cat gga atg tca gaa gag caa gaa aca gaa gct ttt	1644
Asn Pro Tyr Leu His Gly Met Ser Glu Glu Gln Glu Thr Glu Ala Phe	
509 514 519 524	
gta gag gaa cct agt aaa aag gga gca ctt aag gaa gaa cag agg gat	1692
Val Glu Glu Pro Ser Lys Lys Gly Ala Leu Lys Glu Glu Gln Arg Asp	
525 530 535 540	
aaa ttg gaa gaa atc ttg cgg gga tta act cca agg aaa aat gat att	1740
Lys Leu Glu Glu Ile Leu Arg Gly Leu Thr Pro Arg Lys Asn Asp Ile	
541 546 551 556	

gga gat gca atg gtt ttc tgt ctt aat aat gct gaa gct gct gaa gaa	1788
Gly Asp Ala Met Val Phe Cys Leu Asn Asn Ala Glu Ala Ala Glu Glu	
557 562 567 572	
ata gtg gat tgc att act gag tgc ttg tcc atc tta aag aca ccc ctt	1836
Ile Val Asp Cys Ile Thr Glu Ser Leu Ser Ile Leu Lys Thr Pro Leu	
573 578 583 588	
cct aaa aag att gcc aga tta tat ttg gtt tct gat gtt ttg tac aac	1884
Pro Lys Lys Ile Ala Arg Leu Tyr Leu Val Ser Asp Val Leu Tyr Asn	
589 594 599 604	
tct tca gcc aaa gtt gct aat gct tca tat tat aga aaa ttt ttt gaa	1932
Ser Ser Ala Lys Val Ala Asn Ala Ser Tyr Tyr Arg Lys Phe Phe Glu	
605 610 615 620	
aca aag tta tgt cag ata ttt tca gac ctc aat gcc acc tat cgt aca	1980
Thr Lys Leu Cys Gln Ile Phe Ser Asp Leu Asn Ala Thr Tyr Arg Thr	
621 626 631 636	
att caa ggc cat tta caa tct gaa aac ttt aag caa cgg gta atg act	2028
Ile Gln Gly His Leu Gln Ser Glu Asn Phe Lys Gln Arg Val Met Thr	
637 642 647 652	
tgc ttc aga gca tgg gaa gat tgg gca att tat cca gaa cca ttt ttg	2076
Cys Phe Arg Ala Trp Glu Asp Trp Ala Ile Tyr Pro Glu Pro Phe Leu	
653 658 663 668	
atc aaa cta caa aat att ttc tta gga ctt gta aat att att gaa gaa	2124
Ile Lys Leu Gln Asn Ile Phe Leu Gly Leu Val Asn Ile Ile Glu Glu	
669 674 679 684	
aag gaa aca gag gat gtt cca gat gac ctt gat ggt gcc ccc atc gag	2172
Lys Glu Thr Glu Asp Val Pro Asp Asp Leu Asp Gly Ala Pro Ile Glu	
685 690 695 700	
gaa gag ctt gat ggt gca cct ctg gaa gat gta gat gga att cct att	2220
Glu Glu Leu Asp Gly Ala Pro Leu Glu Asp Val Asp Gly Ile Pro Ile	
701 706 711 716	
gat gct act ccc atc gat gat ctt gat gga gtc cct ata aaa agt ctt	2268
Asp Ala Thr Pro Ile Asp Asp Leu Asp Gly Val Pro Ile Lys Ser Leu	
717 722 727 732	
gat gat gat ctt gat gga gtg cct ttg gat gca act gaa gac tca aaa	2316
Asp Asp Asp Leu Asp Gly Val Pro Leu Asp Ala Thr Glu Asp Ser Lys	
733 738 743 748	
aag aat gag cct ata ttt aaa gtt gcc cca tca aaa tgg gaa gct gtg	2364
Lys Asn Glu Pro Ile Phe Lys Val Ala Pro Ser Lys Trp Glu Ala Val	
749 754 759 764	
gat gaa tct gaa ttg gaa gca cag gct gtt aca act tct aaa tgg gaa	2412
Asp Glu Ser Glu Leu Glu Ala Gln Ala Val Thr Thr Ser Lys Trp Glu	
765 770 775 780	
tta ttt gac cag cat gaa gaa tca gaa gaa gaa gaa aat caa aat caa	2460

Leu Phe Asp Gln His Glu Glu Ser Glu Glu Glu Glu Asn Gln Asn Gln	
781 786 791 796	
gaa gaa gaa agt gaa gat gaa gaa gat act caa agt tcc aaa tct gaa	2508
Glu Glu Glu Ser Glu Asp Glu Glu Asp Thr Gln Ser Ser Lys Ser Glu	
797 802 807 812	
gaa cat cat ttg tac tct aat cca atc aaa gaa gaa atg act gag tct	2556
Glu His His Leu Tyr Ser Asn Pro Ile Lys Glu Glu Met Thr Glu Ser	
813 818 823 828	
aag ttc tct aag tac tct gaa atg agt gag gaa aaa cga gcc aaa ctt	2604
Lys Phe Ser Lys Tyr Ser Glu Met Ser Glu Glu Lys Arg Ala Lys Leu	
829 834 839 844	
cgt gaa att gag ctc aaa gtt atg aag ttt cag gat gaa ttg gaa tct	2652
Arg Glu Ile Glu Leu Lys Val Met Lys Phe Gln Asp Glu Leu Glu Ser	
845 850 855 860	
ggg aaa aga cct aaa aaa cca ggc cag agt ttt cag gag caa gta gaa	2700
Gly Lys Arg Pro Lys Lys Pro Gly Gln Ser Phe Gln Glu Gln Val Glu	
861 866 871 876	
cac tac aga gat aaa ctt ctt caa cga gag aaa gag aaa gag tta gaa	2748
His Tyr Arg Asp Lys Leu Leu Gln Arg Glu Lys Glu Lys Glu Leu Glu	
877 882 887 892	
aga gaa cga gaa aga gac aag aaa gat aaa gaa aaa ttg gaa tct cgc	2796
Arg Glu Arg Glu Arg Asp Lys Lys Asp Lys Glu Lys Leu Glu Ser Arg	
893 898 903 908	
tcc aaa gac aag aag gaa aaa gat gag tgt act ccg aca agg aag gaa	2844
Ser Lys Asp Lys Lys Glu Lys Asp Glu Cys Thr Pro Thr Arg Lys Glu	
909 914 919 924	
agg aag agg cga cac agt aca tcc ccc agc cca tct cgc agt agc agt	2892
Arg Lys Arg Arg His Ser Thr Ser Pro Ser Pro Ser Arg Ser Ser Ser	
925 930 935 940	
ggt aga cga gtg aaa tcc cca tca cca aaa tcg gag cga tca gag cgt	2940
Gly Arg Arg Val Lys Ser Pro Ser Pro Lys Ser Glu Arg Ser Glu Arg	
941 946 951 956	
tca gaa aga tct cat aaa gag agc tca cgg tcc agg tca tct cac aaa	2988
Ser Glu Arg Ser His Lys Glu Ser Ser Arg Ser Arg Ser Ser His Lys	
957 962 967 972	
gat tct cct aga gat gtt agc aaa aaa gcc aaa aga tca cca tct ggt	3036
Asp Ser Pro Arg Asp Val Ser Lys Lys Ala Lys Arg Ser Pro Ser Gly	
973 978 983 988	
tca agg aca cct aaa agg tct agg cga tca cgg tct aga tct cct aaa	3084
Ser Arg Thr Pro Lys Arg Ser Arg Arg Ser Arg Ser Arg Ser Pro Lys	
989 994 999 1004	
aaa tca gga aag aag tcc aga tcc cag tcc aga tct cca cac agg tct	3132
Lys Ser Gly Lys Lys Ser Arg Ser Gln Ser Arg Ser Pro His Arg Ser	

1005	1010	1015	1020	
cat aaa aag tca aag aaa aac aaa cac tga c gtaaattttt aagatgctgt				3183
His Lys Lys Ser Lys Lys Asn Lys His *				
1021	1026			
cacttattgg aaatgcgatt tgttttgtgc ctgaacggtc tgttttttaa aaaaacaaaa				3243
aatcaaataa aagagcattc ctgggggtttt ttgtttgttt gtgtatgcat gtgtaaactc				3303
atgagcaact gcatctgtag atctgtcatt gttttatatt gtgtaaatta ctttcattgt				3363
ggctattttct caagatgaaa tttttattgt tctaattgat ttcattcagaa atgtgtataa				3423
tggatctgct gacagtagta gtattttgtt ttaggatgtt gtgacttagc aaaaataata				3483
cagatgtctt cccccctttt gtagctttga caatttgaat tagatttcaa ataaaatctg				3543
aacagaaaaac tataatgttg tttttttgcc ccaccgggtga tattaagtcc cttaaagtcc				3603
tactgagttt cacactactg ttgtgcttct tatacctgat gcactttata agccccagtg				3663
ttcaagtagc ttaagtttta tatttactaa gatgactatc caaattaagg gacctgagac				3723
tcctatttgg tggtttgcta accatttgc tttgataagt ttctcttggg taataactaat				3783
accagatat caaagactag gtagatatgg catggcggtt tgttagtgga atgcctggct				3843
aaaacatttt tttcacagaa gcaatatgat ttccatacat ccaaccatg ttctgagcaa				3903
ctacttactt ttagggggaa attaaatata ttttcatttc ctcttctatt atgaaagaag				3963
tttatttgta aaacaaattt tctaacaagg tttggccata gaattctctt gtatgattgt				4023
tgacctttta taatcttctg taggctatct ttcaaact ggcattcagaa tattttttat				4083
aagtttgtgt ttaaacagct tagttgggtcc cccccccac tccaagaga cttgggttta				4143
gttatagctt taagtataat ttaaaaataa aatgtttttc aggaaacttc gtatctaata				4203
gtttgtaaat tcaagtgca aaaagttgat ttaaaccatt tgcagagttg aactctatta				4263
tgaaaataaa tttgctacgg tatgaggaag aaataaaact tgtgtaattgt tggtcataat				4323
actgctataa atataataaa gggttatgta gaattgaact gacactatta tttgtgaatc				4383
ttgatttcag ttttttatgt aggcacttca tacactgggt tgatgggttt tttttttcct				4443
ccctaaaaga gaaagtagaa aactattcta acaatggatt attttgattt agcttgcttt				4503
ttaaaaaaat cttttcaact tgttttactt aatcttgctt agtcacaaaa taagatgtgc				4563
acctatgggt tggagagttc ctatattagc tgagcagtgata gatacactat ttccaaacgg				4623
tgcacacctt cagtagcttt ggaaatgagc caatcactgt tttacttaat ggttcttatt				4683
agcatgcaaa tattgcttga aagttatttc cttattcact gttttgttag tccattttgt				4743

taggaaacat taattcctaa aaatttggtc agaataatta aaagtgaaca tttggtgctg	4803
atactcaaaa acctacaaat gtagccattt aaaaagtaac atgtttttct cccctgctca	4863
ttgcctggga gaatggaatt ttatataact acctttcttt gcaaaaataa cggctgctgc	4923
gagttggtgg tgattttggc attccatctt gcaactggtt ctagtatagg cttataaata	4983
attggtcagg taataatctt tccagtcaag ttgcaaggga tgcttatttc tcttcaaaaa	5043
aagacatcct gcgggattga gtagaaaatt ttaggtcagt tttgggtgct tatttgtaat	5103
atTTTTccta ctacattgga gtttagcagt tctTTTTttc tggatccaga tacaagtgtc	5163
atggtttato ttacagtggg tgaaactgac tttcttttgg ttgggtgggt gaggatttct	5223
taggcctgat agaatatata ttctgtgaag tttgttaatg tacatattag attgtattgg	5283
atTTTTTTTT cttgaattgc aaatggtatt attagatagg ttatttccag ttttacttca	5343
tgacaaatta cctagagtaa acctacttaa tactccaatg gattctatga aagtttaatg	5403
ggatcagaaa ttggtgactt ataaggggga agatattcta ccatattttt ataatagctt	5463
attattcatg tttcttgtct gaaggacact caagttacag agcaaaattt ctatagggtg	5523
actagaatgt tcataagcat ggtcttccag ttgcaggaaa gatcatgttc tatctgtgga	5583
cacttactgt cctctaccac agctacgtgc cagagttggt ttccacagtt cttataaagg	5643
gcatgactta ggctctttac cctccaactt aatgtttata cacagggtt gtttactagg	5703
ttaatgacat ttaactcccc tctcttctgt aggtgagaga aaataagtaa gtcttgatct	5763
gtttcttacc aaagagagac agacctatga tggaaaatga tcacgtctct gaattttttc	5823
tttaacgtta tagttcctta ttacagatag taagcatatg ggaatttctg agctataaca	5883
tgttgagaag ttagaaatta aaactaacac aacaaaaggc gctgaatcaa aagatctttg	5943
cttttatttg gtcagaatg tttttggctt ttctgctaaa gatggcagaa attactctac	6003
acagacctga tttttcttta ttgcagacca ttcttggtgg cttaccctga gacttttato	6063
ccaattagtg aatcttggag ggaatacttg cttatttatg acttaggtat ttcccccaa	6123
actttaatat tcttgagcac ttgaaaatac ttttgagaaa ttttaactgt gattaaattt	6183
aggtttatta gaaatattct gtacacattt gctccatgg tggcgtaagt tctgaaaaat	6243
tatatgaccg tgacaatagt ttatcatcat cattattggt attcaaaata agggtaaata	6303
aatctctgta ttgccaaagt gacttaaaact gttctgatga ccacacagtg tgatttcttt	6363
agcagagaaa gttggtttta aaaataaata gtaccacttt tctaagactg tacagtttac	6423

aaataagggtt tttttctttg ttgttttctt cttctattaa gttttagtga aaagcctaata 6483
 tacagaaaat tgtgcagata ctagtgaaga tactagtata agtttaaagg aacatgtgac 6543
 tgtaaaatct cacatttaca aagtgccttg tctcttcata tttcacacgc atgttttaga 6603
 atagatttta gggagtggtt aattcattat ccttttgact taaaattttt gttaccaact 6663
 tcctaggact tagataatat ataaataagt acaaatccca ggggaagtgt tgtgatgcta 6723
 gactaaaagg tgggaatgtg ctgctgttcc gtgagccttg ttccattgtt gaaaatttga 6783
 tgccctcagt tttattcagt accacctcat ggagcttcaa tgtaaagtga ttatatgtat 6843
 aattggtaat ttgtatagtt ttgtagattg tagattaaat gcactcatca tgtcacatgt 6903
 aattgtgctt ggagtatttg tgttttattc ttttacttca acgggttctt gtctgttaca 6963
 tctctggtga tttgaaatat caggaaagac agtttgtcag aaatgagaat aatatagttg 7023
 aaatcagttg ggctaaaata ttctacagca agacaatttc ttttgggtga actgattcta 7083
 taatttactt acttttaatg taaggattag atttattggt gagctgcttt ccagatcaga 7143
 ctgtcacttt atagtttttc tatataaaga ttatatagtt gcaaacaaag gttgtgaaat 7203
 ttcccttttg ttgtttttga cttttaatta ataaaagtac attgttttca tagcaaaaaa 7263
 aaaaaa 7269

<210> 252
 <211> 7092
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (73)..(2985)

<400> 252
 aagctggttac gcctgcaggt accggtccgg aattcccggg togacgattt cgtaggaggg 60
 gcaaagctca ag atg gcg gac aaa acg cca ggc gga tct cag aag gcc 108
 Met Ala Asp Lys Thr Pro Gly Gly Ser Gln Lys Ala
 1 5 10
 agt tca aag acg aga tca tca gat gtt cat tca tct gga tct tca gat 156
 Ser Ser Lys Thr Arg Ser Ser Asp Val His Ser Ser Gly Ser Ser Asp
 13 18 23 28
 gca cat atg gat gca tct gga ccc tca gat agt gat atg cca agt cgg 204
 Ala His Met Asp Ala Ser Gly Pro Ser Asp Ser Asp Met Pro Ser Arg
 29 34 39 44

aca cga cct aag agc cca aga aaa cat aat tat agg aat gaa agt gcc	252
Thr Arg Pro Lys Ser Pro Arg Lys His Asn Tyr Arg Asn Glu Ser Ala	
45 50 55 60	
cgt gaa agc ctt tgt gat tct cct cat cag aat ctc tca aga cct ctt	300
Arg Glu Ser Leu Cys Asp Ser Pro His Gln Asn Leu Ser Arg Pro Leu	
61 66 71 76	
ctg gaa aac aaa ctt aaa gca ttc agt att gga aaa atg agt aca gct	348
Leu Glu Asn Lys Leu Lys Ala Phe Ser Ile Gly Lys Met Ser Thr Ala	
77 82 87 92	
aag cga act tta agt aaa aag gaa cag gaa gaa tta aag aaa aag gag	396
Lys Arg Thr Leu Ser Lys Lys Glu Gln Glu Glu Leu Lys Lys Lys Glu	
93 98 103 108	
gat gaa aag gca gct gct gag att tat gag gag ttt ctt gct gct ttt	444
Asp Glu Lys Ala Ala Ala Glu Ile Tyr Glu Glu Phe Leu Ala Ala Phe	
109 114 119 124	
gaa gga agt gat ggt aat aaa gtg aaa aca ttt gtg cga ggg ggt gtt	492
Glu Gly Ser Asp Gly Asn Lys Val Lys Thr Phe Val Arg Gly Gly Val	
125 130 135 140	
gtt aat gca gct aaa gaa gaa cat gaa aca gat gaa aaa aga ggt aaa	540
Val Asn Ala Ala Lys Glu Glu His Glu Thr Asp Glu Lys Arg Gly Lys	
141 146 151 156	
atc tat aag cca tct tca aga ttt gca gat caa aaa aat cct cca aat	588
Ile Tyr Lys Pro Ser Ser Arg Phe Ala Asp Gln Lys Asn Pro Pro Asn	
157 162 167 172	
cag tct tcc aat gaa aga cca cca tct ctt ctt gtg ata gaa acc aaa	636
Gln Ser Ser Asn Glu Arg Pro Pro Ser Leu Leu Val Ile Glu Thr Lys	
173 178 183 188	
aaa cct cca ctt aaa aaa gga gag aaa gaa aag aaa aaa agc aat ttg	684
Lys Pro Pro Leu Lys Lys Gly Glu Lys Glu Lys Lys Lys Ser Asn Leu	
189 194 199 204	
gaa ctc ttc aaa gaa gaa tta aag caa att caa gag gaa cgt gat gag	732
Glu Leu Phe Lys Glu Glu Leu Lys Gln Ile Gln Glu Glu Arg Asp Glu	
205 210 215 220	
aga cat aaa aca aaa ggc aga tta agt cga ttt gaa cct cct cag tca	780
Arg His Lys Thr Lys Gly Arg Leu Ser Arg Phe Glu Pro Pro Gln Ser	
221 226 231 236	
gat tct gat ggt cag cgt cgt tct atg gac gcg cct tca aga aga aat	828
Asp Ser Asp Gly Gln Arg Arg Ser Met Asp Ala Pro Ser Arg Arg Asn	
237 242 247 252	
aga tca tct ggt gtt ctt gat gat tac gca cct ggc tca cat gat gta	876
Arg Ser Ser Gly Val Leu Asp Asp Tyr Ala Pro Gly Ser His Asp Val	
253 258 263 268	
gga gat cca agc act act aat tta tac ctt gga aac att aat cca cag	924

Gly Asp Pro Ser Thr Thr Asn Leu Tyr Leu Gly Asn Ile Asn Pro Gln	
269 274 279 284	
atg aat gaa gaa atg ctg tgc caa gaa ttt gga aga ttt gga ccg tta	972
Met Asn Glu Glu Met Leu Cys Gln Glu Phe Gly Arg Phe Gly Pro Leu	
285 290 295 300	
gcc agt gtg aaa atc atg tgg cct aga act gat gaa gaa aga gcc aga	1020
Ala Ser Val Lys Ile Met Trp Pro Arg Thr Asp Glu Glu Arg Ala Arg	
301 306 311 316	
gag aga aat tgc ggc ttt gtg gcc ttt atg aat aga aga gat gct gaa	1068
Glu Arg Asn Cys Gly Phe Val Ala Phe Met Asn Arg Arg Asp Ala Glu	
317 322 327 332	
aga gct tta aaa aat ttg aat gga aaa atg att atg tct ttt gaa atg	1116
Arg Ala Leu Lys Asn Leu Asn Gly Lys Met Ile Met Ser Phe Glu Met	
333 338 343 348	
aag tta ggt tgg ggt aaa gct gta cct att cct cca cat cca ata tac	1164
Lys Leu Gly Trp Gly Lys Ala Val Pro Ile Pro Pro His Pro Ile Tyr	
349 354 359 364	
att ccg cct tct atg atg gaa cat acg ctt ccc cca cct cca tcc gga	1212
Ile Pro Pro Ser Met Met Glu His Thr Leu Pro Pro Pro Pro Ser Gly	
365 370 375 380	
ctg cct ttt aat gcg cag cct aga gag cgg tta aaa aac cct aat gct	1260
Leu Pro Phe Asn Ala Gln Pro Arg Glu Arg Leu Lys Asn Pro Asn Ala	
381 386 391 396	
cct atg tta ccg cca cct aaa aac aaa gag gat ttt gag aag act ctg	1308
Pro Met Leu Pro Pro Pro Lys Asn Lys Glu Asp Phe Glu Lys Thr Leu	
397 402 407 412	
tcg caa gcc ata gtc aaa gtg gtt atc cca aca gaa agg aat ttg ctc	1356
Ser Gln Ala Ile Val Lys Val Val Ile Pro Thr Glu Arg Asn Leu Leu	
413 418 423 428	
gcc ctg ata cat cga atg ata gag ttt gtt gta cgt gaa ggg cca atg	1404
Ala Leu Ile His Arg Met Ile Glu Phe Val Val Arg Glu Gly Pro Met	
429 434 439 444	
ttt gaa gct atg att atg aac aga gaa atc aac aat cct atg ttc agg	1452
Phe Glu Ala Met Ile Met Asn Arg Glu Ile Asn Asn Pro Met Phe Arg	
445 450 455 460	
ttc tta ttt gaa aac cag aca cca gcc cat gtt tac tat agg tgg aag	1500
Phe Leu Phe Glu Asn Gln Thr Pro Ala His Val Tyr Tyr Arg Trp Lys	
461 466 471 476	
ctt tat tct att ctg cag gga gat tct cca act aaa tgg cgg acg gaa	1548
Leu Tyr Ser Ile Leu Gln Gly Asp Ser Pro Thr Lys Trp Arg Thr Glu	
477 482 487 492	
gat ttt cgt atg ttc aaa aat gga tct ttt tgg agg cca cca cca tta	1596
Asp Phe Arg Met Phe Lys Asn Gly Ser Phe Trp Arg Pro Pro Pro Leu	

493	498	503	508	
aat ccg tac ttg cat gga atg tca gaa gag caa gaa aca gaa gct ttt				1644
Asn Pro Tyr Leu His Gly Met Ser Glu Glu Gln Glu Thr Glu Ala Phe				
509	514	519	524	
gta gag gaa cct agt aaa aag gga gca ctt aag gaa gaa cag agg gat				1692
Val Glu Glu Pro Ser Lys Lys Gly Ala Leu Lys Glu Glu Gln Arg Asp				
525	530	535	540	
aaa ttg gaa gaa atc ttg cgg gga tta act cca agg aaa aat gat att				1740
Lys Leu Glu Glu Ile Leu Arg Gly Leu Thr Pro Arg Lys Asn Asp Ile				
541	546	551	556	
gga gat gca atg gtt ttc tgt ctt aat aat gct gaa gct gct gaa gaa				1788
Gly Asp Ala Met Val Phe Cys Leu Asn Asn Ala Glu Ala Ala Glu Glu				
557	562	567	572	
ata gtg gat tgc att act gag tgc ttg tcc atc tta aag aca ccc ctt				1836
Ile Val Asp Cys Ile Thr Glu Ser Leu Ser Ile Leu Lys Thr Pro Leu				
573	578	583	588	
cct aaa aag att gcc aga tta tat ttg gtt tct gat gtt ttg tac aac				1884
Pro Lys Lys Ile Ala Arg Leu Tyr Leu Val Ser Asp Val Leu Tyr Asn				
589	594	599	604	
tct tca gcc aaa gtt gct aat gct tca tat tat aga aaa ttt ttt gaa				1932
Ser Ser Ala Lys Val Ala Asn Ala Ser Tyr Tyr Arg Lys Phe Phe Glu				
605	610	615	620	
aca aag tta tgt cag ata ttt tca gac ctc aat gcc acc tat cgt aca				1980
Thr Lys Leu Cys Gln Ile Phe Ser Asp Leu Asn Ala Thr Tyr Arg Thr				
621	626	631	636	
att caa ggc cat tta caa tct gaa aac ttt aag caa cgg gta atg act				2028
Ile Gln Gly His Leu Gln Ser Glu Asn Phe Lys Gln Arg Val Met Thr				
637	642	647	652	
tgc ttc aga gca tgg gaa gat tgg gca att tat cca gaa cca ttt ttg				2076
Cys Phe Arg Ala Trp Glu Asp Trp Ala Ile Tyr Pro Glu Pro Phe Leu				
653	658	663	668	
atc aaa cta caa aat att ttc tta gga ctt gta aat att att gaa gaa				2124
Ile Lys Leu Gln Asn Ile Phe Leu Gly Leu Val Asn Ile Ile Glu Glu				
669	674	679	684	
aag gaa aca gag gat gtt cca gat gac ctt gat ggt gcc ccc atc gag				2172
Lys Glu Thr Glu Asp Val Pro Asp Asp Leu Asp Gly Ala Pro Ile Glu				
685	690	695	700	
gaa gag ctt gat ggt gca cct ctg gaa gat gta gat gga att cct att				2220
Glu Glu Leu Asp Gly Ala Pro Leu Glu Asp Val Asp Gly Ile Pro Ile				
701	706	711	716	
gat gct act ccc atc gat gat ctt gat gga gtc cct ata aaa agt ctt				2268
Asp Ala Thr Pro Ile Asp Asp Leu Asp Gly Val Pro Ile Lys Ser Leu				
717	722	727	732	

gat gat gat ctt gat gga gtg cct ttg gat gca act gaa gac tca aaa	2316
Asp Asp Asp Leu Asp Gly Val Pro Leu Asp Ala Thr Glu Asp Ser Lys	
733 738 743 748	
aag aat gag cct ata ttt aaa gtt gcc cca tca aaa tgg gaa gct gtg	2364
Lys Asn Glu Pro Ile Phe Lys Val Ala Pro Ser Lys Trp Glu Ala Val	
749 754 759 764	
gat gaa tct gaa ttg gaa gca cag gct gtt aca act tct aaa tgg gaa	2412
Asp Glu Ser Glu Leu Glu Ala Gln Ala Val Thr Thr Ser Lys Trp Glu	
765 770 775 780	
tta ttt gac cag cat gaa gaa tca gaa gaa gaa gaa aat caa aat caa	2460
Leu Phe Asp Gln His Glu Glu Ser Glu Glu Glu Glu Asn Gln Asn Gln	
781 786 791 796	
gaa gaa gaa agt gaa gat gaa gaa gat act caa agt tcc aaa tct gaa	2508
Glu Glu Glu Ser Glu Asp Glu Glu Asp Thr Gln Ser Ser Lys Ser Glu	
797 802 807 812	
gaa cat cat ttg tac tct aat cca atc aaa gaa gaa atg act gag tct	2556
Glu His His Leu Tyr Ser Asn Pro Ile Lys Glu Glu Met Thr Glu Ser	
813 818 823 828	
aag ttc tct aag tac tct gaa atg agt gag gaa aaa cga gcc aaa ctt	2604
Lys Phe Ser Lys Tyr Ser Glu Met Ser Glu Glu Lys Arg Ala Lys Leu	
829 834 839 844	
cgt gaa att gag ctc aaa gtt atg aag ttt cag gat gaa ttg gaa tct	2652
Arg Glu Ile Glu Leu Lys Val Met Lys Phe Gln Asp Glu Leu Glu Ser	
845 850 855 860	
ggg aaa aga cct aaa aaa cca ggc cag agt ttt cag gag caa gta gaa	2700
Gly Lys Arg Pro Lys Lys Pro Gly Gln Ser Phe Gln Glu Gln Val Glu	
861 866 871 876	
cac tac aga gat aaa ctt ctt caa cga gag aaa gag aaa gag tta gaa	2748
His Tyr Arg Asp Lys Leu Leu Gln Arg Glu Lys Glu Lys Glu Leu Glu	
877 882 887 892	
aga gaa cga gaa aga gac aag aaa gat aaa gaa aaa ttg gaa tct cgc	2796
Arg Glu Arg Glu Arg Asp Lys Lys Asp Lys Glu Lys Leu Glu Ser Arg	
893 898 903 908	
tcc aaa gac aag aag gaa aaa gat gag tgt act ccg aca agg aag gaa	2844
Ser Lys Asp Lys Lys Glu Lys Asp Glu Cys Thr Pro Thr Arg Lys Glu	
909 914 919 924	
aga tca cca tct ggt tca agg aca cct aaa agg tct agg cga tca cgg	2892
Arg Ser Pro Ser Gly Ser Arg Thr Pro Lys Arg Ser Arg Arg Ser Arg	
925 930 935 940	
tct aga tct cct aaa aaa tca gga aag aag tcc aga tcc cag tcc aga	2940
Ser Arg Ser Pro Lys Lys Ser Gly Lys Lys Ser Arg Ser Gln Ser Arg	
941 946 951 956	

tttagtgaaa agcctaatta cagaaaattg tgcagatact agtgaagata ctagtataag 6348
 tttaaaggaa catgtgactg taaaatctca catttacaaa gtgcttgatc tcttcatatt 6408
 tcacacgcat gttttagaat agatttttagg gagtgtttaa ttcattatcc ttttgactta 6468
 aaatttttgt taccaacttc ctaggactta gataatatat aaataagtac aaatcccagg 6528
 ggaagtgttg tgatgctaga ctaaaagggtg ggaatgtgct gctgttccgt gagccttggt 6588
 ccattgttga aaatttgatg cctcagtgtt tattcagtac cacctcatgg agcttcaatg 6648
 taaatggatt atatgtataa ttggtaattt gtatagtttt gtagattgta gattaaatgc 6708
 actcatcatg tcacatgtaa ttgtgcttgg agtatttgtg ttttattctt ttacttcaac 6768
 gggttcttgt ctgttacatc tctgggtgatt tgaaatatca ggaaagacag tttgtcagaa 6828
 atgagaataa tatagttgaa atcagttggg ctaaaatatt ctacagcaag acaatttctt 6888
 ttgggtgaac tgattctata atttacttac ttttaatgta aggattagat ttattgttga 6948
 gctgctttcc agatcagact gtcactttat agtttttcta tataaagatt atatagttgc 7008
 aaacaaagggt tgtgaaattt cctttttgtt gtttttgact ttttaattaat aaaagtacat 7068
 tgttttcata gcaaaaaaaaa aaaa 7092

<210> 253
 <211> 5574
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (123)..(4529)

<400> 253
 gctgtcggta ccgggtccgga attcccgggt cgacgatttc gtattggctt tcaggctggc 60
 gcctgtctcg gccccgcgc cagttttggg ctggttggcg cggaatcggg agattcggga 120
 cc atg gca cct gtg cac ggc gac gac tgt gag ata ggg gcg agt gct 167
 Met Ala Pro Val His Gly Asp Asp Cys Glu Ile Gly Ala Ser Ala
 1 5 10
 ctg tca gat tca ggg agt ttt gta tct tct cga gcc cgg cga gaa aaa 215
 Leu Ser Asp Ser Gly Ser Phe Val Ser Ser Arg Ala Arg Arg Glu Lys
 16 21 26 31
 aaa tca aag aag ggg cgc caa gaa gcc cta gaa aga ctg aaa aag gct 263
 Lys Ser Lys Lys Gly Arg Gln Glu Ala Leu Glu Arg Leu Lys Lys Ala
 32 37 42 47

aaa	gct	ggg	gag	agg	tat	aaa	tat	gaa	gtc	gag	gac	ttc	aca	ggg	gtt	311
Lys	Ala	Gly	Glu	Arg	Tyr	Lys	Tyr	Glu	Val	Glu	Asp	Phe	Thr	Gly	Val	
48					53					58					63	
tat	gaa	gaa	gtt	gat	gaa	gaa	cag	tat	tcg	aag	ctg	gtt	cag	gca	cgc	359
Tyr	Glu	Glu	Val	Asp	Glu	Glu	Gln	Tyr	Ser	Lys	Leu	Val	Gln	Ala	Arg	
64					69					74					79	
cag	gat	gat	gac	tgg	att	gtg	gat	gat	gat	ggg	att	ggc	tat	gtg	gaa	407
Gln	Asp	Asp	Asp	Trp	Ile	Val	Asp	Asp	Asp	Gly	Ile	Gly	Tyr	Val	Glu	
80					85					90					95	
gat	ggc	cga	gag	att	ttt	gat	gat	gac	ctt	gaa	gat	gat	gcc	ctt	gat	455
Asp	Gly	Arg	Glu	Ile	Phe	Asp	Asp	Asp	Leu	Glu	Asp	Asp	Ala	Leu	Asp	
96					101					106					111	
gct	gat	gag	aaa	gga	aaa	gat	ggg	aaa	gca	cgc	aat	aaa	gac	aag	agg	503
Ala	Asp	Glu	Lys	Gly	Lys	Asp	Gly	Lys	Ala	Arg	Asn	Lys	Asp	Lys	Arg	
112					117					122					127	
aat	gta	aag	aag	ctc	gca	gtg	aca	aaa	ccg	aac	aac	att	aag	tca	atg	551
Asn	Val	Lys	Lys	Leu	Ala	Val	Thr	Lys	Pro	Asn	Asn	Ile	Lys	Ser	Met	
128					133					138					143	
ttc	att	gct	tgt	gct	gga	aag	aaa	act	gca	gat	aaa	gct	gta	gac	ttg	599
Phe	Ile	Ala	Cys	Ala	Gly	Lys	Lys	Thr	Ala	Asp	Lys	Ala	Val	Asp	Leu	
144					149					154					159	
tcc	aag	gat	ggg	ctg	cta	ggg	gac	att	cta	cag	gat	ctt	aac	act	gag	647
Ser	Lys	Asp	Gly	Leu	Leu	Gly	Asp	Ile	Leu	Gln	Asp	Leu	Asn	Thr	Glu	
160					165					170					175	
aca	cct	caa	ata	act	cca	cca	cct	gta	atg	ata	ctg	aag	aag	aaa	aga	695
Thr	Pro	Gln	Ile	Thr	Pro	Pro	Pro	Val	Met	Ile	Leu	Lys	Lys	Lys	Arg	
176					181					186					191	
tcc	att	gga	gct	tca	ccg	aat	cct	ttc	tct	gtg	cac	acc	gcc	acg	gca	743
Ser	Ile	Gly	Ala	Ser	Pro	Asn	Pro	Phe	Ser	Val	His	Thr	Ala	Thr	Ala	
192					197					202					207	
gtt	cct	tca	gga	aaa	att	gct	tcc	cct	gtc	tcc	aga	aag	gag	cct	cca	791
Val	Pro	Ser	Gly	Lys	Ile	Ala	Ser	Pro	Val	Ser	Arg	Lys	Glu	Pro	Pro	
208					213					218					223	
tta	act	cct	gtt	cct	ctt	aaa	cgt	gct	gaa	ttt	gct	ggc	gat	gat	gta	839
Leu	Thr	Pro	Val	Pro	Leu	Lys	Arg	Ala	Glu	Phe	Ala	Gly	Asp	Asp	Val	
224					229					234					239	
cag	gtc	gag	agt	aca	gaa	gaa	gag	cag	gag	tca	ggg	gca	atg	gag	ttt	887
Gln	Val	Glu	Ser	Thr	Glu	Glu	Glu	Gln	Glu	Ser	Gly	Ala	Met	Glu	Phe	
240					245					250					255	
gaa	gat	ggg	gac	ttt	gat	gag	ccc</									

Glu Pro Met Ala Ala Lys Ala Trp Asp Lys Glu Ser Glu Pro Ala Glu	
272 277 282 287	
gaa gtg aaa caa gag gcg gat tct ggg aaa ggg acc gtg tcc tac tta	1031
Glu Val Lys Gln Glu Ala Asp Ser Gly Lys Gly Thr Val Ser Tyr Leu	
288 293 298 303	
gga agt ttt ctc ccg gat gtc tct tgt tgg gac att gat caa gaa ggt	1079
Gly Ser Phe Leu Pro Asp Val Ser Cys Trp Asp Ile Asp Gln Glu Gly	
304 309 314 319	
gat agc agt ttc tca gtg caa gaa gtt caa gtg gat tcc agt cac ctc	1127
Asp Ser Ser Phe Ser Val Gln Glu Val Gln Val Asp Ser Ser His Leu	
320 325 330 335	
cca ttg gta aaa ggg gca gat gag gaa caa gta ttc cac ttt tat tgg	1175
Pro Leu Val Lys Gly Ala Asp Glu Glu Gln Val Phe His Phe Tyr Trp	
336 341 346 351	
ttg gat gct tat gag gat cag tac aac caa cca ggt gtg gta ttt ctg	1223
Leu Asp Ala Tyr Glu Asp Gln Tyr Asn Gln Pro Gly Val Val Phe Leu	
352 357 362 367	
ttt ggg aaa gtt tgg att gaa tca gcc gag acc cat gtg agc tgt tgt	1271
Phe Gly Lys Val Trp Ile Glu Ser Ala Glu Thr His Val Ser Cys Cys	
368 373 378 383	
gtc atg gtg aaa aat atc gag cga acg ctt tac ttc ctt ccc cgt gaa	1319
Val Met Val Lys Asn Ile Glu Arg Thr Leu Tyr Phe Leu Pro Arg Glu	
384 389 394 399	
atg aaa att gat cta aat acg ggg aaa gaa aca gga act cca att tca	1367
Met Lys Ile Asp Leu Asn Thr Gly Lys Glu Thr Gly Thr Pro Ile Ser	
400 405 410 415	
atg aag gat gtt tat gag gaa ttt gat gag aaa ata gca aca aaa tat	1415
Met Lys Asp Val Tyr Glu Glu Phe Asp Glu Lys Ile Ala Thr Lys Tyr	
416 421 426 431	
aaa att atg aag ttc aag tct aag cca gtg gaa aag aac tat gct ttt	1463
Lys Ile Met Lys Phe Lys Ser Lys Pro Val Glu Lys Asn Tyr Ala Phe	
432 437 442 447	
gag ata cct gat gtt cca gaa aaa tct gag tac ttg gaa gtt aaa tac	1511
Glu Ile Pro Asp Val Pro Glu Lys Ser Glu Tyr Leu Glu Val Lys Tyr	
448 453 458 463	
tcg gct gaa atg cca cag ctt cct caa gat ttg aaa gga gaa act ttt	1559
Ser Ala Glu Met Pro Gln Leu Pro Gln Asp Leu Lys Gly Glu Thr Phe	
464 469 474 479	
tct cat gta ttt ggg acc aac aca tct agc ctg gaa ctg ttc ttg atg	1607
Ser His Val Phe Gly Thr Asn Thr Ser Ser Leu Glu Leu Phe Leu Met	
480 485 490 495	
aac aga aag atc aaa gga cct tgt tgg ctt gaa gta aaa aag tcc aca	1655
Asn Arg Lys Ile Lys Gly Pro Cys Trp Leu Glu Val Lys Lys Ser Thr	

496	501	506	511	
gct ctt aat cag cca	gct agt tgg tgt aaa	ggt gag gca atg gct ttg		1703
Ala Leu Asn Gln Pro	Val Ser Trp Cys Lys	Val Glu Ala Met Ala Leu		
512	517	522	527	
aaa cca gac ctg gtg	aat gta att aag gat	gtc agt cca cca ccg ctt		1751
Lys Pro Asp Leu Val	Asn Val Ile Lys Asp	Val Ser Pro Pro Pro Leu		
528	533	538	543	
gtc gtg atg gct ttc	agc atg aag aca atg	cag aat gca aag aac cat		1799
Val Val Met Ala Phe	Ser Met Lys Thr Met	Gln Asn Ala Lys Asn His		
544	549	554	559	
caa aat gag att att	gct atg gca gct ttg	gtc cat cac agt ttt gca		1847
Gln Asn Glu Ile Ile	Ala Met Ala Ala Leu	Val His His Ser Phe Ala		
560	565	570	575	
ttg gat aaa gca gcc	cca aag cct ccc ttt	cag tca cac ttc tgt gtt		1895
Leu Asp Lys Ala Ala	Pro Lys Pro Pro Phe	Gln Ser His Phe Cys Val		
576	581	586	591	
gtg tct aaa cca aag	gac tgt att ttt cca	tat gct ttc aaa gaa gtc		1943
Val Ser Lys Pro Lys	Asp Cys Ile Phe Pro	Tyr Ala Phe Lys Glu Val		
592	597	602	607	
att gag aaa aag aat	gtg aag gtt gag gtt	gct gca aca gaa aga aca		1991
Ile Glu Lys Lys Asn	Val Lys Val Glu Val	Ala Ala Thr Glu Arg Thr		
608	613	618	623	
ctg cta ggt ttt ttc	ctt gca aaa gtt cac	aaa att gat cct gat atc		2039
Leu Leu Gly Phe Phe	Leu Ala Lys Val His	Lys Ile Asp Pro Asp Ile		
624	629	634	639	
att gtg ggt cat aat	att tat ggg ttt gaa	ctg gaa gta cta ctg cag		2087
Ile Val Gly His Asn	Ile Tyr Gly Phe Glu	Leu Glu Val Leu Leu Gln		
640	645	650	655	
aga att aat gtg tgc	aaa gct cct cac tgg	tcc aag ata ggt cga ctg		2135
Arg Ile Asn Val Cys	Lys Ala Pro His Trp	Ser Lys Ile Gly Arg Leu		
656	661	666	671	
aag cga tcc aac atg	cca aag ctt ggg ggc	cgg agt gga ttt ggt gaa		2183
Lys Arg Ser Asn Met	Pro Lys Leu Gly Gly	Arg Ser Gly Phe Gly Glu		
672	677	682	687	
aga aat gct acc tgt	ggt cga atg atc tgt	gat gtg gaa att tca gca		2231
Arg Asn Ala Thr Cys	Gly Arg Met Ile Cys	Asp Val Glu Ile Ser Ala		
688	693	698	703	
aag gaa ttg att cgt	tgt aaa agc tac cat	ctg tct gaa ctt gtt cag		2279
Lys Glu Leu Ile Arg	Cys Lys Ser Tyr His	Leu Ser Glu Leu Val Gln		
704	709	714	719	
cag att cta aaa act	gaa agg gtt gta atc	cca atg gaa aat ata caa		2327
Gln Ile Leu Lys Thr	Glu Arg Val Val Ile	Pro Met Glu Asn Ile Gln		
720	725	730	735	

aat atg tac agt gaa tct tct caa ctg tta tac ctg ttg gaa cac acc	2375
Asn Met Tyr Ser Glu Ser Ser Gln Leu Leu Tyr Leu Leu Glu His Thr	
736 741 746 751	
tggtg aaa gat gcc aag ttc att ttg cag atc atg tgt gag cta aat gtt	2423
Trp Lys Asp Ala Lys Phe Ile Leu Gln Ile Met Cys Glu Leu Asn Val	
752 757 762 767	
ctt cca tta gca ttg cag atc act aac atc gct ggg aac att atg tcc	2471
Leu Pro Leu Ala Leu Gln Ile Thr Asn Ile Ala Gly Asn Ile Met Ser	
768 773 778 783	
agg acg ctg atg ggt gga cga tcc gag cgt aac gag ttc ttg ttg ctt	2519
Arg Thr Leu Met Gly Gly Arg Ser Glu Arg Asn Glu Phe Leu Leu Leu	
784 789 794 799	
cat gca ttt tac gaa aac aac tat att gtg cct gac aag cag att ttc	2567
His Ala Phe Tyr Glu Asn Asn Tyr Ile Val Pro Asp Lys Gln Ile Phe	
800 805 810 815	
aga aag cct cag caa aaa ctg gga gat gaa gat gaa gaa att gat gga	2615
Arg Lys Pro Gln Gln Lys Leu Gly Asp Glu Asp Glu Glu Ile Asp Gly	
816 821 826 831	
gat acc aat aaa tac aag aaa gga cgt aag aaa gga gct tat gct gga	2663
Asp Thr Asn Lys Tyr Lys Lys Gly Arg Lys Lys Gly Ala Tyr Ala Gly	
832 837 842 847	
ggc ttg gtt ttg gac ccc aaa gtt ggt ttt tat gat aag ttc att ttg	2711
Gly Leu Val Leu Asp Pro Lys Val Gly Phe Tyr Asp Lys Phe Ile Leu	
848 853 858 863	
ctt ctg gac ttc aac agt cta tat cct tcc atc att cag gaa ttt aac	2759
Leu Leu Asp Phe Asn Ser Leu Tyr Pro Ser Ile Ile Gln Glu Phe Asn	
864 869 874 879	
att tgt ttt aca aca gta caa aga gtt gct tca gag gca cag aaa gtt	2807
Ile Cys Phe Thr Thr Val Gln Arg Val Ala Ser Glu Ala Gln Lys Val	
880 885 890 895	
aca gag gat gga gaa caa gaa cag atc cct gag ttg cca gat cca agc	2855
Thr Glu Asp Gly Glu Gln Glu Gln Ile Pro Glu Leu Pro Asp Pro Ser	
896 901 906 911	
tta gaa atg ggc att ttg ccc aga gag atc cgg aaa ctg gta gaa cgg	2903
Leu Glu Met Gly Ile Leu Pro Arg Glu Ile Arg Lys Leu Val Glu Arg	
912 917 922 927	
aga aaa caa gtc aaa cag cta atg aaa cag caa gac tta aat cca gac	2951
Arg Lys Gln Val Lys Gln Leu Met Lys Gln Gln Asp Leu Asn Pro Asp	
928 933 938 943	
ctt att ctt cag tat gac att cga cag aag gct ttg aag ctc aca gcg	2999
Leu Ile Leu Gln Tyr Asp Ile Arg Gln Lys Ala Leu Lys Leu Thr Ala	
944 949 954 959	

aac agt atg tat ggt tgc ctg gga ttt tcc tat agc aga ttt tac gcc	3047
Asn Ser Met Tyr Gly Cys Leu Gly Phe Ser Tyr Ser Arg Phe Tyr Ala	
960 965 970 975	
aaa cca ctg gct gcc ttg gtg aca tac aaa gga agg gag att ttg atg	3095
Lys Pro Leu Ala Ala Leu Val Thr Tyr Lys Gly Arg Glu Ile Leu Met	
976 981 986 991	
cat acg aaa gag atg gta caa aag atg aat ctt gaa gtt att tat gga	3143
His Thr Lys Glu Met Val Gln Lys Met Asn Leu Glu Val Ile Tyr Gly	
992 997 1002 1007	
gat aca gat tca att atg ata aac acc aat agc acc aat ctg gaa gaa	3191
Asp Thr Asp Ser Ile Met Ile Asn Thr Asn Ser Thr Asn Leu Glu Glu	
1008 1013 1018 1023	
gta ttt aag ttg gga aac aag gta aaa agt gaa gtg aat aag ttg tac	3239
Val Phe Lys Leu Gly Asn Lys Val Lys Ser Glu Val Asn Lys Leu Tyr	
1024 1029 1034 1039	
aaa ctg ctt gaa ata gac att gat ggg gtt ttc aag tct ctg cta ctg	3287
Lys Leu Leu Glu Ile Asp Ile Asp Gly Val Phe Lys Ser Leu Leu Leu	
1040 1045 1050 1055	
ctg aaa aaa aag aag tac gct gct ctg gtt gtt gag cca acg tcg gat	3335
Leu Lys Lys Lys Lys Tyr Ala Ala Leu Val Val Glu Pro Thr Ser Asp	
1056 1061 1066 1071	
ggg aat tat gtc acc aaa cag gag ctc aaa gga tta gat ata gtt aga	3383
Gly Asn Tyr Val Thr Lys Gln Glu Leu Lys Gly Leu Asp Ile Val Arg	
1072 1077 1082 1087	
aga gat tgg tgt gat ctt gct aaa gac act gga aac ttt gtg att ggc	3431
Arg Asp Trp Cys Asp Leu Ala Lys Asp Thr Gly Asn Phe Val Ile Gly	
1088 1093 1098 1103	
cag att ctt tct gat caa agc cgg gac act ata gtg gaa aac att cag	3479
Gln Ile Leu Ser Asp Gln Ser Arg Asp Thr Ile Val Glu Asn Ile Gln	
1104 1109 1114 1119	
aag agg ctg ata gaa att gga gaa aat gtg cta aat ggc agt gtc cca	3527
Lys Arg Leu Ile Glu Ile Gly Glu Asn Val Leu Asn Gly Ser Val Pro	
1120 1125 1130 1135	
gtg agc cag ttt gaa att aac aag gca ttg aca aag gat ccc cag gat	3575
Val Ser Gln Phe Glu Ile Asn Lys Ala Leu Thr Lys Asp Pro Gln Asp	
1136 1141 1146 1151	
tac cct gat aaa aaa agc cta cct cat gta cat gtt gcc ctc tgg ata	3623
Tyr Pro Asp Lys Lys Ser Leu Pro His Val His Val Ala Leu Trp Ile	
1152 1157 1162 1167	
aat tct caa gga ggc aga aag gtg aaa gct gga gat act gtg tca tat	3671
Asn Ser Gln Gly Gly Arg Lys Val Lys Ala Gly Asp Thr Val Ser Tyr	
1168 1173 1178 1183	
gtc atc tgt cag gat gga tca aac ctc act gca agt cag agg gcc tat	3719

1184
 1200
 1216
 1232
 1248
 1264
 1280
 1296
 1312
 1328
 1344
 1360
 1376
 1392

Val	Ile	Cys	Gln	Asp	Gly	Ser	Asn	Leu	Thr	Ala	Ser	Gln	Arg	Ala	Tyr	
1184					1189					1194					1199	
gcg	cct	gag	cag	ctg	cag	aaa	cag	gat	aat	cta	acc	att	gac	acc	cag	3767
Ala	Pro	Glu	Gln	Leu	Gln	Lys	Gln	Asp	Asn	Leu	Thr	Ile	Asp	Thr	Gln	
1200					1205					1210					1215	
tac	tac	ctg	gcc	cag	cag	atc	cac	cca	gtc	gtg	gct	cgg	atc	tgt	gaa	3815
Tyr	Tyr	Leu	Ala	Gln	Gln	Ile	His	Pro	Val	Val	Ala	Arg	Ile	Cys	Glu	
1216					1221					1226					1231	
cca	ata	gac	gga	att	gat	gct	gtc	ctc	att	gca	acg	tgg	ttg	gga	ctt	3863
Pro	Ile	Asp	Gly	Ile	Asp	Ala	Val	Leu	Ile	Ala	Thr	Trp	Leu	Gly	Leu	
1232					1237					1242					1247	
gac	ccc	acc	caa	ttt	aga	gtt	cat	cat	tat	cat	aaa	gat	gaa	gag	aat	3911
Asp	Pro	Thr	Gln	Phe	Arg	Val	His	His	Tyr	His	Lys	Asp	Glu	Glu	Asn	
1248					1253					1258					1263	
gat	gct	cta	ctt	ggt	ggc	cca	gca	cag	ctc	act	gat	gaa	gag	aaa	tac	3959
Asp	Ala	Leu	Leu	Gly	Gly	Pro	Ala	Gln	Leu	Thr	Asp	Glu	Glu	Lys	Tyr	
1264					1269					1274					1279	
agg	gac	tgt	gaa	aga	ttc	aaa	tgt	cca	tgc	cct	aca	tgt	gga	act	gag	4007
Arg	Asp	Cys	Glu	Arg	Phe	Lys	Cys	Pro	Cys	Pro	Thr	Cys	Gly	Thr	Glu	
1280					1285					1290					1295	
aat	att	tat	gat	aat	gtc	ttt	gat	ggt	tcg	gga	aca	gat	atg	gag	ccc	4055
Asn	Ile	Tyr	Asp	Asn	Val	Phe	Asp	Gly	Ser	Gly	Thr	Asp	Met	Glu	Pro	
1296					1301					1306					1311	
agc	ttg	tat	cgt	tgc	agt	aac	atc	gat	tgt	aag	gct	tca	cct	ctg	acc	4103
Ser	Leu	Tyr	Arg	Cys	Ser	Asn	Ile	Asp	Cys	Lys	Ala	Ser	Pro	Leu	Thr	
1312					1317					1322					1327	
ttt	aca	gta	caa	ctg	agc	aac	aaa	ttg	atc	atg	gac	att	aga	cgt	ttc	4151
Phe	Thr	Val	Gln	Leu	Ser	Asn	Lys	Leu	Ile	Met	Asp	Ile	Arg	Arg	Phe	
1328					1333					1338					1343	
att	aaa	aag	tac	tat	gat	ggc	tgg	ttg	ata	tgt	gaa	gag	cca	acc	tgt	4199
Ile	Lys	Lys	Tyr	Tyr	Asp	Gly	Trp	Leu	Ile	Cys	Glu	Glu	Pro	Thr	Cys	
1344					1349					1354					1359	
cgc	aat	cga	act	cgt	cac	ctt	ccc	ctt	caa	ttc	tcc	cga	act	ggg	cct	4247
Arg	Asn	Arg	Thr	Arg	His	Leu	Pro	Leu	Gln	Phe	Ser	Arg	Thr	Gly	Pro	
1360					1365					1370					1375	
ctt	tgc	cca	gcc	tgc	atg	aaa	gct	aca	ctt	caa	cca	gag	tat	tct	gac	4295
Leu	Cys	Pro	Ala	Cys	Met	Lys	Ala	Thr	Leu	Gln	Pro	Glu	Tyr	Ser	Asp	
1376					1381					1386					1391	
aag	tcc	ctg	tac	acc	cag	ctg	tgc	ttt	tac	cgg	tac	att	ttt	gat	gcg	4343
Lys	Ser	Leu	Tyr	Thr	Gln	Leu	Cys	Phe	Tyr	Arg	Tyr	Ile	Phe	Asp	Ala	
1392					1397					1402					1407	
gag	tgt	gca	ctg	gag	aaa	ctt	act	acc	gat	cat	gag	aaa	gat	aaa	ttg	4391
Glu	Cys	Ala	Leu	Glu	Lys	Leu	Thr	Thr	Asp	His	Glu	Lys	Asp	Lys	Leu	

1408	1413	1418	1423	
aag aag caa ttt ttt acc ccc aaa gtt ctg cag gac tac aga aaa ctc				4439
Lys Lys Gln Phe Phe Thr Pro Lys Val Leu Gln Asp Tyr Arg Lys Leu				
1424	1429	1434	1439	
aag aac aca gca gag caa ttc ttg tcc cga agt ggc tac tcc gaa gtg				4487
Lys Asn Thr Ala Glu Gln Phe Leu Ser Arg Ser Gly Tyr Ser Glu Val				
1440	1445	1450	1455	
aat ctg agc aaa ctc ttc gct ggt tgt gcc gtg aaa tcc taa gggaatc				4536
Asn Leu Ser Lys Leu Phe Ala Gly Cys Ala Val Lys Ser *				
1456	1461	1466		
ccaggagtaa ccaaggaggg ggtagttgaa aaatcccagc ttcctctgtg cctccactct				4596
ggccctaaat gtcctccag catctgtttc tcccttgga ctgtgtctca tgtttgtgtg				4656
aatgtagacc aggaaagggg gctgcaaaaa tgttgagtct aatgttcgta agcatcatag				4716
aaattcctgt cttcatatta agatgtactg ctttaaaaca caactccaga gccctcccc				4776
aagctcccct cccaagctc ctgaagaccc ggtttctgag ggagggaaat tgctacttgg				4836
attgagagta gctggaatgt aagtgacccc aggctttgcc tcagggcctt tagcctatgt				4896
cccccccaca taaagagagc ttctcagagc ctgactgaag agctgacgtt ttgctttttc				4956
atatgccaat taaacccggt ctaaataccaa atgctttctcc agccatccag gagggtgtgt				5016
ccttttctagt cttgtctttt atataggttag ctgaggggga agatttagaa gccttgact				5076
cactaaatag attaaacaga gcaggcttgt ttgttgaatt gctccaaagt ccaacagaca				5136
cacactgagc aggtgtttta cactcacatt ccctttttgc cccttaaata gaaagtgcag				5196
gtaaagggtt atacaacaag aaagcacatt gaaaataatt tgatactcta acaatccatt				5256
aacatgtgta ggggttacgg tgaggatcac tgtgttgtat tcagaaaaac ggggagaggg				5316
atgcttaatt ggccctggcg cttgctattt ttttctcatt tcttcacaat aggaccgtct				5376
ttggcagcag caaaatgtat ttcagtatgg cagtctttcc tctcttacat tattggtaag				5436
attatactaa caaaatgttt ccccttgtag aattatgctg tgtttttaaa aaacattgac				5496
ctgtgtgttt ttataaaaaga aaaagtatgt tgtgccttct tcttaagaat aaagttttct				5556
aaagggaaaa aaaaaaaaa				5574

<210> 254
 <211> 1127
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (147)..(995)

<400> 254

ggcagcagggt cgaggtgaag agcaatttga cgccgagttc cgacgcttcg gctgcctccg	60
cttcggtgag cggcttccag gagttctcgc ggttgctgcg ggcggtgcac cagatccggg	120
cctggacgtg ctacttggtt atacgg atg ctc atg gcg acc tgc tgc ccc tca	173
Met Leu Met Ala Thr Cys Cys Pro Ser	
1 5	
cca acg acg aca gcc tgc acc ggg ccc tgg cag cgg gcc ccg cca ctg	221
Pro Thr Thr Thr Ala Cys Thr Gly Pro Trp Gln Arg Ala Pro Pro Leu	
10 15 20 25	
cgc cta ctg gtg cag aag cgg gaa gct gac tcc agc ggc ctg gct ttt	269
Arg Leu Leu Val Gln Lys Arg Glu Ala Asp Ser Ser Gly Leu Ala Phe	
26 31 36 41	
gcc tcc aac tct ctg cag cgg cgc aag aaa ggg ctc ttg ctg cgg cca	317
Ala Ser Asn Ser Leu Gln Arg Arg Lys Lys Gly Leu Leu Leu Arg Pro	
42 47 52 57	
gtg gca ccc ctg cgc acc cgg cca ccc ttg cta atc agc ctg ccc caa	365
Val Ala Pro Leu Arg Thr Arg Pro Pro Leu Leu Ile Ser Leu Pro Gln	
58 63 68 73	
gat ttc cgc cag gtt tcc tca gtc ata gac gtg gac cta ctg cct gag	413
Asp Phe Arg Gln Val Ser Ser Val Ile Asp Val Asp Leu Leu Pro Glu	
74 79 84 89	
acc cac cga cgg gtg cgg ctg cac aag cat ggt tca gac cgc ccc ctg	461
Thr His Arg Arg Val Arg Leu His Lys His Gly Ser Asp Arg Pro Leu	
90 95 100 105	
ggc ttc tac atc cga gat ggc atg agc gtg cgt gtg gct ccc cag ggc	509
Gly Phe Tyr Ile Arg Asp Gly Met Ser Val Arg Val Ala Pro Gln Gly	
106 111 116 121	
ctg gag cgg gtt cca gga atc ttc atc tcc cgc ctg gta cgt ggg ggt	557
Leu Glu Arg Val Pro Gly Ile Phe Ile Ser Arg Leu Val Arg Gly Gly	
122 127 132 137	
ctg gct gag agt aca ggg ctg ctg gcg gtc agt gat gag atc ctc gag	605
Leu Ala Glu Ser Thr Gly Leu Leu Ala Val Ser Asp Glu Ile Leu Glu	
138 143 148 153	
gtc aat ggc att gaa gta gcc ggg aag acc ttg gac caa gtg acg gac	653
Val Asn Gly Ile Glu Val Ala Gly Lys Thr Leu Asp Gln Val Thr Asp	
154 159 164 169	
atg atg gtt gcc aac agc cat aac ctc att gtc act gtc aag ccc gcc	701
Met Met Val Ala Asn Ser His Asn Leu Ile Val Thr Val Lys Pro Ala	
170 175 180 185	

aac cag cgc aat aac gtg gtg cga ggg gca tct ggg cgt ttg aca ggt	749
Asn Gln Arg Asn Asn Val Val Arg Gly Ala Ser Gly Arg Leu Thr Gly	
186 191 196 201	
cct ccc tct gca ggg cct ggg cct gct gag cct gat agt gac gat gac	797
Pro Pro Ser Ala Gly Pro Gly Pro Ala Glu Pro Asp Ser Asp Asp Asp	
202 207 212 217	
agc agt gac ctg gtc att gag aac cgc cag cct ccc agt tcc aat ggg	845
Ser Ser Asp Leu Val Ile Glu Asn Arg Gln Pro Pro Ser Ser Asn Gly	
218 223 228 233	
ctg tct cag ggg ccc ccg tgc tgg gac ctg cac cct ggc tgc cga cat	893
Leu Ser Gln Gly Pro Pro Cys Trp Asp Leu His Pro Gly Cys Arg His	
234 239 244 249	
cct ggt acc cgc agc tct ctg ccc tcc ctg gat gac cag gag cag gcc	941
Pro Gly Thr Arg Ser Ser Leu Pro Ser Leu Asp Asp Gln Glu Gln Ala	
250 255 260 265	
agt tct ggc tgg ggg agt cgc att cga gga gat ggt agt ggc ttc agc	989
Ser Ser Gly Trp Gly Ser Arg Ile Arg Gly Asp Gly Ser Gly Phe Ser	
266 271 276 281	
ctc tga cagtcaggat gaagcccat gccactccac actgctggga catggcaggg	1045
Leu *	
282	
acttcacagt ggggggttttt agctgggtca cagggtccc tcagcctggg gaacattaaa	1105
ggttttctac aaaaaaaaaa aa	1127

<210> 255
 <211> 6470
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (118)..(1653)

<400> 255	
attgaacgcc tgcagtaccg gtccggaatt cccgggtoga cccacgcgtc cggctcatca	60
taacttatgt tccatatttt ttaacccaca tcaactottga aatcgactgt tcagttg	117
atg tgc agg ctt tta cag gat aag cgc tac cag tgt gtc tat tcc ttg	165
Met Cys Arg Leu Leu Gln Asp Lys Arg Tyr Gln Cys Val Tyr Ser Leu	
1 5 10 15	
gca gaa atc ttt aag gtc ctg gct tca ttt tat gtc att ttg gtt ata	213
Ala Glu Ile Phe Lys Val Leu Ala Ser Phe Tyr Val Ile Leu Val Ile	
17 22 27 32	

ctt tat ggt ctg acc tct tcc tac agc ctg tgg tgg atg ctg agg agt	261
Leu Tyr Gly Leu Thr Ser Ser Tyr Ser Leu Trp Trp Met Leu Arg Ser	
33 38 43 48	
tcc ctg aag caa tat tcc ttt gag gcg tta aga gaa aaa agc aac tac	309
Ser Leu Lys Gln Tyr Ser Phe Glu Ala Leu Arg Glu Lys Ser Asn Tyr	
49 54 59 64	
agt gac atc cct gat gtc aag aat gac ttt gcc ttc atc ctt cat ctg	357
Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Ile Leu His Leu	
65 70 75 80	
gct gat cag tat gat cct ctt tat tcc aaa cgc ttc tcc ata ttc cta	405
Ala Asp Gln Tyr Asp Pro Leu Tyr Ser Lys Arg Phe Ser Ile Phe Leu	
81 86 91 96	
tca gag gtc agt gag aac aaa ctg aaa cag atc aac ctc aat aat gaa	453
Ser Glu Val Ser Glu Asn Lys Leu Lys Gln Ile Asn Leu Asn Asn Glu	
97 102 107 112	
tgg aca gtt gag aaa ctg aaa agt aag ctt gtg aaa aat gcc cag gac	501
Trp Thr Val Glu Lys Leu Lys Ser Lys Leu Val Lys Asn Ala Gln Asp	
113 118 123 128	
aag ata gaa ctg cat ctt ttt atg ctc aac ggt ctt cca gac aat gtc	549
Lys Ile Glu Leu His Leu Phe Met Leu Asn Gly Leu Pro Asp Asn Val	
129 134 139 144	
ttt gag tta act gaa atg gaa gtg cta agc ctg gag ctt atc cca gag	597
Phe Glu Leu Thr Glu Met Glu Val Leu Ser Leu Glu Leu Ile Pro Glu	
145 150 155 160	
gtg aag ctg ccc tct gca gtc tca cag ctg gtc aac ctc aag gag ctt	645
Val Lys Leu Pro Ser Ala Val Ser Gln Leu Val Asn Leu Lys Glu Leu	
161 166 171 176	
cgt gtg tac cat tca tct ctg gtc gta gac cat cct gca ctg gcc ttt	693
Arg Val Tyr His Ser Ser Leu Val Val Asp His Pro Ala Leu Ala Phe	
177 182 187 192	
cta gag gag aat tta aaa atc ctc cgc ctg aaa ttt act gaa atg gga	741
Leu Glu Glu Asn Leu Lys Ile Leu Arg Leu Lys Phe Thr Glu Met Gly	
193 198 203 208	
aaa atc cca cgc tgg gta ttt cac ctc aag aat ctc aag gaa ctt tat	789
Lys Ile Pro Arg Trp Val Phe His Leu Lys Asn Leu Lys Glu Leu Tyr	
209 214 219 224	
ctt tcg ggc tgt gtt ctc cct gaa cag ttg agt act atg cag ttg gag	837
Leu Ser Gly Cys Val Leu Pro Glu Gln Leu Ser Thr Met Gln Leu Glu	
225 230 235 240	
ggc ttt cag gac tta aaa aat cta agg acc ctg tac ttg aag agc agc	885
Gly Phe Gln Asp Leu Lys Asn Leu Arg Thr Leu Tyr Leu Lys Ser Ser	
241 246 251 256	
ctc tcc cgg atc cca caa gtt gtt aca gac ctc ctg cct tca ttg cag	933

Leu Ser Arg Ile Pro Gln Val Val Thr Asp Leu Leu Pro Ser Leu Gln	
257 262 267 272	
aaa ctg tcc ctt gat aat gag gga agc aaa ctg gtt gtg ttg aac aac	981
Lys Leu Ser Leu Asp Asn Glu Gly Ser Lys Leu Val Val Leu Asn Asn	
273 278 283 288	
ttg aaa aag atg gtc aat ctg aaa agc cta gaa ctg atc agc tgt gac	1029
Leu Lys Lys Met Val Asn Leu Lys Ser Leu Glu Leu Ile Ser Cys Asp	
289 294 299 304	
ctg gaa cgc atc cca cat tcc att ttc agc ctg aat aat ttg cat gag	1077
Leu Glu Arg Ile Pro His Ser Ile Phe Ser Leu Asn Asn Leu His Glu	
305 310 315 320	
tta gac cta agg gaa aat aac ctt aaa act gtg gaa gag atc att agc	1125
Leu Asp Leu Arg Glu Asn Asn Leu Lys Thr Val Glu Glu Ile Ile Ser	
321 326 331 336	
ttt cag cat ctt cag aat ctt tcc tgc tta aag ttg tgg cac aat aac	1173
Phe Gln His Leu Gln Asn Leu Ser Cys Leu Lys Leu Trp His Asn Asn	
337 342 347 352	
att gct tat att cct gca cag att ggg gca tta tct aac cta gag cag	1221
Ile Ala Tyr Ile Pro Ala Gln Ile Gly Ala Leu Ser Asn Leu Glu Gln	
353 358 363 368	
ctc tct ttg gac cat aat aat att gag aat ctg ccc ttg cag ctt ttc	1269
Leu Ser Leu Asp His Asn Asn Ile Glu Asn Leu Pro Leu Gln Leu Phe	
369 374 379 384	
cta tgc act aaa cta cat tat ttg gat cta agc tat aac cac ttg acc	1317
Leu Cys Thr Lys Leu His Tyr Leu Asp Leu Ser Tyr Asn His Leu Thr	
385 390 395 400	
ttc att cca gaa gaa atc cag tat ctg agt aat ttg cag tac ttt gct	1365
Phe Ile Pro Glu Glu Ile Gln Tyr Leu Ser Asn Leu Gln Tyr Phe Ala	
401 406 411 416	
gtg acc aac aac aat att gag atg cta cca gat ggg ctg ttt cag tgc	1413
Val Thr Asn Asn Asn Ile Glu Met Leu Pro Asp Gly Leu Phe Gln Cys	
417 422 427 432	
aaa aag ctg cag tgt tta ctt ttg ggg aaa aat agc ttg atg aat ttg	1461
Lys Lys Leu Gln Cys Leu Leu Leu Gly Lys Asn Ser Leu Met Asn Leu	
433 438 443 448	
tcc cct cat gtg ggt gag ctg tca aac ctt act cat ctg gag ctc att	1509
Ser Pro His Val Gly Glu Leu Ser Asn Leu Thr His Leu Glu Leu Ile	
449 454 459 464	
ggg aat tac ctg gaa aca ctt cct cct gaa cta gaa gga tgt cag tcc	1557
Gly Asn Tyr Leu Glu Thr Leu Pro Pro Glu Leu Glu Gly Cys Gln Ser	
465 470 475 480	
cta aaa cgg aac tgt ctg att gtt gag gag aac ttg ctc aat act ctt	1605
Leu Lys Arg Asn Cys Leu Ile Val Glu Glu Asn Leu Leu Asn Thr Leu	

481	486	491	496	
cct ctc cct gta aca gaa cgt tta cag acg tgc tta gac aaa tgt tga				1653
Pro Leu Pro Val Thr Glu Arg Leu Gln Thr Cys Leu Asp Lys Cys *				
497	502	507	512	
cttaaagaaa agagacccgt gtttcaaaat cattttttaa agtatgctcg gccgggctg				1713
gtggctcatg cctataatcc cagcaccttg ggaggccaag atgggcggat tgcttgaggt				1773
caggagtctg agaccagtct ggccaacctg gtgaaacccc atctctgcta aaactacaaa				1833
aaaattagcc aggcgtggtg gcgtagcct gtaatcccag ctacttggga ggctgacgca				1893
ggggaattgc ttgaaccagg gaggtggagg ttgcagttag ccgagattgt gccactgtac				1953
accagcctgg gtgacagagc aagactctta tctcaaaaaa aaaaaaaaaa tgctccaggg				2013
ctttaaatga gaagtaaaat tttctaagtt aataaagatg aagaatgggt gactattatg				2073
atgaaccata actaaatgtc ttattaaagc aactgagtgt ctagccctaa attaaccagg				2133
taaaaactgt taacactaac ctgaagtttt gtgaataact gttctttaac ttattgagat				2193
gttgcaagaa atgcacatcc aggggtggact gggagctatg aaatgactaa attcctcctt				2253
gcagtgttta ccttcaagat tgtataggta ttctctcttc ttcttcccc agtccccatt				2313
acttatttgc acacttgttt taactgactt cctgttttga tatttatcac caagaccata				2373
aactcatcaa tatgaatttt cttgatgtat actcacgact gtctttgatt tatgttctta				2433
aattttttta gatagggtat gttgtgcttg gcagaattct tttttggctt aatttttact				2493
tcctttccca gcttgcttga gtcttcttta acctgggttt ctcttaacac caatgatgaa				2553
ccctgagaaa atgcctgcat ttggcctttg cctagaacag gagctgagta ttttaagatgt				2613
attatcctcg ggtcatcctg aaaattaatg tattccctaa aatttcttct tgtctatcat				2673
caaggccttt ttttatttgt taagaatttt tatattaaat gtaaaacata taaatatttt				2733
ctattgtata atcttggatt caacatctgt gaggatcatt tttgtaagat acgtagaatt				2793
tgtgcatttc tttatgaact tactgttagt gttcttgggt tcggctgttt atgactcatg				2853
tttatgtaca ttctgtcca aaatgttttt gtactctgca actaattact tttggataac				2913
aaaagccttg tgtttaatgc cctaaagtat ttgggggttt ctttgtgaga ggggtggcca				2973
atcatctacc tctctcttcc atagttgctg tgcaatcgta cgggtaaaaat tcttaattac				3033
ttacaaaaac tgtgatagag gggagaggta cagatttggt ttttaaattg attttaaaat				3093
actttataga aatttagtaa gagttaaaagc aaaagacttt ttttccctcc atctatgtaa				3153
tctctagcta tgattataat gtaaaacagc ctctattcag tgtctaaaaat gagttctcaa				3213

cttttcattc	ttcaactocca	gtottaat	ctttccctg	tatgtcactg	tattttatgt	4953
cacttcacat	tgtgttaa	agggtaa	gagatcctca	gtatctcagt	gctgtggcat	5013
agctccaata	gggtgtgctgt	gggtgcactgc	agtgatgtat	ttgcataaca	ttgtttgata	5073
gtgaaaaatt	ttttttcgg	tcaagtgttt	tgtgattaaa	attttatgtt	taattaaaa	5133
attgcataat	attgatgggt	tcaaaaacca	ttaaaataat	caaacaatta	ttctgtgccc	5193
ttaacattat	tttctgtgt	tttcaataaa	attttctttt	catctttcca	tcttcacatt	5253
ctcttagcat	catctatgc	acataaggta	tgttgttttc	cttctccact	cacctaccgc	5313
actaaatttg	atcagcaatt	gtacagtaac	agaatatatt	tgtgccagaa	gatttgcaat	5373
gatatttgag	catgtattta	tttaggagga	agccagtgcc	tgtaattatg	totcattgag	5433
tagttttact	ttgcccattc	tgcagtattt	agagctgatc	tgtacccaaa	gcaggacaat	5493
gtaactgtag	atctgctttg	ttttcagtaa	ctgtacattg	catcagaatc	tgttttatttc	5553
tatctggaaa	cagacagaat	gggtgggggag	ggaaggagtt	attttgcattc	ctagtttgta	5613
ttatgaagtc	atcatatata	tatttgaaat	agtataagct	aattactggt	gcagaatgcc	5673
ctcgatataa	ttatttcttt	tcagctggat	gtgaaaagct	gaagcagtga	aaacctgcag	5733
tcttatttca	ctggtttcct	tctgtttctt	gtccatcact	tctgtatcca	caggagcta	5793
tctactacat	acctttggta	acaggctaca	ttctcttcag	attttttata	tgaataattt	5853
catcagcact	aaagcattaa	catagaataa	tgagccaaag	tactgagtcg	agatggcttt	5913
cagttgagtt	taatttcata	tttaactttt	gcatttaact	tgtataatac	actactgctg	5973
agaaaaacaa	ttatgaatgc	cttctgcatg	ttgtacatta	tctctaacag	agatgggtgc	6033
aattttaaga	atacaaaggg	gtatagagtt	agaatggatg	tgttcgtgca	tatatatggt	6093
gtattttaa	attaatgttt	acaagaagat	tttttttaa	ttcttcaa	acttcactta	6153
gtgaaataat	gggccaatct	ggaatagaga	cattttat	ggttagtgca	agagtgaag	6213
ctagcatttg	ttaaccttca	catatttatc	tgtgtacaat	tgtttttgct	tctggtaatg	6273
aattattaga	aaatggaaga	ttttgttcaa	tgtttttg	cctcagggtt	actgtgtaaa	6333
tctgcatttt	tggtggtaaa	tccttttgcc	acagattcag	tagcttttgg	taaacttcac	6393
tgttttttaa	gtaccttttg	tgtaaaataa	agatccaatt	tttataacaa	atggcaaata	6453
aaaacagtaa	atgctgg					6470

<210> 256
 <211> 1997
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (479)..(1882)

<400> 256

```

tttttttttt ttctatttat tttaaataca cacacccaga gggctctgcc ccctgtaaaa      60

gaaaaaaaaat caaaacaaac aaataaataa ccccaaagag atggacccag gggagaacgc      120

gtaagtgtga ggggcatgag tatacacgag tgtgcgtgtc tttccctctc ccttatttgt      180

ctcogtatga gtctctcctt gtaccctccc cctgcctcga tgatattact cccccagact      240

tggaagccgc tgccagagtg acgctttgat ggtatctgca agcgtttttg ctgatcttat      300

ctctgcccc tgaatattaa ttccctaatac tggtagcaat ccatctcccc agtgaaggac      360

ctactagagg caggtggggg gagccaccat cagatcataa gcataagaat aatacaaagg      420

ggagggattc ttctgcaacc aagaggcaag aggcgagaga aggaaaaaaaa aaaaagcg      478
atg agt tca cca aat ata tgg agc aca gga agc tca gtc tac tcg act      526
Met Ser Ser Pro Asn Ile Trp Ser Thr Gly Ser Ser Val Tyr Ser Thr
  1             5             10             15

cct gta ttt tca cag aaa atg acg gtg tgg att ctg ctc ctg ctg tcg      574
Pro Val Phe Ser Gln Lys Met Thr Val Trp Ile Leu Leu Leu Leu Ser
  17             22             27             32

ctc tac cct ggc ttc act agc cag aaa tct gat gat gac tat gaa gat      622
Leu Tyr Pro Gly Phe Thr Ser Gln Lys Ser Asp Asp Asp Tyr Glu Asp
  33             38             43             48

tat gct tct aac aaa aca tgg gtc ttg act cca aaa gtt cct gag ggt      670
Tyr Ala Ser Asn Lys Thr Trp Val Leu Thr Pro Lys Val Pro Glu Gly
  49             54             59             64

gat gtc act gtc atc tta aac aac ctg ctg gaa gga tat gac aat aaa      718
Asp Val Thr Val Ile Leu Asn Asn Leu Leu Glu Gly Tyr Asp Asn Lys
  65             70             75             80

ctt cgg cct gat ata gga gtg aag cca acg tta att cac aca gac atg      766
Leu Arg Pro Asp Ile Gly Val Lys Pro Thr Leu Ile His Thr Asp Met
  81             86             91             96

tat gtg aat agc att ggt cca gtg aat gct atc aat atg gaa tac act      814
Tyr Val Asn Ser Ile Gly Pro Val Asn Ala Ile Asn Met Glu Tyr Thr
  97             102            107            112

att gat ata ttt ttt gcg caa acg tgg tat gac aga cgt ttg aaa ttt      862
Ile Asp Ile Phe Phe Ala Gln Thr Trp Tyr Asp Arg Arg Leu Lys Phe
  113            118            123            128

```


aac agc acc att aaa gtc ctc cga ttg aac agc aac atg gtg ggg aaa	910
Asn Ser Thr Ile Lys Val Leu Arg Leu Asn Ser Asn Met Val Gly Lys	
129 134 139 144	
atc tgg att cca gac act ttc ttc aga aat tcc aaa aaa gct gat gca	958
Ile Trp Ile Pro Asp Thr Phe Phe Arg Asn Ser Lys Lys Ala Asp Ala	
145 150 155 160	
cac tgg atc acc acc ccc aac agg atg ctg aga att tgg aat gat ggt	1006
His Trp Ile Thr Thr Pro Asn Arg Met Leu Arg Ile Trp Asn Asp Gly	
161 166 171 176	
cga gtg ctc tac tcc cta agg ttg aca att gat gct gag tgc caa tta	1054
Arg Val Leu Tyr Ser Leu Arg Leu Thr Ile Asp Ala Glu Cys Gln Leu	
177 182 187 192	
caa ttg cac aat ttt cca atg gat gaa cac tcc tgc ccc ttg gag ttc	1102
Gln Leu His Asn Phe Pro Met Asp Glu His Ser Cys Pro Leu Glu Phe	
193 198 203 208	
tcc agt tat ggc tat cca cgt gaa gaa att gtt tat caa tgg aag cga	1150
Ser Ser Tyr Gly Tyr Pro Arg Glu Glu Ile Val Tyr Gln Trp Lys Arg	
209 214 219 224	
agt tct gtt gaa gtg ggc gac aca aga tcc tgg agg ctt tat caa ttc	1198
Ser Ser Val Glu Val Gly Asp Thr Arg Ser Trp Arg Leu Tyr Gln Phe	
225 230 235 240	
tca ttt gtt ggt cta aga aat acc acc gaa gta gtg aag aca act tcc	1246
Ser Phe Val Gly Leu Arg Asn Thr Thr Glu Val Val Lys Thr Thr Ser	
241 246 251 256	
gga gat tat gtg gtc atg tct gtc tac ttt gat ctg agc aga aga atg	1294
Gly Asp Tyr Val Val Met Ser Val Tyr Phe Asp Leu Ser Arg Arg Met	
257 262 267 272	
gga tac ttt acc atc cag acc tat atc ccc tgc aca ctc att gtc gtc	1342
Gly Tyr Phe Thr Ile Gln Thr Tyr Ile Pro Cys Thr Leu Ile Val Val	
273 278 283 288	
cta tcc tgg gtg tct ttc tgg atc aat aag gat gct gtt cca gcc aga	1390
Leu Ser Trp Val Ser Phe Trp Ile Asn Lys Asp Ala Val Pro Ala Arg	
289 294 299 304	
aca tct tta ggt atc acc act gtc ctg aca atg acc acc ctc agc acc	1438
Thr Ser Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr Leu Ser Thr	
305 310 315 320	
att gcc cgg aaa tcg ctc ccc aag gtc tcc tat gtc aca gcg atg gat	1486
Ile Ala Arg Lys Ser Leu Pro Lys Val Ser Tyr Val Thr Ala Met Asp	
321 326 331 336	
ctc ttt gta tct gtt tgt ttc atc ttt gtc ttc tct gct ctg gtg gag	1534
Leu Phe Val Ser Val Cys Phe Ile Phe Val Phe Ser Ala Leu Val Glu	
337 342 347 352	
tat ggc acc ttg cat tat ttt gtc agc aac cgg aaa cca agc aag gac	1582

Tyr Gly Thr Leu His	Tyr Phe Val Ser Asn Arg Lys Pro Ser Lys Asp	
353	358	363 368
aaa gat aaa aag aag	aaa aac cct gcc cct acc att gat atc cgc cca	1630
Lys Asp Lys Lys Lys	Lys Asn Pro Ala Pro Thr Ile Asp Ile Arg Pro	
369	374 379	384
aga tca gca acc att	caa atg aat aat gct aca cac ctt caa gag aga	1678
Arg Ser Ala Thr Ile	Gln Met Asn Asn Ala Thr His Leu Gln Glu Arg	
385	390 395	400
gat gaa gag tac ggc	tat gag tgt ctg gac ggc aag gac tgt gcc agt	1726
Asp Glu Glu Tyr Gly	Tyr Glu Cys Leu Asp Gly Lys Asp Cys Ala Ser	
401	406 411	416
ttt ttc tgc tgt ttt	gaa gat tgt cga aca gga gct tgg aga cat ggg	1774
Phe Phe Cys Cys Phe	Glu Asp Cys Arg Thr Gly Ala Trp Arg His Gly	
417	422 427	432
agg ata cat atc cgc	att gcc aaa atg gac tcc tat gct cgg atc ttc	1822
Arg Ile His Ile Arg	Ile Ala Lys Met Asp Ser Tyr Ala Arg Ile Phe	
433	438 443	448
ttc ccc act gcc ttc	tgc ctg ttt aat ctg gtc tat tgg gtc tcc tac	1870
Phe Pro Thr Ala Phe	Cys Leu Phe Asn Leu Val Tyr Trp Val Ser Tyr	
449	454 459	464
ctc tac ctg tga gga	ggtatgggtt ttactgatat ggttcttatt cactgagtct	1925
Leu Tyr Leu *		
465		
catggagaga tgtctgttct	aagtccactt aaataatcct ctatgtgggtt gataagtatc	1985
tgaatctgtt tc		1997

<210> 257
 <211> 2215
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (72)..(1430)

<400> 257	
atttggccct cgaggccaag aattcggcac gagcgcggag cccggctcgg ccacaccgat	60
pgcccgccgc c atg ggc tcc tgc caa agc gtc gag atc ccg ggc ggg ggc	110
Met Gly Ser Ser Gln Ser Val Glu Ile Pro Gly Gly Gly	
1 5 10	
acc gag ggc tac cac gtt ctg cgg gta caa gaa aat tcc cca gga cac	158
Thr Glu Gly Tyr His Val Leu Arg Val Gln Glu Asn Ser Pro Gly His	
14 19 24 29	

aga gct ggt ttg gag cct ttc ttt gat ttt att gtt tct att aat ggt	206
Arg Ala Gly Leu Glu Pro Phe Phe Asp Phe Ile Val Ser Ile Asn Gly	
30 35 40 45	
tca aga tta aat aaa gac aat gac act ctt aag gat ctg ctg aaa gca	254
Ser Arg Leu Asn Lys Asp Asn Asp Thr Leu Lys Asp Leu Leu Lys Ala	
46 51 56 61	
aac gtt gaa aag cct gta aag atg ctt atc tat agc agc aaa aca ttg	302
Asn Val Glu Lys Pro Val Lys Met Leu Ile Tyr Ser Ser Lys Thr Leu	
62 67 72 77	
gaa ctg cga gag acc tca gtc aca cca agt aac ctg tgg ggc ggc cag	350
Glu Leu Arg Glu Thr Ser Val Thr Pro Ser Asn Leu Trp Gly Gly Gln	
78 83 88 93	
ggc tta ttg gga gtg agc att cgt ttc tgc agc ttt gat ggg gca aat	398
Gly Leu Leu Gly Val Ser Ile Arg Phe Cys Ser Phe Asp Gly Ala Asn	
94 99 104 109	
gaa aat gtt tgg cat gtg ctg gag gtg gaa tca aat tct cct gca gca	446
Glu Asn Val Trp His Val Leu Glu Val Glu Ser Asn Ser Pro Ala Ala	
110 115 120 125	
ctg gca ggt ctt aga cca cac agt gat tat ata att gga gca gat aca	494
Leu Ala Gly Leu Arg Pro His Ser Asp Tyr Ile Ile Gly Ala Asp Thr	
126 131 136 141	
gtc atg aat gag tct gaa gat cta ttc agc ctt atc gaa aca cat gaa	542
Val Met Asn Glu Ser Glu Asp Leu Phe Ser Leu Ile Glu Thr His Glu	
142 147 152 157	
gca aaa cca ttg aaa ctg tat gtg tac aac aca gac act gat aac tgt	590
Ala Lys Pro Leu Lys Leu Tyr Val Tyr Asn Thr Asp Thr Asp Asn Cys	
158 163 168 173	
cga gaa gtg att att aca cca aat tct gca tgg ggt gga gaa ggc agc	638
Arg Glu Val Ile Ile Thr Pro Asn Ser Ala Trp Gly Gly Glu Gly Ser	
174 179 184 189	
cta gga tgt ggc att gga tat ggt tat ttg cat cga ata cct aca cgc	686
Leu Gly Cys Gly Ile Gly Tyr Gly Tyr Leu His Arg Ile Pro Thr Arg	
190 195 200 205	
cca ttt gag gaa gga aag aaa att tct ctt cca gga caa atg gct ggt	734
Pro Phe Glu Glu Gly Lys Lys Ile Ser Leu Pro Gly Gln Met Ala Gly	
206 211 216 221	
aca cct att aca cct ctt aaa gat ggg ttt aca gag gtc cag ctg tcc	782
Thr Pro Ile Thr Pro Leu Lys Asp Gly Phe Thr Glu Val Gln Leu Ser	
222 227 232 237	
tca gtt aat ccc ccg tct ttg tca cca cca gga act aca gga att gaa	830
Ser Val Asn Pro Pro Ser Leu Ser Pro Pro Gly Thr Thr Gly Ile Glu	
238 243 248 253	

cag agt ctg act gga ctt tct att agc tca act cca cca gct gtc agt	878
Gln Ser Leu Thr Gly Leu Ser Ile Ser Ser Thr Pro Pro Ala Val Ser	
254 259 264 269	
agt gtt ctc agt aca ggt gta cca aca gta ccg tta ttg cca cca caa	926
Ser Val Leu Ser Thr Gly Val Pro Thr Val Pro Leu Leu Pro Pro Gln	
270 275 280 285	
gta aac cag tcc ctc act tct gtg cca cca atg aat cca gct act aca	974
Val Asn Gln Ser Leu Thr Ser Val Pro Pro Met Asn Pro Ala Thr Thr	
286 291 296 301	
tta cca ggt ctg atg cct tta cca gca gga ctg ccg aac ctc ccc aac	1022
Leu Pro Gly Leu Met Pro Leu Pro Ala Gly Leu Pro Asn Leu Pro Asn	
302 307 312 317	
ctc aac ctc cgc ctc cca gca cca cac atc atg cca ggg gtt ggc tta	1070
Leu Asn Leu Arg Leu Pro Ala Pro His Ile Met Pro Gly Val Gly Leu	
318 323 328 333	
cca gaa ctt gta aac cca ggt ctg cca cct ctt cct tcc atg cct ccc	1118
Pro Glu Leu Val Asn Pro Gly Leu Pro Pro Leu Pro Ser Met Pro Pro	
334 339 344 349	
cga aac tta cct ggc att gca cct ctc ccc ctg cca tcc gag ttc ctc	1166
Arg Asn Leu Pro Gly Ile Ala Pro Leu Pro Leu Pro Ser Glu Phe Leu	
350 355 360 365	
ccg tca ttc ccc ttg gtt cca gag agc tct tct gca gca agc tca gga	1214
Pro Ser Phe Pro Leu Val Pro Glu Ser Ser Ser Ala Ala Ser Ser Gly	
366 371 376 381	
gag ctg ctg tct tcc ctc ccg ccc acc agc aac gca ccc tct gac cct	1262
Glu Leu Leu Ser Ser Leu Pro Pro Thr Ser Asn Ala Pro Ser Asp Pro	
382 387 392 397	
gcc aca act act gca aag gca gac gct gcc tcc tca ctc act gtg gat	1310
Ala Thr Thr Thr Ala Lys Ala Asp Ala Ala Ser Ser Leu Thr Val Asp	
398 403 408 413	
gtg acg ccc ccc act gcc aag gcc ccc acc acc gtt gag gac aga gtc	1358
Val Thr Pro Pro Thr Ala Lys Ala Pro Thr Thr Val Glu Asp Arg Val	
414 419 424 429	
ggc gac tcc acc cca gtc agc gag aag cct gtt tct gcg gct gtg gat	1406
Gly Asp Ser Thr Pro Val Ser Glu Lys Pro Val Ser Ala Ala Val Asp	
430 435 440 445	
gcc aat gct tct gag tca cct taa ctttgaacca ttctttggaa ttggcgtggt	1460
Ala Asn Ala Ser Glu Ser Pro *	
446 451	
atatttaacc acgggagcgt gtctggaaac gcaaaactatc attaatattca tactagtttg	1520
taccgtatct gtaggcattcc tgtaaataat tccaagggga aaactaaacg aggacgtggg	1580
ttgtatcctg ccagggttgag tggggctcac acgctagggt gagatgtcag aaagcgcttg	1640

tattttaaac aacaaaaaag aattgtaagg gtggcttgct gccaggcttg cactgccgtt 1700
cctgggggtg tgcattctcg ggaaaggtgg tggcggggcg tccactaggt ttctgtccc 1760
ctgctgctcc ttccgtaaga aaatgaaata ttctatgcct aatactcaca cgcaacattt 1820
cttgtaacttt gtaagtcggt tgcgagaatg cagaccacct cactaaactg taaacggtaa 1880
agagattttt acttttggtc tccgtgagtc gcatctctac taaggtttac acaggaattc 1940
cacctgaaga cttgtgttaa agttctacag cgcgcaactgt taactgaacg tctttttctt 2000
cagcctatac gcggatcctt gttttgagct ctgagaatca ctgagacaac attttgtaac 2060
tgctgctggt gctttctaca tacaccttat aaagtgacat ttcaaaagaa ataaggtgcc 2120
acagttttta accagaaggt ggcaactctgt ggctccttgt agtattatag ctatactggg 2180
aaagcataga tacagcaata aagtacagta atttt 2215

<210> 258
<211> 2074
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (169)..(585)

<400> 258
tttgaattct gagagcgtac gaaggcccta ccggaccgga attcccgggt cgacgatttc 60
gtccgccatc accaccgcga cccgttcggg gtttcgtgcc tgccgcgagc ccaccaccag 120
gtgcgctggc gcgcggacgg cccttccttg gagaagctgc ctgtgcac atg ggc ctg 177
Met Gly Leu
1
gtg atc acc gag gtg gag cag gaa ccc agc ttc tcg gac atc gag agc 225
Val Ile Thr Glu Val Glu Gln Glu Pro Ser Phe Ser Asp Ile Glu Ser
4 9 14 19
ctc gtg gtg tgg tgt atg gcc gtg ggc atc tcc tac att agc gtc tac 273
Leu Val Val Trp Cys Met Ala Val Gly Ile Ser Tyr Ile Ser Val Tyr
20 25 30 35
gac cac qaa ggt att ttc aaa aga aat aat tcc aga ttg atg gat gga 321
Asp His Gln Gly Ile Phe Lys Arg Asn Asn Ser Arg Leu Met Asp Gly
36 41 46 51
att tta aaa caa cag caa gaa ctt ctg ggc cta gat tgt tca aaa tgc 369
Ile Leu Lys Gln Gln Gln Glu Leu Leu Gly Leu Asp Cys Ser Lys Cys
52 57 62 67

tca cca gag ttt gca aat agt aat gac aaa gat gat caa gtt tta aat	417
Ser Pro Glu Phe Ala Asn Ser Asn Asp Lys Asp Asp Gln Val Leu Asn	
68 73 78 83	
tgc cat ttg gca gtg aag gtg cta tcc ccg gaa gat gga aaa gca gat	465
Cys His Leu Ala Val Lys Val Leu Ser Pro Glu Asp Gly Lys Ala Asp	
84 89 94 99	
att gtg aga gcc gct cag gac ttt tgc cag tta gta gcc cag aag caa	513
Ile Val Arg Ala Ala Gln Asp Phe Cys Gln Leu Val Ala Gln Lys Gln	
100 105 110 115	
agg aga ccc aaa gat ttg gat gta gat atg tta gtt tac tca gtt caa	561
Arg Arg Pro Lys Asp Leu Asp Val Asp Met Leu Val Tyr Ser Val Gln	
116 121 126 131	
atg gtt gtc ctg atc ctg att tag tactgaagtt cggctcctgtg gacagcacac	615
Met Val Val Leu Ile Leu Ile *	
132 137	
gaggctttct tacctggcac atcagattga ctgagattgt ctctttgcct tcccatctaa	675
acatcagtta tgaggacttt ttctctgccc ttctgtcatta tgcagcctgt gaacagcgtc	735
tgaggaaagtc gtggtcattg gttgcataat tccatttgag cttatggagg aaaggaccaa	795
gtgactctga ttttagaaaag cacctatgaa accctgtaca cacctatgaa accctgtaca	855
cacctagttc ataattttca taatttatca acaaacacaa aaaagtgtct tacttgagag	915
tgagtgtgtg cgtgtgtgcg tgcacacatg tgcacgtttg tatgtgtgga aataaacata	975
aatggggacg tgttgagaa ggaaatacat agacctacaa ctttgagcat atagcagtga	1035
tgttttagga actgaaatgt cacacttaat aaagtcttca gccagctac ttccctattt	1095
ttgtggggag aagagggcct gattagaact gttctggttg tgtttggcgg gaggggaata	1155
atttttgttc agtccttctt agtgacccaa ctttaatttt taagaataat atattgactt	1215
actgaactga agcattctga gttgaaagga gctccagagg agtggagtgc tgtgttgctc	1275
acatgttaaa atcttgctca ccttcagagc agagggaata cctatcttca gatataccgc	1335
cattttcatc tottaattgt agtcaaaagt atgacttgag agtgttgctc tggattctg	1395
ggttctgaag tctggtattc tggattctg ggttcaaaag tatgacttga gagtgttgct	1455
ctggtattct gagagttgct ctgtattctg ggttctgaag attatttgaa aaataactcc	1515
tactacattg aaatgcagac ttaaaaattt aaacattgga ttaggcagtc aaaaaacca	1575
agcaagcata aaaggtcaat aagttgtaat cttgatagta aaggtggaaa acttattata	1635
aatggaaaga aagttttatt tccttttttg tttgatgggc agtatgcat attataccca	1695

aagttctttt aaaaaatatt tccatcaacc atttttattt aaaataaaca tttgagggaa 1755
gttaccaagg cagctttttt cctcaaaagt aacctgttcc tctttggaat agcacatttt 1815
aggggcatgg ttaatacctg agattttttac tcagtaaadc ctgatgggta ctgtgtgtaa 1875
aatatcttta agtaggattg aaggcctctg tgggggaata aaatattacc aaagtctata 1935
aaaataaatt ttacatgttc tcttttatga cagagagcag cactgggttct gttattttta 1995
aaatgaataa ttgatttctt gatagggtgtt taatatttct tccctcactg atggattcta 2055
ggtaggaacc attcttata 2074

<210> 259
<211> 7313
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (13) .. (6147)

<400> 259
cgtgggtttgt ag atg tgc ttg ggg aga atg ggg gcc tct tct cca aga 48
Met Cys Leu Gly Arg Met Gly Ala Ser Ser Pro Arg
1 5 10
agc ccg gag cct gtc ggg ccg ccg gcg ccc ggt ctc ccc ttc tgc tgc 96
Ser Pro Glu Pro Val Gly Pro Pro Ala Pro Gly Leu Pro Phe Cys Cys
13 18 23 28
gga gga tcc ctg ctg gcg gtt gtg gtg ctg ctt gcg ctg ccg gtg gcc 144
Gly Gly Ser Leu Leu Ala Val Val Val Leu Leu Ala Leu Pro Val Ala
29 34 39 44
tgg ggt caa tgc aat gcc cca gaa tgg ctt cca ttt gcc agg cct acc 192
Trp Gly Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr
45 50 55 60
aac cta act gat gag ttt gag ttt ccc att ggg aca tat ctg aac tat 240
Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr
61 66 71 76
gaa tgc cgc cct ggt tat tcc gga aga ccg ttt tct atc atc tgc cta 288
Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu
77 82 87 92
aaa aac tca gtc tgg act ggt gct aag gac agg tgc aga cgt aaa tca 336
Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser
93 98 103 108
tgt cgt aat cct cca gat cct gtg aat ggc atg gtg cat gtg atc aaa 384
Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys

109	114	119	124	
ggc atc cag ttc gga tcc caa att aaa tat tct tgt act aaa gga tac				432
Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr				
125	130	135	140	
cga ctc att ggt tcc tcg tct gcc aca tgc atc atc tca ggt gat act				480
Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr				
141	146	151	156	
gtc att tgg gat aat gaa aca cct att tgt gac aga att cct tgt ggg				528
Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly				
157	162	167	172	
cta ccc ccc acc atc acc aat gga gat ttc att agc acc aac aga gag				576
Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu				
173	178	183	188	
aat ttt cac tat gga tca gtg gtg acc tac cgc tgc aat cct gga agc				624
Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser				
189	194	199	204	
gga ggg aga aag gtg ttt gag ctt gtg ggt gag ccc tcc ata tac tgc				672
Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys				
205	210	215	220	
acc agc aat gac gat caa gtg ggc atc tgg agc ggc ccc gcc cct cag				720
Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln				
221	226	231	236	
tgc att ata cct aac aaa tgc acg cct cca aat gtg gaa aat gga ata				768
Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile				
237	242	247	252	
ttg gta tct gac aac aga agc tta ttt tcc tta aat gaa gtt gtg gag				816
Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu				
253	258	263	268	
ttt agg tgt cag cct ggc ttt gtc atg aaa gga ccc cgc cgt gtg aag				864
Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys				
269	274	279	284	
tgc cag gcc ctg aac aaa tgg gag ccg gag cta cca agc tgc tcc agg				912
Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg				
285	290	295	300	
gta tgt cag cca cct cca gat gtc ctg cat gct gag cgt acc caa agg				960
Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg				
301	306	311	316	
gac aag gac aac ttt tca cct ggg cag gaa gtg ttc tac agc tgt gag				1008
Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu				
317	322	327	332	
ccc ggc tac gac ctc aga ggg gct gcg tct atg cgc tgc aca ccc cag				1056
Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln				
333	338	343	348	

gga gac tgg agc cct gca gcc ccc aca tgt gaa gtg aaa tcc tgt gat	1104
Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp	
349 354 359 364	
gac ttc atg ggc caa ctt ctt aat ggc cgt gtg cta ttt cca gta aat	1152
Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn	
365 370 375 380	
ctc cag ctt gga gca aaa gtg gat ttt gtt tgt gat gaa gga ttt caa	1200
Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln	
381 386 391 396	
tta aaa ggc agc tct gct agt tac tgt gtc ttg gct gga atg gaa agc	1248
Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser	
397 402 407 412	
ctt tgg aat agc agt gtt cca gtg tgt gaa caa atc ttt tgt cca agt	1296
Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser	
413 418 423 428	
cct cca gtt att cct aat ggg aga cac aca gga aaa cct ctg gaa gtc	1344
Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val	
429 434 439 444	
ttt ccc ttt ggg aaa aca gta aat tac aca tgc gac ccc cac cca gac	1392
Phe Pro Phe Gly Lys Thr Val Asn Tyr Thr Cys Asp Pro His Pro Asp	
445 450 455 460	
aga ggg acg agc ttc gac ctc att gga gag agc acc atc cgc tgc aca	1440
Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr	
461 466 471 476	
agt gac cct caa ggg aat ggg gtt tgg agc agc cct gcc cct cgc tgt	1488
Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys	
477 482 487 492	
gga att ctg ggt cac tgt caa gcc cca gat cat ttt ctg ttt gcc aag	1536
Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys	
493 498 503 508	
ttg aaa acc caa acc aat gca tct gac ttt ccc att ggg aca tct tta	1584
Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu	
509 514 519 524	
aag tac gaa tgc cgt cct gag tac tac ggg agg cca ttc tct atc aca	1632
Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr	
525 530 535 540	
tgt cta gat aac ctg gtc tgg tca agt ccc aaa gat gtc tgt aaa cgt	1680
Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg	
541 546 551 556	
aaa tca tgt aaa act cct cca gat cca gtg aat ggc atg gtg cat gtg	1728
Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val	
557 562 567 572	

atc aca gac atc cag gtt gga tcc aga atc aac tat tct tgt act aca	1776
Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr	
573 578 583 588	
ggg cac cga ctc att ggt cac tca tct gct gaa tgt atc ctc tcg ggc	1824
Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly	
589 594 599 604	
aat gct gcc cat tgg agc acg aag ccg cca att tgt caa cga att cct	1872
Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro	
605 610 615 620	
tgt ggg cta ccc ccc acc atc gcc aat gga gat ttc att agc acc aac	1920
Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn	
621 626 631 636	
aga gag aat ttt cac tat gga tca gtg gtg acc tac cgc tgc aat ccc	1968
Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro	
637 642 647 652	
gga agc gga ggg aga aag gtg ttt gag ctt gtg ggt gag ccc tcc ata	2016
Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile	
653 658 663 668	
tac tgc acc agc aat gac gat caa gtg ggc atc tgg agc ggc ccg gcc	2064
Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala	
669 674 679 684	
cct cag tgc att ata cct aac aaa tgc acg cct cca aat gtg gaa aat	2112
Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn	
685 690 695 700	
gga ata ttg gta tct gac aac aga agc tta ttt tcc tta aat gaa gtt	2160
Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val	
701 706 711 716	
gtg gag ttt agg tgt cag cct ggc ttt gtc atg aaa gga ccc cgc cgt	2208
Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg	
717 722 727 732	
gtg aag tgc cag gcc ctg aac aaa tgg gag ccg gag cta cca agc tgc	2256
Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys	
733 738 743 748	
tcc agg gta tgt cag cca cct cca gat gtc ctg cat gct gag cgt acc	2304
Ser Arg Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr	
749 754 759 764	
caa agg gac aag gac aac ttt tca ccc ggg cag gaa gtg ttc tac agc	2352
Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser	
765 770 775 780	
tgt gag ccc ggc tat gac ctc aga ggg gct gcg tct atg cgc tgc aca	2400
Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr	
781 786 791 796	
ccc cag gga gac tgg agc cct gca gcc ccc aca tgt gaa gtg aaa tcc	2448

Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser	
797 802 807 812	
tgt gat gac ttc atg ggc caa ctt ctt aat ggc cgt gtg cta ttt cca	2496
Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro	
813 818 823 828	
gta aat ctc cag ctt gga gca aaa gtg gat ttt gtt tgt gat gaa gga	2544
Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly	
829 834 839 844	
ttt caa tta aaa ggc agc tct gct agt tat tgt gtc ttg gct gga atg	2592
Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met	
845 850 855 860	
gaa agc ctt tgg aat agc agt gtt cca gtg tgt gaa caa atc ttt tgt	2640
Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys	
861 866 871 876	
cca agt cct cca gtt att cct aat ggg aga cac aca gga aaa cct ctg	2688
Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu	
877 882 887 892	
gaa gtc ttt ccc ttt gga aaa gca gta aat tac aca tgc gac ccc cac	2736
Glu Val Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His	
893 898 903 908	
cca gac aga ggg acg agc ttc gac ctc att gga gag agc acc atc cgc	2784
Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg	
909 914 919 924	
tgc aca agt gac cct caa ggg aat ggg gtt tgg agc agc cct gcc cct	2832
Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro	
925 930 935 940	
cgc tgt gga att ctg ggt cac tgt caa gcc cca gat cat ttt ctg ttt	2880
Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe	
941 946 951 956	
gcc aag ttg aaa acc caa acc aat gca tct gac ttt ccc att ggg aca	2928
Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr	
957 962 967 972	
tct tta aag tac gaa tgc cgt cct gag tac tac ggg agg cca ttc tct	2976
Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser	
973 978 983 988	
atc aca tgt cta gat aac ctg gtc tgg tca agt ccc aaa gat gtc tgt	3024
Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys	
989 994 999 1004	
aaa cgt aaa tca tgt aaa act cct cca gat cca gtg aat ggc atg gtg	3072
Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val	
1005 1010 1015 1020	
cat gtg atc aca gac atc cag gtt gga tcc aga atc aac tat tct tgt	3120
His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys	

1021	1026	1031	1036	
act aca ggg cac cga ctc	att ggt cac tca tct	gct gaa tgt atc ctc	3168	
Thr Thr Gly His Arg Leu	Ile Gly His Ser Ser	Ala Glu Cys Ile Leu		
1037	1042	1047	1052	
tca ggc aat act gcc cat	tgg agc acg aag ccg	cca att tgt caa cga	3216	
Ser Gly Asn Thr Ala His	Trp Ser Thr Lys Pro	Pro Ile Cys Gln Arg		
1053	1058	1063	1068	
att cct tgt ggg cta ccc	cca acc atc gcc aat	gga gat ttc att agc	3264	
Ile Pro Cys Gly Leu Pro	Pro Thr Ile Ala Asn	Gly Asp Phe Ile Ser		
1069	1074	1079	1084	
acc aac aga gag aat ttt	cac tat gga tca gtg	gtg acc tac cgc tgc	3312	
Thr Asn Arg Glu Asn Phe	His Tyr Gly Ser Val	Val Thr Tyr Arg Cys		
1085	1090	1095	1100	
aat ctt gga agc aga ggg	aga aag gtg ttt gag	ctt gtg ggt gag ccc	3360	
Asn Leu Gly Ser Arg Gly	Arg Lys Val Phe Glu	Leu Val Gly Glu Pro		
1101	1106	1111	1116	
tcc ata tac tgc acc agc	aat gac gat caa gtg	ggc atc tgg agc ggc	3408	
Ser Ile Tyr Cys Thr Ser	Asn Asp Asp Gln Val	Gly Ile Trp Ser Gly		
1117	1122	1127	1132	
ccc gcc cct cag tgc att	ata cct aac aaa tgc	acg cct cca aat gtg	3456	
Pro Ala Pro Gln Cys Ile	Ile Pro Asn Lys Cys	Thr Pro Pro Asn Val		
1133	1138	1143	1148	
gaa aat gga ata ttg gta	tct gac aac aga agc	tta ttt tcc tta aat	3504	
Glu Asn Gly Ile Leu Val	Ser Asp Asn Arg Ser	Leu Phe Ser Leu Asn		
1149	1154	1159	1164	
gaa gtt gtg gag ttt agg	tgt cag cct ggc ttt	gtc atg aaa gga ccc	3552	
Glu Val Val Glu Phe Arg	Cys Gln Pro Gly Phe	Val Met Lys Gly Pro		
1165	1170	1175	1180	
cgc cgt gtg aag tgc cag	gcc ctg aac aaa tgg	gag cca gag tta cca	3600	
Arg Arg Val Lys Cys Gln	Ala Leu Asn Lys Trp	Glu Pro Glu Leu Pro		
1181	1186	1191	1196	
agc tgc tcc agg gtg tgt	cag ccg cct cca gaa	atc ctg cat ggt gag	3648	
Ser Cys Ser Arg Val Cys	Gln Pro Pro Pro Glu	Ile Leu His Gly Glu		
1197	1202	1207	1212	
cat acc cca agc cat cag	gac aac ttt tca cct	ggg cag gaa gtg ttc	3696	
His Thr Pro Ser His Gln	Asp Asn Phe Ser Pro	Gly Gln Glu Val Phe		
1213	1218	1223	1228	
tac agc tgt gag cct ggc	tat gac ctc aga ggg	gct gcg tct ctg cac	3744	
Tyr Ser Cys Glu Pro Gly	Tyr Asp Leu Arg Gly	Ala Ala Ser Leu His		
1229	1234	1239	1244	
tgc aca ccc cag gga gac	tgg agc cct gaa gcc	ccg aga tgt gca gtg	3792	
Cys Thr Pro Gln Gly Asp	Trp Ser Pro Glu Ala	Pro Arg Cys Ala Val		
1245	1250	1255	1260	

aaa tcc tgt gat gac ttc ttg ggt caa ctc cct cat ggc cgt gtg cta	3840
Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu	
1261 1266 1271 1276	
ttt cca ctt aat ctc cag ctt ggg gca aag gtg tcc ttt gtc tgt gat	3888
Phe Pro Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe Val Cys Asp	
1277 1282 1287 1292	
gaa ggg ttt cgc tta aag ggc agt tcc gtt agt cat tgt gtc ttg gtt	3936
Glu Gly Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val	
1293 1298 1303 1308	
gga atg aga agc ctt tgg aat aac agt gtt cct gtg tgt gaa cat atc	3984
Gly Met Arg Ser Leu Trp Asn Asn Ser Val Pro Val Cys Glu His Ile	
1309 1314 1319 1324	
ttt tgt cca aat cct cca gct atc ctt aat ggg aga cac aca gga act	4032
Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His Thr Gly Thr	
1325 1330 1335 1340	
ccc tct gga gat att ccc tat gga aaa gaa ata tct tac aca tgt gac	4080
Pro Ser Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp	
1341 1346 1351 1356	
ccc cac cca gac aga ggg atg acc ttc aac ctc att ggg gag agc acc	4128
Pro His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr	
1357 1362 1367 1372	
atc cgc tgc aca agt gac cct cat ggg aat ggg gtt tgg agc agc cct	4176
Ile Arg Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro	
1373 1378 1383 1388	
gcc cct cgc tgt gaa ctt tct gtt cgt gct ggt cac tgt aaa acc cca	4224
Ala Pro Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro	
1389 1394 1399 1404	
gag cag ttt cca ttt gcc agt cct acg atc cca att aat gac ttt gag	4272
Glu Gln Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu	
1405 1410 1415 1420	
ttt cca gtc ggg aca tct ttg aat tat gaa tgc cgt cct ggg tat ttt	4320
Phe Pro Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe	
1421 1426 1431 1436	
ggg aaa atg ttc tct atc tcc tgc cta gaa aac ttg gtc tgg tca agt	4368
Gly Lys Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser	
1437 1442 1447 1452	
gtt gaa gac aac tgt aga cga aaa tca tgt gga cct cca cca gaa ccc	4416
Val Glu Asp Asn Cys Arg Arg Lys Ser Cys Gly Pro Pro Pro Glu Pro	
1453 1458 1463 1468	
ttc aat gga atg gtg cat ata aac aca gat aca cag ttt gga tca aca	4464
Phe Asn Gly Met Val His Ile Asn Thr Asp Thr Gln Phe Gly Ser Thr	
1469 1474 1479 1484	

gtt	aat	tat	tct	tgt	aat	gaa	ggg	ttt	cga	ctc	att	ggg	tcc	cca	tct	4512
Val	Asn	Tyr	Ser	Cys	Asn	Glu	Gly	Phe	Arg	Leu	Ile	Gly	Ser	Pro	Ser	
1485					1490					1495					1500	
act	act	tgt	ctc	gtc	tca	ggc	aat	aat	gtc	aca	tgg	gat	aag	aag	gca	4560
Thr	Thr	Cys	Leu	Val	Ser	Gly	Asn	Asn	Val	Thr	Trp	Asp	Lys	Lys	Ala	
1501					1506					1511					1516	
cct	att	tgt	gag	atc	ata	tct	tgt	gag	cca	cct	cca	acc	ata	tcc	aat	4608
Pro	Ile	Cys	Glu	Ile	Ile	Ser	Cys	Glu	Pro	Pro	Pro	Thr	Ile	Ser	Asn	
1517					1522					1527					1532	
gga	gac	ttc	tac	agc	aac	aat	aga	aca	tct	ttt	cac	aat	gga	acg	gtg	4656
Gly	Asp	Phe	Tyr	Ser	Asn	Asn	Arg	Thr	Ser	Phe	His	Asn	Gly	Thr	Val	
1533					1538					1543					1548	
gta	act	tac	cag	tgc	cac	act	gga	cca	gat	gga	gaa	cag	ctg	ttt	gag	4704
Val	Thr	Tyr	Gln	Cys	His	Thr	Gly	Pro	Asp	Gly	Glu	Gln	Leu	Phe	Glu	
1549					1554					1559					1564	
ctt	gtg	gga	gaa	cgg	tca	ata	tat	tgc	acc	agc	aaa	gat	gat	caa	gtt	4752
Leu	Val	Gly	Glu	Arg	Ser	Ile	Tyr	Cys	Thr	Ser	Lys	Asp	Asp	Gln	Val	
1565					1570					1575					1580	
ggg	gtt	tgg	agc	agc	cct	ccc	cct	cgg	tgt	att	tct	act	aat	aaa	tgc	4800
Gly	Val	Trp	Ser	Ser	Pro	Pro	Pro	Arg	Cys	Ile	Ser	Thr	Asn	Lys	Cys	
1581					1586					1591					1596	
aca	gct	cca	gaa	gtt	gaa	aat	gca	att	aga	gta	cca	gga	aac	agg	agt	4848
Thr	Ala	Pro	Glu	Val	Glu	Asn	Ala	Ile	Arg	Val	Pro	Gly	Asn	Arg	Ser	
1597					1602					1607					1612	
ttc	ttt	tcc	ctc	act	gag	atc	atc	aga	ttt	aga	tgt	cag	ccc	ggg	ttt	4896
Phe	Phe	Ser	Leu	Thr	Glu	Ile	Ile	Arg	Phe	Arg	Cys	Gln	Pro	Gly	Phe	
1613					1618					1623					1628	
gtc	atg	gta	ggg	tcc	cac	act	gtg	cag	tgc	cag	acc	aat	ggc	aga	tgg	4944
Val	Met	Val	Gly	Ser	His	Thr	Val	Gln	Cys	Gln	Thr	Asn	Gly	Arg	Trp	
1629					1634					1639					1644	
ggg	ccc	aag	ctg	cca	cac	tgc	tcc	agg	gtg	tgt	cag	ccg	cct	cca	gaa	4992
Gly	Pro	Lys	Leu	Pro	His	Cys	Ser	Arg	Val	Cys	Gln	Pro	Pro	Pro	Glu	
1645					1650					1655					1660	
atc	ctg	cat	ggg	gag	cat	acc	cta	agc	cat	cag	gac	aac	ttt	tca	cct	5040
Ile	Leu	His	Gly	Glu	His	Thr	Leu	Ser	His	Gln	Asp	Asn	Phe	Ser	Pro	
1661					1666					1671					1676	
ggg	cag	gaa	gtg	ttc	tac	agc	tgt	gag	ccc	agc	tat	gac	ctc	aga	ggg	5088
Gly	Gln	Glu	Val	Phe	Tyr	Ser	Cys	Glu	Pro	Ser	Tyr	Asp	Leu	Arg	Gly	
1677																

1933	1938	1943	1948	
ctg gaa ggc agt ccc tgg agc cag tgc cag gcg gat gac aga tgg gac				5904
Leu Glu Gly Ser Pro Trp Ser Gln Cys Gln Ala Asp Asp Arg Trp Asp				
1949	1954	1959	1964	
cct cct ctg gcc aaa tgt acc tct cgt gca cat gat gct ctc ata gtt				5952
Pro Pro Leu Ala Lys Cys Thr Ser Arg Ala His Asp Ala Leu Ile Val				
1965	1970	1975	1980	
ggc act tta tct ggt acg atc ttc ttt att tta ctc atc att ttc ctc				6000
Gly Thr Leu Ser Gly Thr Ile Phe Phe Ile Leu Leu Ile Ile Phe Leu				
1981	1986	1991	1996	
tct tgg ata att cta aag cac aga aaa ggc aat aat gca cat gaa aac				6048
Ser Trp Ile Ile Leu Lys His Arg Lys Gly Asn Asn Ala His Glu Asn				
1997	2002	2007	2012	
cct aaa gaa gtg gct atc cat tta cat tct caa gga ggc agc agc gtt				6096
Pro Lys Glu Val Ala Ile His Leu His Ser Gln Gly Gly Ser Ser Val				
2013	2018	2023	2028	
cat ccc cga act ctg caa aca aat gaa gaa aat agc agg gtc ctt cct				6144
His Pro Arg Thr Leu Gln Thr Asn Glu Glu Asn Ser Arg Val Leu Pro				
2029	2034	2039	2044	
tga caaa gtactataca gctgaagaac atctogaata caattttggt gggaaaggag				6201
*				
2045				
ccaattgatt tcaacagaat cagatctgag cttcataaag tctttgaagt gacttcacag				6261
agacgcagac atgtgcactt gaagatgctg ccccttcctt ggtacctagc aaagctcctg				6321
cctctttgtg tgcgtcactg tgaaaccccc acccttctgc ctggtgctaa acgcacacag				6381
tatctagtca ggggaaaaga ctgcatttag gagatagaaa atagtttgga ttacttaaag				6441
gaataagggtg ttgcctggaa tttctgggtt gtaagggtggt cactgttctt ttttaaaata				6501
tttgtaatat ggaatgggct cagtaagaag agcttggaag atgcagaaag ttatgaaaaa				6561
taagtcactt ataattatgc tacctactga taacctctcc taatattttg attcattttc				6621
tgcctatctt ctttcacatg tgttttttta catacgtact tttccccctt agtttgtttc				6681
cttttatttt atagagcaga accctagtct tttaaacagt ttagagtgaag atatatgcta				6741
tatcagtttt tactttctct agggagaaaa attaattttac tagaaaggca tgaaatgatc				6801
atgggaagag tgggtaagac tactgaagag aaatattttg aaaataagat ttcgatatct				6861
tctttttttt tgagatggag tctggctctg tctcccaggc tggagtgcag tggcgtaatc				6921
tgggctcact gcaacgtccg cctcccgggt tcacaccatt ctctgcctc agcctcctga				6981
gtagctggga ctataggccc ccgccaccat gcctagctaa tttttttgta tttttagtag				7041

agacagggtt tcaccgtgtt agccaggctg gtctcgatct cctgacctcg tgatctgccc 7101
gccttggcct cccaaagtgc tgggattaca ggcattgagca ccacacctgg cccatgtcca 7161
catattctaa acatcagaaa acaacaaata cattgtagtt ctgttcaaatt ttctacttct 7221
aaagttatgt gtgcaactag ggacacactg agatttatgg agaaaaggat aaaagcaaag 7281
atttaaaatt acatgctaga ctttagtaaca ta 7313

<210> 260
<211> 5473
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(4482)

<400> 260

atg aga ata gca cag gaa aga ccc acc gcc atg agt aaa gga att gtg 48
Met Arg Ile Ala Gln Glu Arg Pro Thr Ala Met Ser Lys Gly Ile Val
1 5 10

gga gtg atg gtg ttt gta cat gct cga aat gcc act gta aga aca gct 96
Gly Val Met Val Phe Val His Ala Arg Asn Ala Thr Val Arg Thr Ala
17 22 27 32

atg tct cta ata gaa aga gca aaa aat tgt ggc cat att ccc ttc ttt 144
Met Ser Leu Ile Glu Arg Ala Lys Asn Cys Gly His Ile Pro Phe Phe
33 38 43 48

ttt cct acc caa gga cat gac tat gta ctt gca gaa aaa cag gta caa 192
Phe Pro Thr Gln Gly His Asp Tyr Val Leu Ala Glu Lys Gln Val Gln
49 54 59 64

agg tcg aga aat aag caa gta cga gaa tta ttc cca gat ggt ttt agt 240
Arg Ser Arg Asn Lys Gln Val Arg Glu Leu Phe Pro Asp Gly Phe Ser
65 70 75 80

att cat cat gca gga atg ctt cgg cag gac aga aat tta gtt gaa aac 288
Ile His His Ala Gly Met Leu Arg Gln Asp Arg Asn Leu Val Glu Asn
81 86 91 96

ttg ttt tct aat ggg cat atc aaa gtc cta gtg tgt aca gct acg tta 336
Leu Phe Ser Asn Gly His Ile Lys Val Leu Val Cys Thr Ala Thr Leu
97 102 107 112

gcc tgg ggt gtc aat ctt ccc gcc cat gct gtt att att aag gga aca 384
Ala Trp Gly Val Asn Leu Pro Ala His Ala Val Ile Ile Lys Gly Thr
113 118 123 128

caa ata tat gct gca aaa aga ggc tcc ttt gtt gac ctt gga att tta 432

Gln Ile Tyr Ala Ala Lys Arg Gly Ser Phe Val Asp Leu Gly Ile Leu	
129 134 139 144	
gat gtc atg cag ata ttt ggt cga gct gga cga cca caa ttt gac aaa	480
Asp Val Met Gln Ile Phe Gly Arg Ala Gly Arg Pro Gln Phe Asp Lys	
145 150 155 160	
ttt ggg gaa gga ata att ata aca acg cat gat aaa ctc agc cat tac	528
Phe Gly Glu Gly Ile Ile Ile Thr Thr His Asp Lys Leu Ser His Tyr	
161 166 171 176	
ctc act ttg ctc act caa cga aac cca att gag agt cag ttt ctg gaa	576
Leu Thr Leu Leu Thr Gln Arg Asn Pro Ile Glu Ser Gln Phe Leu Glu	
177 182 187 192	
agc ctt gca gat aac cta aat gca gag att gct ctg gga aca gtt act	624
Ser Leu Ala Asp Asn Leu Asn Ala Glu Ile Ala Leu Gly Thr Val Thr	
193 198 203 208	
aat gtg gaa gaa gca gtg aag tgg ata agt tac act tat ctt tat gta	672
Asn Val Glu Glu Ala Val Lys Trp Ile Ser Tyr Thr Tyr Leu Tyr Val	
209 214 219 224	
cgg atg aga gca aat cca tta gca tat ggc atc agt cac aag gct tat	720
Arg Met Arg Ala Asn Pro Leu Ala Tyr Gly Ile Ser His Lys Ala Tyr	
225 230 235 240	
cag att gac cca aca tta aga aag cat cga gaa cag ttg gtc att gaa	768
Gln Ile Asp Pro Thr Leu Arg Lys His Arg Glu Gln Leu Val Ile Glu	
241 246 251 256	
gtt gga cga aaa cta gac aaa gct cag atg att cgt ttt gag gag cga	816
Val Gly Arg Lys Leu Asp Lys Ala Gln Met Ile Arg Phe Glu Glu Arg	
257 262 267 272	
act gga tat ttt tcc tca act gat ttg ggt aga act gcc agc cat tac	864
Thr Gly Tyr Phe Ser Ser Thr Asp Leu Gly Arg Thr Ala Ser His Tyr	
273 278 283 288	
tat att aaa tac aac acc att gag acc ttt aat gaa ctc ttt gat gct	912
Tyr Ile Lys Tyr Asn Thr Ile Glu Thr Phe Asn Glu Leu Phe Asp Ala	
289 294 299 304	
cac aaa aca gaa ggt gat atc ttt gcc ata gtc tcc aaa gct gaa gaa	960
His Lys Thr Glu Gly Asp Ile Phe Ala Ile Val Ser Lys Ala Glu Glu	
305 310 315 320	
ttt gat caa att aag gtc aga gaa gag gaa ata gag gag tta gat acc	1008
Phe Asp Gln Ile Lys Val Arg Glu Glu Glu Ile Glu Glu Leu Asp Thr	
321 326 331 336	
tta tta agc aat ttt tgt gaa ctc tcc act cct gga ggt gta gag aat	1056
Leu Leu Ser Asn Phe Cys Glu Leu Ser Thr Pro Gly Gly Val Glu Asn	
337 342 347 352	
agt tat ggg aaa ata aac atc tta ctt caa act tat atc agc cga gga	1104
Ser Tyr Gly Lys Ile Asn Ile Leu Leu Gln Thr Tyr Ile Ser Arg Gly	

353	358	363	368	
gaa atg gac agt ttc tcc ctt ata tca gat tct gca tat gtt gca cag				1152
Glu Met Asp Ser Phe Ser Leu Ile Ser Asp Ser Ala Tyr Val Ala Gln				
369	374	379	384	
aat gca gct aga att gtc cgt gct ctt ttt gaa att gct ctg agg aaa				1200
Asn Ala Ala Arg Ile Val Arg Ala Leu Phe Glu Ile Ala Leu Arg Lys				
385	390	395	400	
cgt tgg cct acc atg acc tac agg ctc ctg aat ctt agt aaa gtc att				1248
Arg Trp Pro Thr Met Thr Tyr Arg Leu Leu Asn Leu Ser Lys Val Ile				
401	406	411	416	
gac aag agg ctt tgg ggt tgg gct agc cct ttg aga caa ttt tca atc				1296
Asp Lys Arg Leu Trp Gly Trp Ala Ser Pro Leu Arg Gln Phe Ser Ile				
417	422	427	432	
cta cca cca cac atc cta aca aga tta gaa gaa aaa aag ctt act gtg				1344
Leu Pro Pro His Ile Leu Thr Arg Leu Glu Glu Lys Lys Leu Thr Val				
433	438	443	448	
gat aag ctg aaa gac atg agg aaa gat gaa ata ggt cac att tta cat				1392
Asp Lys Leu Lys Asp Met Arg Lys Asp Glu Ile Gly His Ile Leu His				
449	454	459	464	
cat gtg aat att gga ctg aag gtc aaa caa tgt gtt cat cag att cct				1440
His Val Asn Ile Gly Leu Lys Val Lys Gln Cys Val His Gln Ile Pro				
465	470	475	480	
tct gtt atg atg gaa gca ttc att cag cct atc aca agg act gtc ctc				1488
Ser Val Met Met Glu Ala Phe Ile Gln Pro Ile Thr Arg Thr Val Leu				
481	486	491	496	
cga gtg aca ctc agc atc tat gct gat ttc act tgg aat gat cag gta				1536
Arg Val Thr Leu Ser Ile Tyr Ala Asp Phe Thr Trp Asn Asp Gln Val				
497	502	507	512	
cat ggg aca gta gga gaa cct tgg tgg att tgg gta gaa gat cct aca				1584
His Gly Thr Val Gly Glu Pro Trp Trp Ile Trp Val Glu Asp Pro Thr				
513	518	523	528	
aat gat cat att tat cat tca gag tat ttt cta gct cta aaa aaa caa				1632
Asn Asp His Ile Tyr His Ser Glu Tyr Phe Leu Ala Leu Lys Lys Gln				
529	534	539	544	
gtc att agt aaa gaa gcc caa cta ctg gta ttt aca atc cct att ttt				1680
Val Ile Ser Lys Glu Ala Gln Leu Leu Val Phe Thr Ile Pro Ile Phe				
545	550	555	560	
gag cct ttg cct tcc caa tac tac atc cga gca gtg tct gat aga tgg				1728
Glu Pro Leu Pro Ser Gln Tyr Tyr Ile Arg Ala Val Ser Asp Arg Trp				
561	566	571	576	
ttg ggt gct gag gca gta tgt att atc aac ttt caa cat cta att cta				1776
Leu Gly Ala Glu Ala Val Cys Ile Ile Asn Phe Gln His Leu Ile Leu				
577	582	587	592	

cca gag aga cat cct cct cat aca gaa tta ctg gat ctt cag cct tta	1824
Pro Glu Arg His Pro Pro His Thr Glu Leu Leu Asp Leu Gln Pro Leu	
593 598 603 608	
cca atc aca gct ttg gga tgt aaa gca tat gaa gcc ctg tac aac ttc	1872
Pro Ile Thr Ala Leu Gly Cys Lys Ala Tyr Glu Ala Leu Tyr Asn Phe	
609 614 619 624	
agc cac ttt aac cct gta cag aca caa ata ttt cat aca ttg tat cac	1920
Ser His Phe Asn Pro Val Gln Thr Gln Ile Phe His Thr Leu Tyr His	
625 630 635 640	
acg gat tgt aat gtc cta ctt gga gca cct act gga tcg gga aag act	1968
Thr Asp Cys Asn Val Leu Leu Gly Ala Pro Thr Gly Ser Gly Lys Thr	
641 646 651 656	
gtt gca gct gaa tta gcc att ttc aga gtc ttc aac aaa tac cct act	2016
Val Ala Ala Glu Leu Ala Ile Phe Arg Val Phe Asn Lys Tyr Pro Thr	
657 662 667 672	
tca aag gcg gta tat att gca ccc cta aaa gcc cta gta cgt gaa aga	2064
Ser Lys Ala Val Tyr Ile Ala Pro Leu Lys Ala Leu Val Arg Glu Arg	
673 678 683 688	
atg gat gat tgg aaa gtt aga ata gaa gaa aaa ctt ggt aaa aaa gtt	2112
Met Asp Asp Trp Lys Val Arg Ile Glu Glu Lys Leu Gly Lys Lys Val	
689 694 699 704	
att gaa cta aca ggg gat gtg act cct gat atg aaa tcc att gcc aag	2160
Ile Glu Leu Thr Gly Asp Val Thr Pro Asp Met Lys Ser Ile Ala Lys	
705 710 715 720	
gct gac ctt atc gtc act acg cca gag aag tgg gat gga gtc agc aga	2208
Ala Asp Leu Ile Val Thr Pro Glu Lys Trp Asp Gly Val Ser Arg	
721 726 731 736	
agc tgg caa aat agg aac tat gtt cag caa gtc act att ctc atc ata	2256
Ser Trp Gln Asn Arg Asn Tyr Val Gln Gln Val Thr Ile Leu Ile Ile	
737 742 747 752	
gat gag atc cat ctg ctt ggg gag gaa aga ggc cct gtt cta gag gtc	2304
Asp Glu Ile His Leu Leu Gly Glu Glu Arg Gly Pro Val Leu Glu Val	
753 758 763 768	
att gta tct cga aca aat ttt atc tca tca cac aca gaa aag cct gtt	2352
Ile Val Ser Arg Thr Asn Phe Ile Ser Ser His Thr Glu Lys Pro Val	
769 774 779 784	
aga ata gtt gga cta tct act gca tta gct aat gcc aga gac ctt gct	2400
Arg Ile Val Gly Leu Ser Thr Ala Leu Ala Asn Ala Arg Asp Leu Ala	
785 790 795 800	
gat tgg ctc aat att aag cag atg ggc ttg ttt aac ttc cga cca tca	2448
Asp Trp Leu Asn Ile Lys Gln Met Gly Leu Phe Asn Phe Arg Pro Ser	
801 806 811 816	

gta cgc cca gtt cca ctg gaa gtt cac att caa ggc ttt cca ggt caa	2496
Val Arg Pro Val Pro Leu Glu Val His Ile Gln Gly Phe Pro Gly Gln	
817 822 827 832	
cat tac tgt cct cgt atg gct agt atg aac aag cct gca ttt cag gca	2544
His Tyr Cys Pro Arg Met Ala Ser Met Asn Lys Pro Ala Phe Gln Ala	
833 838 843 848	
att aga agc cat tct cca gcc aaa cct gtt ttg ata ttt gtc tca tca	2592
Ile Arg Ser His Ser Pro Ala Lys Pro Val Leu Ile Phe Val Ser Ser	
849 854 859 864	
aga cgt caa act cgt ctt act gct ttg gaa ttg atc gcc ttc ctg gct	2640
Arg Arg Gln Thr Arg Leu Thr Ala Leu Glu Leu Ile Ala Phe Leu Ala	
865 870 875 880	
act gaa gaa gat cca aag cag tgg tta aac atg gat gaa aga gag atg	2688
Thr Glu Glu Asp Pro Lys Gln Trp Leu Asn Met Asp Glu Arg Glu Met	
881 886 891 896	
gag aac atc att gca aca gta aga gat tcc aac ctc aag ctg acc ctt	2736
Glu Asn Ile Ile Ala Thr Val Arg Asp Ser Asn Leu Lys Leu Thr Leu	
897 902 907 912	
gct ttc ggg ata gga atg cat cat gct gga cta cat gag agg gac cga	2784
Ala Phe Gly Ile Gly Met His His Ala Gly Leu His Glu Arg Asp Arg	
913 918 923 928	
aaa aca gta gag gaa cta ttt gta aac tgt aaa gtt cag gtt ctt att	2832
Lys Thr Val Glu Glu Leu Phe Val Asn Cys Lys Val Gln Val Leu Ile	
929 934 939 944	
gct aca agc aca tta gcc tgg ggt gta aac ttt cca gct cat tta gta	2880
Ala Thr Ser Thr Leu Ala Trp Gly Val Asn Phe Pro Ala His Leu Val	
945 950 955 960	
att att aag gga aca gaa tac tat gat gga aaa aca aga cgt tat gtg	2928
Ile Ile Lys Gly Thr Glu Tyr Tyr Asp Gly Lys Thr Arg Arg Tyr Val	
961 966 971 976	
gat ttt ccc att aca gat gtc ctc cag atg atg ggg cgt gct ggg agg	2976
Asp Phe Pro Ile Thr Asp Val Leu Gln Met Met Gly Arg Ala Gly Arg	
977 982 987 992	
ccg cag ttc gat gac caa ggc aaa gct gta att cta gtt cat gac ata	3024
Pro Gln Phe Asp Asp Gln Gly Lys Ala Val Ile Leu Val His Asp Ile	
993 998 1003 1008	
aag aaa gac ttt tat aaa aaa ttt ctt tat gaa cct ttc cca gta gaa	3072
Lys Lys Asp Phe Tyr Lys Lys Phe Leu Tyr Glu Pro Phe Pro Val Glu	
1009 1014 1019 1024	
tca agt tta tta gga gtg ctc tct gac cac tta aat gca gag att gct	3120
Ser Ser Leu Leu Gly Val Leu Ser Asp His Leu Asn Ala Glu Ile Ala	
1025 1030 1035 1040	
ggg ggt aca att aca tct aag caa gat gca ttg gat tat atc acc tgg	3168

Gly	Gly	Thr	Ile	Thr	Ser	Lys	Gln	Asp	Ala	Leu	Asp	Tyr	Ile	Thr	Trp	
1041					1046					1051					1056	
act	tac	ttt	ttc	cga	cgt	ctt	atc	atg	aat	ccc	agc	tat	tac	aat	ttg	3216
Thr	Tyr	Phe	Phe	Arg	Arg	Leu	Ile	Met	Asn	Pro	Ser	Tyr	Tyr	Asn	Leu	
1057					1062					1067					1072	
ggt	gat	gtg	agc	cat	gat	tct	gtg	aac	aag	ttt	ctg	tcc	cat	ctg	att	3264
Gly	Asp	Val	Ser	His	Asp	Ser	Val	Asn	Lys	Phe	Leu	Ser	His	Leu	Ile	
1073					1078					1083					1088	
gag	aag	tcc	ctg	att	gaa	ttg	gaa	ctt	tcc	tac	tgt	att	gaa	att	gga	3312
Glu	Lys	Ser	Leu	Ile	Glu	Leu	Glu	Leu	Ser	Tyr	Cys	Ile	Glu	Ile	Gly	
1089					1094					1099					1104	
gag	gat	aat	cgc	agc	att	gaa	cct	cta	act	tat	ggc	cga	att	gcc	tcc	3360
Glu	Asp	Asn	Arg	Ser	Ile	Glu	Pro	Leu	Thr	Tyr	Gly	Arg	Ile	Ala	Ser	
1105					1110					1115					1120	
tat	tac	tat	ttg	aag	cat	caa	aca	gtt	aaa	atg	ttc	aag	gac	cgc	ttg	3408
Tyr	Tyr	Tyr	Leu	Lys	His	Gln	Thr	Val	Lys	Met	Phe	Lys	Asp	Arg	Leu	
1121					1126					1131					1136	
aag	cct	gaa	tgc	agt	act	gaa	gaa	ctg	ctt	tca	att	cta	agt	gat	gca	3456
Lys	Pro	Glu	Cys	Ser	Thr	Glu	Glu	Leu	Leu	Ser	Ile	Leu	Ser	Asp	Ala	
1137					1142					1147					1152	
gaa	gaa	tat	aca	gat	ttg	cca	gtg	aga	cac	aat	gaa	gat	cat	atg	aat	3504
Glu	Glu	Tyr	Thr	Asp	Leu	Pro	Val	Arg	His	Asn	Glu	Asp	His	Met	Asn	
1153					1158					1163					1168	
agt	gaa	ctg	gca	aaa	tgt	ctt	ccc	att	gaa	tca	aat	cct	cat	tca	ttt	3552
Ser	Glu	Leu	Ala	Lys	Cys	Leu	Pro	Ile	Glu	Ser	Asn	Pro	His	Ser	Phe	
1169					1174					1179					1184	
gac	agc	cct	cac	acc	aaa	gca	cat	ctc	ctg	cta	cag	gca	cat	ctc	agc	3600
Asp	Ser	Pro	His	Thr	Lys	Ala	His	Leu	Leu	Leu	Gln	Ala	His	Leu	Ser	
1185					1190					1195					1200	
cga	gcc	atg	cta	ccc	tgc	cca	gat	tat	gac	act	gat	acc	aaa	aca	gtc	3648
Arg	Ala	Met	Leu	Pro	Cys	Pro	Asp	Tyr	Asp	Thr	Asp	Thr	Lys	Thr	Val	
1201					1206					1211					1216	
ttg	gac	caa	gct	ctc	aga	gta	tgt	cag	gca	atg	ctg	gac	gtg	gct	gca	3696
Leu	Asp	Gln	Ala	Leu	Arg	Val	Cys	Gln	Ala	Met	Leu	Asp	Val	Ala	Ala	
1217					1222					1227					1232	
aac	cag	ggc	tgg	ctg	gtg	act	gtc	ctg	aat	atc	acc	aac	ctg	att	cag	3744
Asn	Gln	Gly	Trp	Leu	Val	Thr	Val	Leu	Asn	Ile	Thr	Asn	Leu	Ile	Gln	
1233					1238					1243					1248	

1265	1270	1275	1280	
att atg aag ggc cca cat gct agg ggt cgg act tcc atc gag tgc ctt				3888
Ile Met Lys Gly Pro His Ala Arg Gly Arg Thr Ser Ile Glu Cys Leu				
1281	1286	1291	1296	
cct gaa ctg atc cat gcc tgt gga ggg aaa gac cat gta ttt agc tcc				3936
Pro Glu Leu Ile His Ala Cys Gly Gly Lys Asp His Val Phe Ser Ser				
1297	1302	1307	1312	
atg gta gaa agt gag cta cat gct gca aaa acg aaa cag gca tgg aat				3984
Met Val Glu Ser Glu Leu His Ala Ala Lys Thr Lys Gln Ala Trp Asn				
1313	1318	1323	1328	
ttc tta tct cac ttg cca gtg ata aat gtt ggc ata agt gtt aaa ggc				4032
Phe Leu Ser His Leu Pro Val Ile Asn Val Gly Ile Ser Val Lys Gly				
1329	1334	1339	1344	
tcg tgg gat gac tta gtt gaa gga cat aat gaa ctc tct gtc tca act				4080
Ser Trp Asp Asp Leu Val Glu Gly His Asn Glu Leu Ser Val Ser Thr				
1345	1350	1355	1360	
ctg act gca gac aaa cga gat gac aac aaa tgg atc aaa ttg cat gct				4128
Leu Thr Ala Asp Lys Arg Asp Asp Asn Lys Trp Ile Lys Leu His Ala				
1361	1366	1371	1376	
gac caa gag tat gtg ctt caa gtg agc ttg cag aga gtc cac ttt ggg				4176
Asp Gln Glu Tyr Val Leu Gln Val Ser Leu Gln Arg Val His Phe Gly				
1377	1382	1387	1392	
ttc cac aag gga aag cca gag agc tgt gca gtt act cct cga ttt ccc				4224
Phe His Lys Gly Lys Pro Glu Ser Cys Ala Val Thr Pro Arg Phe Pro				
1393	1398	1403	1408	
aaa tca aaa gac gaa gga tgg ttt ttg ata tta gga gaa gtg gat aag				4272
Lys Ser Lys Asp Glu Gly Trp Phe Leu Ile Leu Gly Glu Val Asp Lys				
1409	1414	1419	1424	
aga gaa ctt att gct ttg aaa aga gta gga tat att cga aat cat cat				4320
Arg Glu Leu Ile Ala Leu Lys Arg Val Gly Tyr Ile Arg Asn His His				
1425	1430	1435	1440	
gtt gct tcc ctt tct ttt tat acc cct gaa ata cct gga agg tat atc				4368
Val Ala Ser Leu Ser Phe Tyr Thr Pro Glu Ile Pro Gly Arg Tyr Ile				
1441	1446	1451	1456	
tac aca tta tat ttc atg agt gac tgc tac ctt ggc ctg gac cag cag				4416
Tyr Thr Leu Tyr Phe Met Ser Asp Cys Tyr Leu Gly Leu Asp Gln Gln				
1457	1462	1467	1472	
tat gac aat cta tct caa cgt tac aca agc gag tct ttc tgc aca ggt				4464
Tyr Asp Asn Leu Ser Gln Arg Tyr Thr Ser Glu Ser Phe Cys Thr Gly				
1473	1478	1483	1488	
caa cac caa ggt ctc tga ttccct gactgacctg gcattaaagt aacttgacct				4518
Gln His Gln Gly Leu *				
1489	1494			

gaacaatcca tttgaaagga gtggctaaga attctctctg ttcagtcac tagacaaatc 4578
 gaattacttg atgtttgcct tgaaagaatc aacttctaac ctcaaccatc caggaaattg 4638
 acagtggctg cagtattgac tccagtgaca taaagttaac cacagtggcc ttttaacaaa 4698
 tgttgccttt tataatgtta tctttatgag tttcttgata tgtaagatga aaaagcattt 4758
 agaataatct ttttaattgt gtatatattg gatgatattt aggagctatc aatcaaattt 4818
 tacatctcac aatgtactgt ttacatggat attggctgct ttttttaagg aaaaccacat 4878
 tgagatgtga caagtgttag gacttgtcac agatttctaa ctctgccgca taaactataa 4938
 atctgtaagg tggtagacag cgtgtcttgt tagcaaaatt tatactttga tatgatcaca 4998
 tgtagaagta gcttcaagaa tttctttag tcataaatgt ttaataatat atgatgtaa 5058
 attatattat ggagcctaata gatgataaca aagaaaacaa tatactgatc ttagaaaatg 5118
 tagacatggt taactgggaa ataaaatata gaggggcact tcaagacaag ctgactcaat 5178
 gttttctttc tgcttccctt taaataatat ccccttactc atctgttctt cttttctttc 5238
 ccttctactt caaggcttta tttctattat ctttctgaca tatttattta cagaagtaga 5298
 gaagtataat ctaattcatg ttgtagcact tacagatcat atagtacaat tatttgtctt 5358
 tatgctctcc aggaaaaatc tgagacagaa aatttttcac ccctatggat aggatttcgc 5418
 ctgtaataaa gaaaatttct aaatgtccaa acaaaaaaaaa aaacaaaaaa aaaaa 5473

<210> 261
 <211> 2392
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (49) .. (2274)

<400> 261

atttggccct cgaggccaag aattcggcac gagagcagtt gggccaag atg gcg gcc 57
 Met Ala Ala
 1

gcc gag gga ccg gtg ggc gac ggc gag ctg tgg cag acc tgg ctt cct 105
 Ala Glu Gly Pro Val Gly Asp Gly Glu Leu Trp Gln Thr Trp Leu Pro
 4 9 14 19

aac cac gtc gtg ttc ttg cgg ctc cgg gag gga ctg aaa aac cag agt 153
 Asn His Val Val Phe Leu Arg Leu Arg Glu Gly Leu Lys Asn Gln Ser
 20 25 30 35

cca acc gaa gct gag aaa cca gct tct tcg tcg ttg cct tcg tcg ccg	201
Pro Thr Glu Ala Glu Lys Pro Ala Ser Ser Leu Pro Ser Ser Pro	
36 41 46 51	
ccg ccg cag ttg ctg acg aga aac gtg gtc ttt ggc ctc ggc gga gag	249
Pro Pro Gln Leu Leu Thr Arg Asn Val Val Phe Gly Leu Gly Gly Glu	
52 57 62 67	
ctt ttc ctg tgg gac gga gaa gac agc tcc ttc tta gtc gtt cgc ctt	297
Leu Phe Leu Trp Asp Gly Glu Asp Ser Ser Phe Leu Val Val Arg Leu	
68 73 78 83	
cgg ggc ccc agc ggc ggc ggc gaa gag ccc gcc ctg tcc cag tac cag	345
Arg Gly Pro Ser Gly Gly Gly Glu Glu Pro Ala Leu Ser Gln Tyr Gln	
84 89 94 99	
aga ttg ctt tgc ata aat cca ccc ctg ttt gaa atc tat caa gtc ttg	393
Arg Leu Leu Cys Ile Asn Pro Pro Leu Phe Glu Ile Tyr Gln Val Leu	
100 105 110 115	
tta agc cca aca caa cat cat gta gca ctt ata gga ata aaa gga ctt	441
Leu Ser Pro Thr Gln His His Val Ala Leu Ile Gly Ile Lys Gly Leu	
116 121 126 131	
atg gta tta gaa tta cct aaa aga tgg ggg aag aat tct gaa ttt gaa	489
Met Val Leu Glu Leu Pro Lys Arg Trp Gly Lys Asn Ser Glu Phe Glu	
132 137 142 147	
ggt gga aaa tca aca gtg aat tgt agt acc act cca gtt gcg gag aga	537
Gly Gly Lys Ser Thr Val Asn Cys Ser Thr Thr Pro Val Ala Glu Arg	
148 153 158 163	
ttt ttc acc agt tcc acc tct ctg act cta aag cat gct gca tgg tat	585
Phe Phe Thr Ser Ser Thr Ser Leu Thr Leu Lys His Ala Ala Trp Tyr	
164 169 174 179	
cca agt gaa atc ctg gat ccc cac gta gtg ctg tta aca tca gac aac	633
Pro Ser Glu Ile Leu Asp Pro His Val Val Leu Leu Thr Ser Asp Asn	
180 185 190 195	
gta atc aga att tac tca cta cgt gag ccg cag aca ccc act aac gtg	681
Val Ile Arg Ile Tyr Ser Leu Arg Glu Pro Gln Thr Pro Thr Asn Val	
196 201 206 211	
ata ata ctt tca gaa gcc gaa gag gaa agt cta gta ctc aat aaa gga	729
Ile Ile Leu Ser Glu Ala Glu Glu Glu Ser Leu Val Leu Asn Lys Gly	
212 217 222 227	
agg gcg tat acc gca tct cta gga gag aca gca gtt gca ttt gac ttt	777
Arg Ala Tyr Thr Ala Ser Leu Gly Glu Thr Ala Val Ala Phe Asp Phe	
228 233 238 243	
ggg cca ttg gca gca gtc cca aag act cta ttt gga caa aac ggc aaa	825
Gly Pro Leu Ala Ala Val Pro Lys Thr Leu Phe Gly Gln Asn Gly Lys	
244 249 254 259	

gat gaa gta gtg gca tac cca ctg tac atc tta tat gaa aat gga gag	873
Asp Glu Val Val Ala Tyr Pro Leu Tyr Ile Leu Tyr Glu Asn Gly Glu	
260 265 270 275	
act ttc ctg aca tac atc agt ctg tta cac agc cct gga aat att tgg	921
Thr Phe Leu Thr Tyr Ile Ser Leu Leu His Ser Pro Gly Asn Ile Trp	
276 281 286 291	
aaa gct gtt ggg tcc att gcc cat gca tct gcg gct gaa gat aac tat	969
Lys Ala Val Gly Ser Ile Ala His Ala Ser Ala Ala Glu Asp Asn Tyr	
292 297 302 307	
ggg tat gat gcg tgt gct gta ctc tgc tta ccc tgt gtc ccc aat atc	1017
Gly Tyr Asp Ala Cys Ala Val Leu Cys Leu Pro Cys Val Pro Asn Ile	
308 313 318 323	
tta gtg atc gct act gaa tca gga atg ctg tat cac tgt gtc gtg cta	1065
Leu Val Ile Ala Thr Glu Ser Gly Met Leu Tyr His Cys Val Val Leu	
324 329 334 339	
gaa ggg gaa gaa gaa gat gac cac acg tca gaa aag tcc tgg gat tcc	1113
Glu Gly Glu Glu Glu Asp Asp His Thr Ser Glu Lys Ser Trp Asp Ser	
340 345 350 355	
agg att gac ctc att cct tct ctg tat gtg ttt gaa tgt gtt gag ttg	1161
Arg Ile Asp Leu Ile Pro Ser Leu Tyr Val Phe Glu Cys Val Glu Leu	
356 361 366 371	
gag ctt gct ttg aaa ctg gca tct gga gag gat gac cct ttt gat tct	1209
Glu Leu Ala Leu Lys Leu Ala Ser Gly Glu Asp Asp Pro Phe Asp Ser	
372 377 382 387	
gac ttt tct tgt cca gtc aaa ctt cat aga gat ccc aag tgt cct tca	1257
Asp Phe Ser Cys Pro Val Lys Leu His Arg Asp Pro Lys Cys Pro Ser	
388 393 398 403	
aga tat cac tgt act cat gaa gct ggt gta cat agt gtt ggg cta act	1305
Arg Tyr His Cys Thr His Glu Ala Gly Val His Ser Val Gly Leu Thr	
404 409 414 419	
tgg att cat aaa ctt cac aaa ttt ctt gga tca gat gaa gaa gat aag	1353
Trp Ile His Lys Leu His Lys Phe Leu Gly Ser Asp Glu Glu Asp Lys	
420 425 430 435	
gat agt tta cag gaa ctc tct aca gaa cag aaa tgc ttt gtt gaa cac	1401
Asp Ser Leu Gln Glu Leu Ser Thr Glu Gln Lys Cys Phe Val Glu His	
436 441 446 451	
atc ctt tgt acg agg cca ttg ccc tgc agg cag cca gct cca att cga	1449
Ile Leu Cys Thr Arg Pro Leu Pro Cys Arg Gln Pro Ala Pro Ile Arg	
452 457 462 467	
gga ttt tgg att gta cct gac att ctg gga ccc acg atg atc tgc atc	1497
Gly Phe Trp Ile Val Pro Asp Ile Leu Gly Pro Thr Met Ile Cys Ile	
468 473 478 483	
acc agt acc tat gaa tgc ctc ata tgg ccg tta tta agt aca gtc cat	1545

708	713	718	723	
cat ata agg gaa atg gtg aag caa atc aat gat atc cgc aat cat gta				2265
His Ile Arg Glu Met Val Lys Gln Ile Asn Asp Ile Arg Asn His Val				
724	729	734	739	
aac ttc tga caccacc aggagctgac tcacacctga actgaacacc attgaaggct				2321
Asn Phe *				
740				
taaacccata ttgtaaaaca ggtagaatta totaatttat aaaaagggtgt tttgatgaca				2381
aaaaaaaaa a				2392

<210> 262
 <211> 5006
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (464)..(3427)

<400> 262	
tcagtgtggt ggaattccac agagtatatc agtcctatcc agctcattac cgatgaatgt	60
gagaataact tacatggcta atagtagtag agtatctctc ctgggttttt cttttcttca	120
agtgcattata gctaaatata ttctgggaac acttagaact tgctaattca gtattgctac	180
ttttacagat gagcctgaag tcttgacaga acctccaagt gccacaacca ctactaccat	240
aggtatatct gcaacctgga caactttggc aggttctcat ggtaaaagaa ataataccat	300
aactacaacc agttcaaaga ggaaaaacag gaaaaataaa attactccag aaaacgttca	360
aattatattt gatgatccac taccaatttc atacagtcag ccagagaagg tgaatggaga	420
gtccaagagc agcagtagca gcgagagtgg ggacagtgat aac atg agg att tcc	475
	Met Arg Ile Ser
	1
agc tgc agc gat gaa agt agt aac agc aac agc agt cgt aag agt gac	523
Ser Cys Ser Asp Glu Ser Ser Asn Ser Asn Ser Ser Arg Lys Ser Asp	
5 10 15 20	
aat cat tca cca gct gtg gtc act acc act gtg agc agc aaa aag cag	571
Asn His Ser Pro Ala Val Val Thr Thr Thr Val Ser Ser Lys Lys Gln	
21 26 31 36	
cca tca gtt gtt gtt aca ttt cca aag gaa gag aga aaa tct gtt tct	619
Pro Ser Val Leu Val Thr Phe Pro Lys Glu Glu Arg Lys Ser Val Ser	
37 42 47 52	

ggc aag gct tca ata aaa ttg tca gaa act atc agt gaa ggg acc agt Gly Lys Ala Ser Ile Lys Leu Ser Glu Thr Ile Ser Glu Gly Thr Ser 53 58 63 68	667
aat tct cta tct act tgt aca aaa tct ggt cca tct ccc ctt tct tct Asn Ser Leu Ser Thr Cys Thr Lys Ser Gly Pro Ser Pro Leu Ser Ser 69 74 79 84	715
cca aat ggg aag tta aca gta gca agt cct aag cgt ggg caa aag agg Pro Asn Gly Lys Leu Thr Val Ala Ser Pro Lys Arg Gly Gln Lys Arg 85 90 95 100	763
gaa gaa gga tgg aaa gaa gtt gta aga agg tca aag aaa gta tct gtt Glu Glu Gly Trp Lys Glu Val Val Arg Arg Ser Lys Lys Val Ser Val 101 106 111 116	811
cca tca act gtg ata tcc aga gtg att gga aga gga ggc tgt aat atc Pro Ser Thr Val Ile Ser Arg Val Ile Gly Arg Gly Gly Cys Asn Ile 117 122 127 132	859
aat gct att cgg gag ttt act ggt gca cac ata gat att gat aaa cag Asn Ala Ile Arg Glu Phe Thr Gly Ala His Ile Asp Ile Asp Lys Gln 133 138 143 148	907
aaa gac aag act gga gac cgg ata atc act ata agg ggt ggc act gaa Lys Asp Lys Thr Gly Asp Arg Ile Ile Thr Ile Arg Gly Gly Thr Glu 149 154 159 164	955
tca aca aga caa gca act caa ttg att aat gct ttg atc aag gat cca Ser Thr Arg Gln Ala Thr Gln Leu Ile Asn Ala Leu Ile Lys Asp Pro 165 170 175 180	1003
gac aaa gaa att gat gaa ctt att cca aag aat cgt ttg aaa agc tcc Asp Lys Glu Ile Asp Glu Leu Ile Pro Lys Asn Arg Leu Lys Ser Ser 181 186 191 196	1051
tca gca aat tcc aaa ata ggg tca tca gca cct acc acc act gct gct Ser Ala Asn Ser Lys Ile Gly Ser Ser Ala Pro Thr Thr Thr Ala Ala 197 202 207 212	1099
aac act tcc tta atg gga att aaa atg aca act gta gct ctg tca tca Asn Thr Ser Leu Met Gly Ile Lys Met Thr Thr Val Ala Leu Ser Ser 213 218 223 228	1147
aca tct caa act gcc aca gca ctc act gtg cct gca att tct tct gca Thr Ser Gln Thr Ala Thr Ala Leu Thr Val Pro Ala Ile Ser Ser Ala 229 234 239 244	1195
tcc act cac aaa acc att aag aac cca gtg aat aat gtg agg cct ggt Ser Thr His Lys Thr Ile Lys Asn Pro Val Asn Asn Val Arg Pro Gly 245 250 255 260	1243
ttt cca gtt tct ctt cca tta gca tat cct cct cca cag ttt gca cat Phe Pro Val Ser Leu Pro Leu Ala Tyr Pro Pro Pro Gln Phe Ala His 261 266 271 276	1291
gct ttg ctt gct gct cag act ttc cag cag atc cgt cca cca agg ttg	1339

Ala Leu Leu Ala Ala Gln Thr Phe Gln Gln Ile Arg Pro Pro Arg Leu	
277	282 287 292
ccc atg acc cac ttt gga ggt act ttt cca cca gct caa tcc act tgg	1387
Pro Met Thr His Phe Gly Gly Thr Phe Pro Pro Ala Gln Ser Thr Trp	
293	298 303 308
ggt ccg ttt cct gtc agg cct ttg agc cct gcc aga gct act aac tcg	1435
Gly Pro Phe Pro Val Arg Pro Leu Ser Pro Ala Arg Ala Thr Asn Ser	
309	314 319 324
cct aag cct cac atg gtg cct cgc cat agc aat caa aat agc agt ggt	1483
Pro Lys Pro His Met Val Pro Arg His Ser Asn Gln Asn Ser Ser Gly	
325	330 335 340
tct cag gtg aat tca gca ggt tct tta act tca agc cca aca act aca	1531
Ser Gln Val Asn Ser Ala Gly Ser Leu Thr Ser Ser Pro Thr Thr Thr	
341	346 351 356
acc agt tca tca gct tca acg gtg cct ggt aca tct aca aat ggc agt	1579
Thr Ser Ser Ser Ala Ser Thr Val Pro Gly Thr Ser Thr Asn Gly Ser	
357	362 367 372
cca agt tca cct tct gtc cga agg cag ctt ttt gtc aca gtt gtg aag	1627
Pro Ser Ser Pro Ser Val Arg Arg Gln Leu Phe Val Thr Val Val Lys	
373	378 383 388
aca tcc aat gcc acc aca aca aca gtc aca acc acg gca agc aac aac	1675
Thr Ser Asn Ala Thr Thr Thr Thr Val Thr Thr Thr Ala Ser Asn Asn	
389	394 399 404
aac act gca ccc aca aat gcc aca tat cct atg cct act gcc aaa gaa	1723
Asn Thr Ala Pro Thr Asn Ala Thr Tyr Pro Met Pro Thr Ala Lys Glu	
405	410 415 420
cac tat cca gta tca tcc cca tct tcc cca tca cca cca gcc cag cca	1771
His Tyr Pro Val Ser Ser Pro Ser Ser Pro Ser Pro Pro Ala Gln Pro	
421	426 431 436
gga ggg gtt tct aga aac agc cct ttg gat tgt gga tca gca tct cca	1819
Gly Gly Val Ser Arg Asn Ser Pro Leu Asp Cys Gly Ser Ala Ser Pro	
437	442 447 452
aat aaa gtg gca tct tcc tcc gaa cag gaa gca ggt agt cca cca gta	1867
Asn Lys Val Ala Ser Ser Ser Glu Gln Glu Ala Gly Ser Pro Pro Val	
453	458 463 468
gta gaa aca aca aac act aga cct cca aac agc agc agt tct tct ggg	1915
Val Glu Thr Thr Asn Thr Arg Pro Pro Asn Ser Ser Ser Ser Ser Gly	
469	474 479 484
agt tca tca gct cat tct aat cag caa caa cct ccg gga tct gtt tct	1963
Ser Ser Ser Ala His Ser Asn Gln Gln Gln Pro Pro Gly Ser Val Ser	
485	490 495 500
cag gaa cca aga cca cct ctt cag cag tct cag gtt cct ccc ccg gaa	2011
Gln Glu Pro Arg Pro Pro Leu Gln Gln Ser Gln Val Pro Pro Pro Glu	

501	506	511	516	
gtt aga atg act gtt cct cct tta gca aca agt tct gct cca gtg gcg				2059
Val Arg Met Thr Val Pro Pro Leu Ala Thr Ser Ser Ala Pro Val Ala				
517	522	527	532	
gtg cct tct act gcc cca gtg act tac cct atg cct cag aca cca atg				2107
Val Pro Ser Thr Ala Pro Val Thr Tyr Pro Met Pro Gln Thr Pro Met				
533	538	543	548	
gga tgc ccc cag cct act cct aaa atg gaa acc cct gct att aga cca				2155
Gly Cys Pro Gln Pro Thr Pro Lys Met Glu Thr Pro Ala Ile Arg Pro				
549	554	559	564	
ccc cct cat ggc aca act gcc cct cac aag aat tca gct tca gtg caa				2203
Pro Pro His Gly Thr Thr Ala Pro His Lys Asn Ser Ala Ser Val Gln				
565	570	575	580	
aat tca tct gtt gca gtc ctc agt gtc aat cac att aaa aga cct cac				2251
Asn Ser Ser Val Ala Val Leu Ser Val Asn His Ile Lys Arg Pro His				
581	586	591	596	
agt gtt ccc tct tct gtc cag cta cct tcg acc tta agt aca caa agt				2299
Ser Val Pro Ser Ser Val Gln Leu Pro Ser Thr Leu Ser Thr Gln Ser				
597	602	607	612	
gct tgt cag aat tca gta cat cca gca aat aag cct att gct ccc aat				2347
Ala Cys Gln Asn Ser Val His Pro Ala Asn Lys Pro Ile Ala Pro Asn				
613	618	623	628	
ttc agt gcc ccc tta cca ttt ggg ccc ttt agc aca ttg ttt gaa aac				2395
Phe Ser Ala Pro Leu Pro Phe Gly Pro Phe Ser Thr Leu Phe Glu Asn				
629	634	639	644	
agc cct act tct gct cat gcc ttc tgg gga gga tct gtt gtt tca tct				2443
Ser Pro Thr Ser Ala His Ala Phe Trp Gly Gly Ser Val Val Ser Ser				
645	650	655	660	
cag tca aca cca gaa tct atg cta tca gga aaa tcc tca tat ttg cca				2491
Gln Ser Thr Pro Glu Ser Met Leu Ser Gly Lys Ser Ser Tyr Leu Pro				
661	666	671	676	
aat tca gat cct tta cat cag tct gat act tcc aaa gct cca ggt ttt				2539
Asn Ser Asp Pro Leu His Gln Ser Asp Thr Ser Lys Ala Pro Gly Phe				
677	682	687	692	
aga cca cca tta cag aga cct gct cca agt ccc tca ggt att gtc aat				2587
Arg Pro Pro Leu Gln Arg Pro Ala Pro Ser Pro Ser Gly Ile Val Asn				
693	698	703	708	
atg gac tcg cca tat ggt tct gta aca cct tct tca aca cat ttg gga				2635
Met Asp Ser Pro Tyr Gly Ser Val Thr Pro Ser Ser Thr His Leu Gly				
709	714	719	724	
aac ttt gct tca aac att tca gga ggt cag atg tac gga cct ggg gca				2683
Asn Phe Ala Ser Asn Ile Ser Gly Gly Gln Met Tyr Gly Pro Gly Ala				
725	730	735	740	

ccc ctt gga gga gca ccc gca gct gct aac ttt aac aga caa cat ttt	2731
Pro Leu Gly Gly Ala Pro Ala Ala Ala Asn Phe Asn Arg Gln His Phe	
741 746 751 756	
tcc ccg ctt agt ttg ttg act ccg tgt tca tca gca tca aat gat tct	2779
Ser Pro Leu Ser Leu Leu Thr Pro Cys Ser Ser Ala Ser Asn Asp Ser	
757 762 767 772	
tct gca cag tca gta tcc tcg gga gtt cgt gca cca tct cct gcc cca	2827
Ser Ala Gln Ser Val Ser Ser Gly Val Arg Ala Pro Ser Pro Ala Pro	
773 778 783 788	
tca tca gta ccg tta ggg tca gaa aag ccc agc aat gtg tct cag gac	2875
Ser Ser Val Pro Leu Gly Ser Glu Lys Pro Ser Asn Val Ser Gln Asp	
789 794 799 804	
agg aaa gtt cca gtc cct att ggg act gaa cgt tct gca cgt atc agg	2923
Arg Lys Val Pro Val Pro Ile Gly Thr Glu Arg Ser Ala Arg Ile Arg	
805 810 815 820	
caa act gga acg tca gct cca tct gtt att ggg agc aat ttg tct aca	2971
Gln Thr Gly Thr Ser Ala Pro Ser Val Ile Gly Ser Asn Leu Ser Thr	
821 826 831 836	
tca gta gga cat agt ggc atc tgg tcc ttt gaa ggg att ggt ggc aat	3019
Ser Val Gly His Ser Gly Ile Trp Ser Phe Glu Gly Ile Gly Gly Asn	
837 842 847 852	
caa gac aaa gta gac tgg tgt aac cct ggg atg gga aat cct atg atc	3067
Gln Asp Lys Val Asp Trp Cys Asn Pro Gly Met Gly Asn Pro Met Ile	
853 858 863 868	
cac aga ccg atg tct gac cca gga gta ttt tca caa cat caa gca atg	3115
His Arg Pro Met Ser Asp Pro Gly Val Phe Ser Gln His Gln Ala Met	
869 874 879 884	
gag cga gat agt aca gga att gta act cct tct ggt aca ttc cat cag	3163
Glu Arg Asp Ser Thr Gly Ile Val Thr Pro Ser Gly Thr Phe His Gln	
885 890 895 900	
cat gtt cct gca ggc tac atg gac ttt cct aaa gtt ggg ggt atg cct	3211
His Val Pro Ala Gly Tyr Met Asp Phe Pro Lys Val Gly Gly Met Pro	
901 906 911 916	
ttt tct gtg tat ggg aat gca atg att cct cca gta gca cct atc cct	3259
Phe Ser Val Tyr Gly Asn Ala Met Ile Pro Pro Val Ala Pro Ile Pro	
917 922 927 932	
gat ggt gct gga gga ccc ata ttt aat ggc cct cat gct gca gac cct	3307
Asp Gly Ala Gly Gly Pro Ile Phe Asn Gly Pro His Ala Ala Asp Pro	
933 938 943 948	
tct tgg aac tca ctg ata aag atg gtt tcc agc tcc acg gaa aat aat	3355
Ser Trp Asn Ser Leu Ile Lys Met Val Ser Ser Ser Thr Glu Asn Asn	
949 954 959 964	

ggc cct caa acg gtg tgg act gga ccc tgg gca cct cac atg aac agt	3403
Gly Pro Gln Thr Val Trp Thr Gly Pro Trp Ala Pro His Met Asn Ser	
965 970 975 980	
gtg cat atg aac cag ctt ggc tga tgaggatcag cttggttagcc tgcagattcc	3457
Val His Met Asn Gln Leu Gly *	
981 986	
ttttcatttg gaggaatca caagtggccg aaaaaaaaaa ttatgctccc aaatcattct	3517
actgatgtgc ttgactgaag tgtgtaggct ttttgcagaa gatcttacta actgacctat	3577
tttctgtgaa catttgtgac tgcccattcc ccatcatcat ccgttttacc ttagttagca	3637
tttttcttat catttttctt tttttcttcc cctcttcccc tttggacata actttctggt	3697
gaagctgttc tttggctggt tggttttagt actgtaaact gcttctgagc aaacacggaa	3757
atthagcaaa attatgtaaa cttgatcctg aagttttaga atggcaaata aatgtacaat	3817
tgtttacata acagaaaagg ctaagcagaa agtaaatttc aatatgtcag tatagaggct	3877
ctactttatg tagacttaaa ttaatgtgag atatgtacct tcatattcag aaatctggat	3937
gtttccttca tacattaaac tattaataag cataactttt ctactgggtg aatttaagta	3997
taaagtaaaa taatgggcat tatcattgga tgtttcccca cattggcttt taaaataccc	4057
atcttgcttt ctttttggtt tatttgtagc aaggcacata tagaagaaga aatttctggc	4117
ttttccatgt tgttttatta ccttttctca cttttaaaac taatacagac ttatctcttc	4177
actccttttt ctctccttac ctttaccact aataccagta aaattatctt tctgatagtg	4237
aaaaggttct gtcaagattt tcaactgtaat ggctgtaca gagatggacc atcttcatca	4297
tcaccagtgg tttcttctaa ttataaaatg tttaaacttt ctgagaattt aaaaagccac	4357
cactgttccc agtcagcata tacaagctct taatattctg tttattaaat aattcaatgt	4417
actattttat attggatgat attgattctt aacattggct tttcagtcac caacagtcaa	4477
cataaaaatt tcaattttca gtaatttagt ggaaaatata ttatttcttt tttcaatttt	4537
aaaggcttcc tgctttttta cccttgtata ttatcagtga aaaggatcaa cagttaattt	4597
gagccaagta ataaaagaaa ttctgcattt gtcacgaaga caatttatgg tagacagata	4657
aatacacaga ttacagtga aagtctccat ttaacctgtt tataaaagat acaaggccac	4717
actaaactac tcagtgggat ttatatattc catccacttg aaacaataaa cagtaatgta	4777
tccaagaaga ttatgtgtcc taccctgtct catggaaaaa ttaattatat ggttgaaatg	4837
taaaagaaag taagcataaa aatcgagtaa tgtatatata aaaaaaaaag tcgatcggcc	4897
gcgaagttag tagtagtagc gacagctcta gaggatccaa gcttacgtac gcgtgcatgc	4957

gacgtcatta gctcttctat agtgtcacct aaattcaatt gacgagatg

5006

<210> 263
<211> 1878
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (616)..(1686)

<220>
<221> misc_feature
<222> (1)...(1878)
<223> n = a,t,c or g

<400> 263

```

agcctgnggg gnnnnaaatc gagagcactt cnagnngncn ggaattcgtg gattcctggc      60
tccagaaaaat gggcttggag cggggggccac gttgaggaag gcgaagggca ttgtgggggc      120
gttatgtaaa agtaggaccc caaccgacag atcctattgc tcgcgccacc tgggcgcgcg      180
gagctttgct cgtttactat tgaaaaagtt ccagcgcggg aaactgaacc cggagctttg      240
cgcacgccc agccctcaag taatgtgggt tgtggttttt gttgttgttg tcgccacgca      300
tgcgtcttcg tgccgtgtgg ctatttgatt gtgtcaactc ttctgattag aatggcgcca      360
ttttgcggta cggaagctac acagcaacac gtataggaga ctctccccga gatcttctag      420
ggagtgaccc atctatTTTT gtttggaag aggaaactcc gaaatgggat cgcggaagac      480
ttaaagggcc aggctgattt ttttttcta ctgcaggtct ctgaggctgt ggttgctaca      540
gggtcaccac gagcttggct tacttgtctc atccttccct tgcttggat cattttctca      600
gttctcccaa aagcc atg tcc cgg ccc ttg ctc atc acc ttc acc cca gcc      651
          Met Ser Arg Pro Leu Leu Ile Thr Phe Thr Pro Ala
          1              5              10

act gac ccc agc gac ctc tgg aag gat ggg cag cag cag cca cag ccc      699
Thr Asp Pro Ser Asp Leu Trp Lys Asp Gly Gln Gln Gln Pro Gln Pro
13              18              23              28

gag aag cca gag tcc acc ctg gat ggg gct gca gcc cga gct ttc tat      747
Glu Lys Pro Glu Ser Thr Leu Asp Gly Ala Ala Ala Arg Ala Phe Tyr
29              34              39              44

gag gcc ctg att ggg gat gag agc agc gct cct gac tcc cag aga tct      795
Glu Ala Leu Ile Gly Asp Glu Ser Ser Ala Pro Asp Ser Gln Arg Ser
45              50              55              60

```

cag act gaa cct gcc aga gaa aga aag aga aaa aaa aaa aaa acg	843
Gln Thr Glu Pro Ala Arg Glu Arg Lys Arg Lys Lys Lys Lys Thr	
61 66 71 76	
aag gca cca gca gca gaa gca gtg gca gaa gga gca tca gga aga cat	891
Lys Ala Pro Ala Ala Glu Ala Val Ala Glu Gly Ala Ser Gly Arg His	
77 82 87 92	
gga caa ggg aga tcc ctt gag gct gag gat aag atg act cac cgg ata	939
Gly Gln Gly Arg Ser Leu Glu Ala Glu Asp Lys Met Thr His Arg Ile	
93 98 103 108	
ctg agg gca gcc cag gag ggg gac ctg cca gaa ctt agg aga ctg ctg	987
Leu Arg Ala Ala Gln Glu Gly Asp Leu Pro Glu Leu Arg Arg Leu Leu	
109 114 119 124	
gaa ccg cat gag gca gga gga gct ggg ggg aat atc aac gcc cgg gat	1035
Glu Pro His Glu Ala Gly Gly Ala Gly Gly Asn Ile Asn Ala Arg Asp	
125 130 135 140	
gcc ttc tgg tgg acc cca ctg atg tgt gct gct cga gcg ggc cag ggg	1083
Ala Phe Trp Trp Thr Pro Leu Met Cys Ala Ala Arg Ala Gly Gln Gly	
141 146 151 156	
gca gct gtg agc tat ctc ctg ggc cgt ggg gct gcc tgg gtg ggg gtc	1131
Ala Ala Val Ser Tyr Leu Leu Gly Arg Gly Ala Ala Trp Val Gly Val	
157 162 167 172	
tgt gag ctg agt ggc agg gat gcg gct cag ctc gct gaa gaa gct ggc	1179
Cys Glu Leu Ser Gly Arg Asp Ala Ala Gln Leu Ala Glu Glu Ala Gly	
173 178 183 188	
ttc cct gag gta gcc cgc atg gtc agg gag agc cat gga gag aca agg	1227
Phe Pro Glu Val Ala Arg Met Val Arg Glu Ser His Gly Glu Thr Arg	
189 194 199 204	
agc ccg gaa aac cgg tct cct act ccc tcc ctc cag tac tgc gag aac	1275
Ser Pro Glu Asn Arg Ser Pro Thr Pro Ser Leu Gln Tyr Cys Glu Asn	
205 210 215 220	
tgt gac acc cac ttc caa gat tcc aac cac cgc aca tcc act gct cac	1323
Cys Asp Thr His Phe Gln Asp Ser Asn His Arg Thr Ser Thr Ala His	
221 226 231 236	
ctg ctg tca ctg tcg cag ggt cct cag cct ccc aac ctt cca ctt ggg	1371
Leu Leu Ser Leu Ser Gln Gly Pro Gln Pro Pro Asn Leu Pro Leu Gly	
237 242 247 252	
gtg ccc atc tcc agc ccg ggc ttc aaa ctg ctg ctg agg ggg ggc tgg	1419
Val Pro Ile Ser Ser Pro Gly Phe Lys Leu Leu Leu Arg Gly Gly Trp	
253 258 263 268	
gag cca gga atg ggg ctg gga ccc cgg ggt gag ggc cgt gcc aat ccc	1467
Glu Pro Gly Met Gly Leu Gly Pro Arg Gly Glu Gly Arg Ala Asn Pro	
269 274 279 284	
atc ccc act gtc ctc aag agg gac cag gaa gga cta ggc tac aga tca	1515

Ile	Pro	Thr	Val	Leu	Lys	Arg	Asp	Gln	Glu	Gly	Leu	Gly	Tyr	Arg	Ser	
285					290					295					300	
gca	ccc	cag	ccc	cga	gtg	aca	cat	ttc	cca	gct	tgg	gat	acc	cga	gct	1563
Ala	Pro	Gln	Pro	Arg	Val	Thr	His	Phe	Pro	Ala	Trp	Asp	Thr	Arg	Ala	
301					306					311					316	
gtg	gct	ggg	agg	gag	aga	ccc	cct	cgg	gtg	gcc	aca	ctg	agc	tgg	agg	1611
Val	Ala	Gly	Arg	Glu	Arg	Pro	Pro	Arg	Val	Ala	Thr	Leu	Ser	Trp	Arg	
317					322					327					332	
gag	gag	aga	agg	agg	gag	gag	aaa	gac	agg	gct	tgg	gag	cgg	gat	cta	1659
Glu	Glu	Arg	Arg	Arg	Glu	Glu	Lys	Asp	Arg	Ala	Trp	Glu	Arg	Asp	Leu	
333					338					343					348	
agg	act	tac	atg	aac	ctc	gag	ttc	tga	ctttg	gtaaagtctg	accctagtct					1711
Arg	Thr	Tyr	Met	Asn	Leu	Glu	Phe	*								
349					354											
gctgctgaag	tctgaacttg	ggcctctgac	ctgggccctt	tgacttcccc	ttcctgggat											1771
ctgcccagat	gcagatcctg	aagtttttgg	tcaataggct	ctgtcttcgt	gagagacggg											1831
ctgagagtca	gaaataaatc	aaccatttgt	ggttttaaaaa	aaaaaaaa												1878

<210> 264
 <211> 2562
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (259)..(1770)

<400> 264																
ttttgtccta	aaaacagaaa	atagccgcat	tcacataaac	tctgataggg	tcctgaagaa											60
catacaggat	ctcaagaact	tttcagttct	gaagatgaac	tgccacccaaa	tgagatacgt											120
attgagttgt	gtagctcagg	aatactgtgt	tcccaactaa	ataccttcca	caaaagtgtc											180
attaaaagaa	gctgtacctc	tgaagataaa	gtgggccagt	ctgaagctct	atctagagtc											240
cttcaagtag	ctaagaaa	atg aag ttg	att tct aat	gga gga	gat tct gct											291
		Met Lys Leu	Ile Ser Asn	Gly Gly	Asp Ser Ala											
		1		5												
gta gaa atg	gat cgg aga	aat gtg tct	gaa ttt aag	agt att aaa	aaa											339
Val Glu Met	Asp Arg Arg	Asn Val Ser	Glu Phe Lys	Ser Ile Lys	Lys											
12		17		22	27											
aca tca tta	ata aaa aac	tgt gat tct	aaa agc cag	aag tat aat	tgt											387
Thr Ser Leu	Ile Lys Asn	Cys Asp Ser	Lys Ser Gln	Lys Tyr Asn	Cys											
28		33		38	43											

tta gtc atg gag cta tct cca tgc cat gtg aag gaa ata aac ata aaa Leu Val Met Glu Leu Ser Pro Cys His Val Lys Glu Ile Asn Ile Lys	435
44 49 54 59	
ttc gga cca aat tct ggc tct aaa gtg cct tta gca aca gtt aca gta Phe Gly Pro Asn Ser Gly Ser Lys Val Pro Leu Ala Thr Val Thr Val	483
60 65 70 75	
att gat caa tca gaa act aag aag aag gtt ttt ctg tgg agg act gca Ile Asp Gln Ser Glu Thr Lys Lys Lys Val Phe Leu Trp Arg Thr Ala	531
76 81 86 91	
gca ttt tgg gca ttt aca gtg ttt ctt gga gat ata att tta ctc aca Ala Phe Trp Ala Phe Thr Val Phe Leu Gly Asp Ile Ile Leu Leu Thr	579
92 97 102 107	
gat gtt gtt att cat gag gac caa tgg att ggc gag aca gta cta caa Asp Val Val Ile His Glu Asp Gln Trp Ile Gly Glu Thr Val Leu Gln	627
108 113 118 123	
tca aca ttt agc agt cag tta tta aat ctt ggg agt tat tca tct att Ser Thr Phe Ser Ser Gln Leu Leu Asn Leu Gly Ser Tyr Ser Ser Ile	675
124 129 134 139	
cag cct gaa gaa tat tcc agt gta gtt agt gaa gtt gta ctt caa gac Gln Pro Glu Glu Tyr Ser Ser Val Val Ser Glu Val Val Leu Gln Asp	723
140 145 150 155	
tta ctg gca tat gtg tcc tca aaa cat tcc tac ctc aga gat ctt cct Leu Leu Ala Tyr Val Ser Ser Lys His Ser Tyr Leu Arg Asp Leu Pro	771
156 161 166 171	
ccg agg cag cct cag agg gtg aac agt ata gac ttt gta gaa ttg gag Pro Arg Gln Pro Gln Arg Val Asn Ser Ile Asp Phe Val Glu Leu Glu	819
172 177 182 187	
cac ctt caa cct gat gta tta gtc cac gca gta cta aga gtt gtt gat His Leu Gln Pro Asp Val Leu Val His Ala Val Leu Arg Val Val Asp	867
188 193 198 203	
ttc act ata ctg aca gag gca gta tac agt tat aga gga cag aag cag Phe Thr Ile Leu Thr Glu Ala Val Tyr Ser Tyr Arg Gly Gln Lys Gln	915
204 209 214 219	
aaa aaa gtt atg tta aca gtg gaa cag gcc caa gat caa cat tat gcg Lys Lys Val Met Leu Thr Val Glu Gln Ala Gln Asp Gln His Tyr Ala	963
220 225 230 235	
ctt gta tta tgg ggt cct gga gca gcc tgg tac cct caa ctt caa agg Leu Val Leu Trp Gly Pro Gly Ala Ala Trp Tyr Pro Gln Leu Gln Arg	1011
236 241 246 251	
aaa aaa ggt tat att tgg gaa ttt aaa tat ctt ttt gtt cag tgc aat Lys Lys Gly Tyr Ile Trp Glu Phe Lys Tyr Leu Phe Val Gln Cys Asn	1059
252 257 262 267	

tac aca cta gaa aac cta gaa ttg cat aca acg cct tgg tca tcc tgt	1107
Tyr Thr Leu Glu Asn Leu Glu Leu His Thr Thr Pro Trp Ser Ser Cys	
268 273 278 283	
gag tgc ttg ttt gat gat gat ata agg gca att aca ttt aaa gca aaa	1155
Glu Cys Leu Phe Asp Asp Asp Ile Arg Ala Ile Thr Phe Lys Ala Lys	
284 289 294 299	
ttt caa aaa agt gca ccc tcc ttt gtg aag ata tca gac tta gca acc	1203
Phe Gln Lys Ser Ala Pro Ser Phe Val Lys Ile Ser Asp Leu Ala Thr	
300 305 310 315	
cac cta gag gat aag tgt tca gga gtg gtt ctg att aaa gcc cag att	1251
His Leu Glu Asp Lys Cys Ser Gly Val Val Leu Ile Lys Ala Gln Ile	
316 321 326 331	
tca gag ctg gca ttt cct att aca gca tct cag aag ata gcg cta aat	1299
Ser Glu Leu Ala Phe Pro Ile Thr Ala Ser Gln Lys Ile Ala Leu Asn	
332 337 342 347	
gct cac agt tct ctg aag agt att ttt tct tct ctt ccc aac atc gta	1347
Ala His Ser Ser Leu Lys Ser Ile Phe Ser Ser Leu Pro Asn Ile Val	
348 353 358 363	
tat act ggc tgt gca aaa tgt gga ttg gaa cta gaa aca gat gag aac	1395
Tyr Thr Gly Cys Ala Lys Cys Gly Leu Glu Leu Glu Thr Asp Glu Asn	
364 369 374 379	
agg atc tac aaa caa tgt ttt agc tgc ttg cca ttt act atg aag aaa	1443
Arg Ile Tyr Lys Gln Cys Phe Ser Cys Leu Pro Phe Thr Met Lys Lys	
380 385 390 395	
ata tat tat agg cca gcg tta atg act gcc att gat gga aga cat gat	1491
Ile Tyr Tyr Arg Pro Ala Leu Met Thr Ala Ile Asp Gly Arg His Asp	
396 401 406 411	
gtt tgt atc cgt gta gaa tca aag ctg ata gag aag att ctt ctc aac	1539
Val Cys Ile Arg Val Glu Ser Lys Leu Ile Glu Lys Ile Leu Leu Asn	
412 417 422 427	
att tct gca gac tgc ctc aac aga gtg ata gtt cct tcc tca gag atc	1587
Ile Ser Ala Asp Cys Leu Asn Arg Val Ile Val Pro Ser Ser Glu Ile	
428 433 438 443	
acc tat ggg atg gtc gtg gca gac ctg ttc cac tcc ttg ttg gca gtc	1635
Thr Tyr Gly Met Val Val Ala Asp Leu Phe His Ser Leu Leu Ala Val	
444 449 454 459	
agc gca gaa cct tgt gta tta aag att cag agc ctt ttt gtg tta gat	1683
Ser Ala Glu Pro Cys Val Leu Lys Ile Gln Ser Leu Phe Val Leu Asp	
460 465 470 475	
gaa aac agc tat cca tta caa caa gat ttc tcc ctc ctg gat ttt tat	1731
Glu Asn Ser Tyr Pro Leu Gln Gln Asp Phe Ser Leu Leu Asp Phe Tyr	
476 481 486 491	
cct gac att gta aag cat gga gcc aat gcc cgt ctc tga ggccagagga	1780

Pro Asp Ile Val Lys His Gly Ala Asn Ala Arg Leu *

492

497

502

```

agaaattgca ggcatttcaa ggaagaagta ctgaaatgat ttgtcttttg aaataaatga 1840
atgacagggc ttttgctttg gattttttat gaaatatatt ttacaaagag aattgcacta 1900
gatatataaa ttaaaacttt tttctaagaa aatcctgtga ggtttaaaaa gattgttttt 1960
gtcttttggg ttcttccttt ctctggaga aatgatctac cagtcaaggc aatatgtagc 2020
agatccctgg gaattaaagg ttgcccatt tgttcaactgt atttagtccc tgctacattc 2080
caggcattgt actaagtatg gggaaccaca gagaagacat tccctcagaa actgctgcag 2140
tgctttcgct tatccctacc taaaaaacg tcaatgtgaa atcatttcct tgattataac 2200
tataatgata atggattagt ttatataaac ctatgtttag acaagttcaa gacaagcgtg 2260
tctttctata aaaagtattg aaaatgaagg aaatgagatc atgtttcaat ttattaaagc 2320
aggggaagagc gttctgtggg tagttcgtgt ctaggatttg agtgccttac tgaatgcatt 2380
taccagcaaa catgtagcaa tctgttctct cattgtgatt gtggaagaag ctcatgtaaa 2440
atgatatgca ttaatgagga agtatggcgt ggtacttatt ctgtaagttc agagtatgct 2500
gagtgttaat agattatcat attgcctgaa aataaattca tgatgacatg aaaaaaaaaa 2560
aa 2562

```

<210> 265

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (237)..(1502)

<400> 265

```

agggatgatc ggcattgaggc attgccttat tgaggctcta taaaacacgt ctgtacaaaa 60
aagcaggctg gtaccgggtcc ggaattcccg ggatctattg cgccgggcga gtggctgttg 120
agcggcgccg cgggagttcc gcaggtttcc cgtgttcgca gcggagccgg aggccagctg 180
aaccggccg tgggatcccg gataggagga ggaggggacc cataggacgc gttaac 236
atg gac ctg gaa aac aaa gtg aag aag atg ggc tta ggt cac gag caa 284
Met Asp Leu Glu Asn Lys Val Lys Lys Met Gly Leu Gly His Glu Gln
1 5 10 15
gga ttt gga gcc cct tgt tta aaa tgc aaa gaa aaa tgt gaa gga ttc 332
Gly Phe Gly Ala Pro Cys Leu Lys Cys Lys Glu Lys Cys Glu Gly Phe

```

17	22	27	32	
gaa ctg cac ttc tgg aga aaa ata tgt cgt aac tgc aag tgt ggc caa				380
Glu Leu His Phe Trp Arg Lys Ile Cys Arg Asn Cys Lys Cys Gly Gln				
33	38	43	48	
gaa gag cat gat gtc ctc ttg agc aat gaa gag gat cga aaa gtg gga				428
Glu Glu His Asp Val Leu Leu Ser Asn Glu Glu Asp Arg Lys Val Gly				
49	54	59	64	
aaa ctt ttt gaa gac acc aag tat acc act ctg att gca aaa cta aag				476
Lys Leu Phe Glu Asp Thr Lys Tyr Thr Thr Leu Ile Ala Lys Leu Lys				
65	70	75	80	
tca gat gga att ccc atg tat aaa cgc aat gtt atg ata ttg acg aat				524
Ser Asp Gly Ile Pro Met Tyr Lys Arg Asn Val Met Ile Leu Thr Asn				
81	86	91	96	
cca gtt gct gcc aag aag aat gtc tcc atc aat aca gtt acc tat gag				572
Pro Val Ala Ala Lys Lys Asn Val Ser Ile Asn Thr Val Thr Tyr Glu				
97	102	107	112	
tgg gct cct cct gtc cag aat caa gca ttg gcc agg cag tac atg cag				620
Trp Ala Pro Pro Val Gln Asn Gln Ala Leu Ala Arg Gln Tyr Met Gln				
113	118	123	128	
atg cta ccc aag gaa aag cag cca gta gca ggc tca gag ggg gca cag				668
Met Leu Pro Lys Glu Lys Gln Pro Val Ala Gly Ser Glu Gly Ala Gln				
129	134	139	144	
tac cgg aag aag cag ctg gca aag cag ctc cct gca cat gac cag gac				716
Tyr Arg Lys Lys Gln Leu Ala Lys Gln Leu Pro Ala His Asp Gln Asp				
145	150	155	160	
cct tca aag tgc cat gag ttg tct ccc aga gag gtg aag gag atg gag				764
Pro Ser Lys Cys His Glu Leu Ser Pro Arg Glu Val Lys Glu Met Glu				
161	166	171	176	
cag ttt gtg aag aaa tat aag agc gaa gct ctg gga gta gga gat gtc				812
Gln Phe Val Lys Lys Tyr Lys Ser Glu Ala Leu Gly Val Gly Asp Val				
177	182	187	192	
aaa ctt ccc tgt gag atg gat gcc caa ggc ccc aaa caa atg aac att				860
Lys Leu Pro Cys Glu Met Asp Ala Gln Gly Pro Lys Gln Met Asn Ile				
193	198	203	208	
cct gga ggg gat aga agc acc cca gca gca gtg ggg gcc atg gag gac				908
Pro Gly Gly Asp Arg Ser Thr Pro Ala Ala Val Gly Ala Met Glu Asp				
209	214	219	224	
aaa tct gct gag cac aaa aga act caa tat tcc tgc tat tgc tgc aaa				956
Lys Ser Ala Glu His Lys Arg Thr Gln Tyr Ser Cys Tyr Cys Cys Lys				
225	230	235	240	
ctg agt atg aaa gaa ggt gac cca gcc atc tat gcc gaa agg gct ggc				/ 1004
Leu Ser Met Lys Glu Gly Asp Pro Ala Ile Tyr Ala Glu Arg Ala Gly				
241	246	251	256	

tat gat aaa ctg tgg cac cca gct tgt ttt gtc tgc agc acc tgc cat	1052
Tyr Asp Lys Leu Trp His Pro Ala Cys Phe Val Cys Ser Thr Cys His	
257 262 267 272	
gaa ctc ctg gtt gac atg att tat ttt tgg aag aat gag aag cta tac	1100
Glu Leu Leu Val Asp Met Ile Tyr Phe Trp Lys Asn Glu Lys Leu Tyr	
273 278 283 288	
tgt ggc aga cat tac tgt gac agc gag aaa ccc cga tgt gct ggc tgt	1148
Cys Gly Arg His Tyr Cys Asp Ser Glu Lys Pro Arg Cys Ala Gly Cys	
289 294 299 304	
gac gag ctg ata ttc agc aat gag tat acc cag gca gaa aac cag aat	1196
Asp Glu Leu Ile Phe Ser Asn Glu Tyr Thr Gln Ala Glu Asn Gln Asn	
305 310 315 320	
tgg cac ctg aaa cac ttc tgc tgc ttt gac tgt gat agc att cta gct	1244
Trp His Leu Lys His Phe Cys Cys Phe Asp Cys Asp Ser Ile Leu Ala	
321 326 331 336	
ggg gag ata tac gtg atg gtc aat gac aag ccc gtg tgc aag ccc tgc	1292
Gly Glu Ile Tyr Val Met Val Asn Asp Lys Pro Val Cys Lys Pro Cys	
337 342 347 352	
tat gtg aag aat cac gct gtg gtg tgt caa gga tgc cac aat gcc atc	1340
Tyr Val Lys Asn His Ala Val Val Cys Gln Gly Cys His Asn Ala Ile	
353 358 363 368	
gac cca gaa gtg cag cgg gtg acc tat aac aat ttc agc tgg cat gca	1388
Asp Pro Glu Val Gln Arg Val Thr Tyr Asn Asn Phe Ser Trp His Ala	
369 374 379 384	
tcc aca gag tgc ttt ctg tgc tct tgc tgc agc aaa tgc ctc att ggg	1436
Ser Thr Glu Cys Phe Leu Cys Ser Cys Cys Ser Lys Cys Leu Ile Gly	
385 390 395 400	
cag aag ttc atg cca gta gaa ggg atg gtt ttc tgt tca gtg gaa tgt	1484
Gln Lys Phe Met Pro Val Glu Gly Met Val Phe Cys Ser Val Glu Cys	
401 406 411 416	
aag aag agg atg tct tag gaggag ggcacccaga agtatcgagc catagctatc	1538
Lys Lys Arg Met Ser *	
417 422	
caaagtggtc tgcattttcta ctgtaaaatg caatttgaaa aaaataaaac gcaaaaaaag	1598
aaactgtaaa aaaaaaaaaa	1617

<210> 266
 <211> 4549
 <212> DNA
 <213> Homo sapiens

[illegible][illegible]

175	180	185	190	
gac cgc ttt gag aag gag tcg cac tgc gag aac cag aag cag ggc gag				803
Asp Arg Phe Glu Lys Glu Ser His Cys Glu Asn Gln Lys Gln Gly Glu				
191	196	201	206	
cag cag tct ctg atc gac gag gac gcc gtg tgc tgc atc tgc atg gac				851
Gln Gln Ser Leu Ile Asp Glu Asp Ala Val Cys Cys Ile Cys Met Asp				
207	212	217	222	
ggg gag tgt cag aac agc aac gtg atc ctc ttc tgc gac atg tgc aac				899
Gly Glu Cys Gln Asn Ser Asn Val Ile Leu Phe Cys Asp Met Cys Asn				
223	228	233	238	
ctg gcc gtg cac cag gag tgc tac ggg gtg ccc tac atc ccc gag ggc				947
Leu Ala Val His Gln Glu Cys Tyr Gly Val Pro Tyr Ile Pro Glu Gly				
239	244	249	254	
cag tgg ctc tgc cgc cac tgc ctg cag tcg cgg gcc cgg ccc gcc gac				995
Gln Trp Leu Cys Arg His Cys Leu Gln Ser Arg Ala Arg Pro Ala Asp				
255	260	265	270	
tgt gtg ctg tgc ccc aac aag ggt ggt gcc ttc aaa aag aca gat gac				1043
Cys Val Leu Cys Pro Asn Lys Gly Gly Ala Phe Lys Lys Thr Asp Asp				
271	276	281	286	
gac cgc tgg ggt cac gtg gtg tgt gcc ctg tgg atc cca gag gtc ggc				1091
Asp Arg Trp Gly His Val Val Cys Ala Leu Trp Ile Pro Glu Val Gly				
287	292	297	302	
ttt gcc aac acg gtg ttc atc gag ccc atc gat ggg gtg agg aac atc				1139
Phe Ala Asn Thr Val Phe Ile Glu Pro Ile Asp Gly Val Arg Asn Ile				
303	308	313	318	
cct cca gcc cgg tgg aaa ctg aca tgc tac ctc tgt aag cag aag ggc				1187
Pro Pro Ala Arg Trp Lys Leu Thr Cys Tyr Leu Cys Lys Gln Lys Gly				
319	324	329	334	
gtg ggt gcc tgc atc cag tgc cac aaa gca aac tgc tac aca gca ttc				1235
Val Gly Ala Cys Ile Gln Cys His Lys Ala Asn Cys Tyr Thr Ala Phe				
335	340	345	350	
cat gtg acg tgt gcc cag aag gct ggc ctg tac atg aaa atg gag ccc				1283
His Val Thr Cys Ala Gln Lys Ala Gly Leu Tyr Met Lys Met Glu Pro				
351	356	361	366	
gtg aag gaa ctg act ggc ggt ggc acc acc ttc tcc gtc aga aag acc				1331
Val Lys Glu Leu Thr Gly Gly Gly Thr Thr Phe Ser Val Arg Lys Thr				
367	372	377	382	
gct tac tgt gat gtc cac acg cct cca ggc tgc acc cgg agg cct ctg				1379
Ala Tyr Cys Asp Val His Thr Pro Pro Gly Cys Thr Arg Arg Pro Leu				
383	388	393	398	
aat att tac ggg gat gtc gaa atg aaa aat ggc gtc tgt cga aaa gag				1427
Asn Ile Tyr Gly Asp Val Glu Met Lys Asn Gly Val Cys Arg Lys Glu				
399	404	409	414	

agc tgc gtt aaa acg gtc agg tcc aca tcc aag gtc agg aag aag gca	1475
Ser Ser Val Lys Thr Val Arg Ser Thr Ser Lys Val Arg Lys Lys Ala	
415 420 425 430	
aaa aag gct aag aaa gct ctg gct gag ccc tgc gcg gtc ctg ccg acc	1523
Lys Lys Ala Lys Lys Ala Leu Ala Glu Pro Cys Ala Val Leu Pro Thr	
431 436 441 446	
gtg tgc gct cct tat att ccc ccg cag agg tta aat agg att gcg aat	1571
Val Cys Ala Pro Tyr Ile Pro Pro Gln Arg Leu Asn Arg Ile Ala Asn	
447 452 457 462	
cag gtg gcc att cag cgg aag aag cag ttt gtg gag cga gcc cac agc	1619
Gln Val Ala Ile Gln Arg Lys Lys Gln Phe Val Glu Arg Ala His Ser	
463 468 473 478	
tac tgg ctg ctc aag cgg ctg tcc agg aac ggg gcc ccc ctg ctg cgg	1667
Tyr Trp Leu Leu Lys Arg Leu Ser Arg Asn Gly Ala Pro Leu Leu Arg	
479 484 489 494	
cgg ctg cag tcc agc ctg cag tct cag cga agc tca cag cag aga gaa	1715
Arg Leu Gln Ser Ser Leu Gln Ser Gln Arg Ser Ser Gln Gln Arg Glu	
495 500 505 510	
aat gat gag gag atg aag gct gcc aaa gag aag ctg aag tac tgg cag	1763
Asn Asp Glu Glu Met Lys Ala Ala Lys Glu Lys Leu Lys Tyr Trp Gln	
511 516 521 526	
cgg ctg cgg cac gac ctg gag cgc gct cgc ctg ctg atc gag ctg ctg	1811
Arg Leu Arg His Asp Leu Glu Arg Ala Arg Leu Leu Ile Glu Leu Leu	
527 532 537 542	
cgc aag cgg gag aag ctc aag cgt gag cag gtg aag gtg gag cag gtc	1859
Arg Lys Arg Glu Lys Leu Lys Arg Glu Gln Val Lys Val Glu Gln Val	
543 548 553 558	
gcc atg gag ctg cgg ctg acc ccg ctg acg gtg ctg ctg cgc tca gtg	1907
Ala Met Glu Leu Arg Leu Thr Pro Leu Thr Val Leu Leu Arg Ser Val	
559 564 569 574	
ctg gac cag ctg caa gac aag gac ccc gcc agg ata ttt gcg cag ccc	1955
Leu Asp Gln Leu Gln Asp Lys Asp Pro Ala Arg Ile Phe Ala Gln Pro	
575 580 585 590	
gtg agt ctg aag gag gta cca gat tat ttg gat cac att aaa cat ccc	2003
Val Ser Leu Lys Glu Val Pro Asp Tyr Leu Asp His Ile Lys His Pro	
591 596 601 606	
atg gac ttt gcc aca atg agg aaa cgg tta gaa gct caa ggg tat aaa	2051
Met Asp Phe Ala Thr Met Arg Lys Arg Leu Glu Ala Gln Gly Tyr Lys	
607 612 617 622	
aac ctc cat gag ttt gag gag gat ttt gat ctc att ata gat aac tgc	2099
Asn Leu His Glu Phe Glu Glu Asp Phe Asp Leu Ile Ile Asp Asn Cys	
623 628 633 638	

atg aag tac aat gcc agg gac acc gtg ttc tat aga gcc gcg gtg agg	2147
Met Lys Tyr Asn Ala Arg Asp Thr Val Phe Tyr Arg Ala Ala Val Arg	
639 644 649 654	
ctg cgc gat cag gga ggt gtt gtt ctg agg cag gcc cgg cgc gag gtg	2195
Leu Arg Asp Gln Gly Gly Val Val Leu Arg Gln Ala Arg Arg Glu Val	
655 660 665 670	
gac agc atc ggc ttg gaa gag gcc tcg ggg atg cac ctg cct gag cgg	2243
Asp Ser Ile Gly Leu Glu Glu Ala Ser Gly Met His Leu Pro Glu Arg	
671 676 681 686	
cct gct gcg gca ccg cgg cgg cct ttc tcc tgg gaa gac gtg gac agg	2291
Pro Ala Ala Ala Pro Arg Arg Pro Phe Ser Trp Glu Asp Val Asp Arg	
687 692 697 702	
ttg ctg gac ccc gcc aac aga gcc cac ctg ggc ctg gag gag cag ctg	2339
Leu Leu Asp Pro Ala Asn Arg Ala His Leu Gly Leu Glu Glu Gln Leu	
703 708 713 718	
aga gag ctg ctg gac atg ctc gac ctc acc tgc gct atg aag tcc agc	2387
Arg Glu Leu Leu Asp Met Leu Asp Leu Thr Cys Ala Met Lys Ser Ser	
719 724 729 734	
ggc tcc cgg agc aag cgg gca aag ctg ctc aaa aag gaa att gcc ctt	2435
Gly Ser Arg Ser Lys Arg Ala Lys Leu Leu Lys Lys Glu Ile Ala Leu	
735 740 745 750	
ctc cga aac aag ctg agc cag cag cac agc cag ccc ctg ccc acg ggg	2483
Leu Arg Asn Lys Leu Ser Gln Gln His Ser Gln Pro Leu Pro Thr Gly	
751 756 761 766	
cca ggc ttg gaa ggc ttc gaa gag gac gga gct gcg ctg ggg ccg gag	2531
Pro Gly Leu Glu Gly Phe Glu Glu Asp Gly Ala Ala Leu Gly Pro Glu	
767 772 777 782	
gcg ggc gag gaa gtc ctt ccg agg ttg gag act ctt ctg cag cca agg	2579
Ala Gly Glu Glu Val Leu Pro Arg Leu Glu Thr Leu Leu Gln Pro Arg	
783 788 793 798	
aaa agg tcg cgg agc aca tgc gga gac tcc gag gtg gag gag gag tcc	2627
Lys Arg Ser Arg Ser Thr Cys Gly Asp Ser Glu Val Glu Glu Glu Ser	
799 804 809 814	
cca gga aag cgc ctg gac gca ggt ctc acc aac ggc ttt ggg ggt gcg	2675
Pro Gly Lys Arg Leu Asp Ala Gly Leu Thr Asn Gly Phe Gly Gly Ala	
815 820 825 830	
agg agc gag cag gag ccg ggc ggc ggc ctg ggg agg aag gcc aca ccc	2723
Arg Ser Glu Gln Glu Pro Gly Gly Gly Leu Gly Arg Lys Ala Thr Pro	
831 836 841 846	
cga cga cgc tgt gcc tcc gag tcc agc atc tcc tcc agc aac agc ccg	2771
Arg Arg Arg Cys Ala Ser Glu Ser Ser Ile Ser Ser Ser Asn Ser Pro	
847 852 857 862	
ctc tgc gac tcg agc ttt aat gcg ccc aaa tgt ggg cgg ggc aaa ccg	2819

Leu Cys Asp Ser Ser Phe Asn Ala Pro Lys Cys Gly Arg Gly Lys Pro	
863 868 873 878	
gct ctt gtg cga cgg cac acg ctg gag gac cgc agt gag ctg atc tcc	2867
Ala Leu Val Arg Arg His Thr Leu Glu Asp Arg Ser Glu Leu Ile Ser	
879 884 889 894	
tgc atc gag aat ggg aac tac gcc aag gcg gcc agg atc gca gcc gaa	2915
Cys Ile Glu Asn Gly Asn Tyr Ala Lys Ala Arg Ile Ala Ala Glu	
895 900 905 910	
gtc ggc cag agc agc atg tgg atc tcc act gat gcc gcc gcc tcg gtg	2963
Val Gly Gln Ser Ser Met Trp Ile Ser Thr Asp Ala Ala Ala Ser Val	
911 916 921 926	
ctg gag cct ctg aag gtg gtg tgg gcc aag tgc agc ggc tac ccc tcc	3011
Leu Glu Pro Leu Lys Val Val Trp Ala Lys Cys Ser Gly Tyr Pro Ser	
927 932 937 942	
tac ccg gca ctg atc atc gac ccc aag atg ccc cgt gtg cct ggc cac	3059
Tyr Pro Ala Leu Ile Ile Asp Pro Lys Met Pro Arg Val Pro Gly His	
943 948 953 958	
cac aac ggc gtc acc atc ccg gcc cca ccc ctg gac gtg ctg aag att	3107
His Asn Gly Val Thr Ile Pro Ala Pro Pro Leu Asp Val Leu Lys Ile	
959 964 969 974	
ggg gag cac atg cag acc aag tct gat gag aag ctg ttc ctc gtt ctc	3155
Gly Glu His Met Gln Thr Lys Ser Asp Glu Lys Leu Phe Leu Val Leu	
975 980 985 990	
ttt ttt gat aat aag aga agt tgg cag tgg ctt cct aag tcc aaa atg	3203
Phe Phe Asp Asn Lys Arg Ser Trp Gln Trp Leu Pro Lys Ser Lys Met	
991 996 1001 1006	
gtt ccc ctt ggt att gac gaa act ata gac aag tta aag atg atg gaa	3251
Val Pro Leu Gly Ile Asp Glu Thr Ile Asp Lys Leu Lys Met Met Glu	
1007 1012 1017 1022	
ggg agg aat tcc agc atc cgg aag gcc gtg cgg atc gct ttt gac cgc	3299
Gly Arg Asn Ser Ser Ile Arg Lys Ala Val Arg Ile Ala Phe Asp Arg	
1023 1028 1033 1038	
gcc atg aac cac ctg agc cgc gtc cac ggg gag ccg acc agc gac ctc	3347
Ala Met Asn His Leu Ser Arg Val His Gly Glu Pro Thr Ser Asp Leu	
1039 1044 1049 1054	
agt gac att gac tga cggcccgcc gccagcgcg gtcttgtcca tagtgttgat	3402
Ser Asp Ile Asp *	
1055	
aagctgtaca tggttgtata ttgttcaaaa cttaacttat tctgattttt agttatagct	3462
ctttaattct ttttccccgg ggagggggga ggttttattt ccaagttttc taggaaccca	3522
tctccgtctg ggcgctgtga gtgggggtggg cacgtccggg cagcccagtg cgtctgtcgc	3582

acgtccccag gcogtgcctgc tggcgctcact ttctttgata tgtagctttt tottaaagac 3642
 ttttgaatgt ttaataatgt tgtaaatcat gctctttaca cagagtacca cttatttaac 3702
 aagacgggat gtaaatttac aatgacaaat gtgtatttta agaaagaaaa tgacattatt 3762
 ttgaatggta ctttgtggaa agaggggaga ataaagttat gctgtgtaca tcacttgcag 3822
 atcaccaaaa aactccgct gcccgcgacc gccggtgggt gtgtccccgc tcccgctgct 3882
 ccgcccacct caaaccocgc aggtgtgcct ccagcggat tatttattgt agaaagtgt 3942
 ttcatctgct ttataatgaa aaatacattt gcaaaggat attgatatgc atttttatac 4002
 aggacataa aaattcaact tggcttggga gcagaatgca ttgcattgta taaatgactc 4062
 tggcctgtgt gtactttgat ttataactt gtaatctttt gtttacaatg aggggctttc 4122
 tgtaacttgt tttaatttag aacactttgg tagcaataga aactttggat acatttttgt 4182
 atggtacctg tgatgtatat agaattagta ctttattttt atttttaaga ggtaaagcat 4242
 tatgttgggg aaagtagggg ggggttccaa atttgcattt tttatattaa aaataaagtc 4302
 aagatttga cggtgtggcc attttattcc tacagcccta gacggctagg tgagccccaa 4362
 ggacgggtgg ggtgctggct gcagggggcg gggacacgcc tttatcttga aaactgtcat 4422
 gggatggcat tatttgttat ttcacctgat catattttta ttttaaaact tcagttacat 4482
 aaaagtttta aatgcttttt ttaagcctac accgtttgta acatctccat agaaacttgg 4542
 aaatcaa 4549

<210> 267
 <211> 4942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (186)..(3755)

<400> 267
 caatctagtt tcaacatata atgaggattt ctgtctgata cagagaaaga taccagtggt 60
 ctggagggtc tgtcttaaga agtgctcttg aagtctgctg ggatttcctt tcgggactca 120
 cagagggaag cctgctccct gagggctttt tctcaggccc aatagatcag ggtaatcatt 180
 accaa atg agg agg aaa gga cga tgt cat cga ggc tct gca gcg agg 227
 Met Arg Arg Lys Gly Arg Cys His Arg Gly Ser Ala Ala Arg
 1 5 10

cat cct tct tcc cca tgc agt gtt aaa cac tcc cct acg cga gaa acg	275
His Pro Ser Ser Pro Cys Ser Val Lys His Ser Pro Thr Arg Glu Thr	
15 20 25 30	
ctg acc tac gct caa gct caa agg atg gta gag ata gaa att gaa ggg	323
Leu Thr Tyr Ala Gln Ala Gln Arg Met Val Glu Ile Glu Ile Glu Gly	
31 36 41 46	
cgc ttg cac agg atc agt att ttt gat ccc ctg gag atc ata ttg gaa	371
Arg Leu His Arg Ile Ser Ile Phe Asp Pro Leu Glu Ile Ile Leu Glu	
47 52 57 62	
gat gac ctc act gct caa gag atg agt gag tgc aac agc aac aag gaa	419
Asp Asp Leu Thr Ala Gln Glu Met Ser Glu Cys Asn Ser Asn Lys Glu	
63 68 73 78	
aac agc gag cgg cct cct gtc tgc tta aga act aag cgt cac aaa aac	467
Asn Ser Glu Arg Pro Pro Val Cys Leu Arg Thr Lys Arg His Lys Asn	
79 84 89 94	
aac aga gtc aaa aag aaa aac gag gcc ctc ccc agc gcc cac ggc acg	515
Asn Arg Val Lys Lys Lys Asn Glu Ala Leu Pro Ser Ala His Gly Thr	
95 100 105 110	
ccg gcc tcg gcc agt gcc ctc ccg gag ccc aag gtg cgc atc gtg gag	563
Pro Ala Ser Ala Ser Ala Leu Pro Glu Pro Lys Val Arg Ile Val Glu	
111 116 121 126	
tac agc cct ccg tcc gcc ccc agg agg cct cct gtg tac tac aag ttc	611
Tyr Ser Pro Pro Ser Ala Pro Arg Arg Pro Pro Val Tyr Tyr Lys Phe	
127 132 137 142	
atc gag aag tcg gcc gag gaa ctg gac aac gag gtg gag tat gac atg	659
Ile Glu Lys Ser Ala Glu Glu Leu Asp Asn Glu Val Glu Tyr Asp Met	
143 148 153 158	
gac gag gag gac tat gcc tgg ctg gag atc gtc aat gag aag cgc aag	707
Asp Glu Glu Asp Tyr Ala Trp Leu Glu Ile Val Asn Glu Lys Arg Lys	
159 164 169 174	
ggc gac tgc gtc ccc gcc gtg tcg cag agc atg ttt gag ttc ctg atg	755
Gly Asp Cys Val Pro Ala Val Ser Gln Ser Met Phe Glu Phe Leu Met	
175 180 185 190	
gac cgc ttt gag aag gag tcg cac tgc gag aac cag aag cag ggc gag	803
Asp Arg Phe Glu Lys Glu Ser His Cys Glu Asn Gln Lys Gln Gly Glu	
191 196 201 206	
cag cag tct ctg atc gac gag gac gcc gtg tgc tgc atc tgc atg gac	851
Gln Gln Ser Leu Ile Asp Glu Asp Ala Val Cys Cys Ile Cys Met Asp	
207 212 217 222	
ggg gag tgt cag aac agc aac gtg atc ctc ttc tgc gac atg tgc aac	899
Gly Glu Cys Gln Asn Ser Asn Val Ile Leu Phe Cys Asp Met Cys Asn	
223 228 233 238	
ctg gcc gtg cac cag gag tgc tac ggg gtg ccc tac atc ccc gag ggc	947

Leu	Ala	Val	His	Gln	Glu	Cys	Tyr	Gly	Val	Pro	Tyr	Ile	Pro	Glu	Gly	
239					244					249					254	
cag	tgg	ctc	tgc	cgc	cac	tgc	ctg	cag	tgc	cgg	gcc	cgg	ccc	gcc	gac	995
Gln	Trp	Leu	Cys	Arg	His	Cys	Leu	Gln	Ser	Arg	Ala	Arg	Pro	Ala	Asp	
255					260					265					270	
tgt	gtg	ctg	tgc	ccc	aac	aag	ggg	ggg	gcc	ttc	aaa	aag	aca	gat	gac	1043
Cys	Val	Leu	Cys	Pro	Asn	Lys	Gly	Gly	Ala	Phe	Lys	Lys	Thr	Asp	Asp	
271					276					281					286	
gac	cgc	tgg	ggg	cac	gtg	gtg	tgt	gcc	ctg	tgg	atc	cca	gag	gtc	ggc	1091
Asp	Arg	Trp	Gly	His	Val	Val	Cys	Ala	Leu	Trp	Ile	Pro	Glu	Val	Gly	
287					292					297					302	
ttt	gcc	aac	acg	gtg	ttc	atc	gag	ccc	atc	gat	ggg	gtg	agg	aac	atc	1139
Phe	Ala	Asn	Thr	Val	Phe	Ile	Glu	Pro	Ile	Asp	Gly	Val	Arg	Asn	Ile	
303					308					313					318	
cct	cca	gcc	cgg	tgg	aaa	ctg	aca	tgc	tac	ctc	tgt	aag	cag	aag	ggc	1187
Pro	Pro	Ala	Arg	Trp	Lys	Leu	Thr	Cys	Tyr	Leu	Cys	Lys	Gln	Lys	Gly	
319					324					329					334	
gtg	ggg	gcc	tgc	atc	cag	tgc	cac	aaa	gca	aac	tgc	tac	aca	gca	ttc	1235
Val	Gly	Ala	Cys	Ile	Gln	Cys	His	Lys	Ala	Asn	Cys	Tyr	Thr	Ala	Phe	
335					340					345					350	
cat	gtg	acg	tgt	gcc	cag	aag	gct	ggc	ctg	tac	atg	aaa	atg	gag	ccc	1283
His	Val	Thr	Cys	Ala	Gln	Lys	Ala	Gly	Leu	Tyr	Met	Lys	Met	Glu	Pro	
351					356					361					366	
gtg	aag	gaa	ctg	act	ggc	ggg	ggc	acc	acc	ttc	tcc	gtc	aga	aag	acc	1331
Val	Lys	Glu	Leu	Thr	Gly	Gly	Gly	Thr	Thr	Phe	Ser	Val	Arg	Lys	Thr	
367					372					377					382	
gct	tac	tgt	gat	gtc	cac	acg	cct	cca	ggc	tgc	acc	cgg	agg	cct	ctg	1379
Ala	Tyr	Cys	Asp	Val	His	Thr	Pro	Pro	Gly	Cys	Thr	Arg	Arg	Pro	Leu	
383					388					393					398	
aat	att	tac	ggg	gat	gtc	gaa	atg	aaa	aat	ggc	gtc	tgt	cga	aaa	gag	1427
Asn	Ile	Tyr	Gly	Asp	Val	Glu	Met	Lys	Asn	Gly	Val	Cys	Arg	Lys	Glu	
399					404					409					414	
agc	tgc	gtt	aaa	acg	gtc	agg	tcc	aca	tcc	aag	gtc	agg	aag	aag	gca	1475
Ser	Ser	Val	Lys	Thr	Val	Arg	Ser	Thr	Ser	Lys	Val	Arg	Lys	Lys	Ala	
415					420					425					430	
aaa	aag	gct	aag	aaa	gct	ctg	gct	gag	ccc	tgc	gcg	gtc	ctg	ccg	acc	1523
Lys	Lys	Ala	Lys	Lys	Ala	Leu	Ala	Glu	Pro	Cys	Ala	Val	Leu	Pro	Thr	
431					436					441					446	
gtg	tgc	gct	cct	tat	att	ccc	ccg	cag	agg	tta	aat	agg	att	gcg	aat	1571
Val	Cys	Ala	Pro	Tyr	Ile	Pro	Pro	Gln	Arg	Leu	Asn	Arg	Ile	Ala	Asn	
447					452					457					462	
cag	gtg	gcc	att	cag	cgg	aag	aag	cag	ttt	gtg	gag	cga	gcc	cac	agc	1619
Gln	Val	Ala	Ile	Gln	Arg	Lys	Lys	Gln	Phe	Val	Glu	Arg	Ala	His	Ser	

463	468	473	478	
tac tgg ctg ctc aag	cgg ctg tcc agg aac	ggg gcc ccc ctg ctg cgg		1667
Tyr Trp Leu Leu Lys	Arg Leu Ser Arg Asn	Gly Ala Pro Leu Leu Arg		
479	484	489	494	
cgg ctg cag tcc agc	ctg cag tct cag cga	agc tca cag cag aga gaa		1715
Arg Leu Gln Ser Ser	Leu Gln Ser Gln Arg	Ser Ser Gln Gln Arg Glu		
495	500	505	510	
aat gat gag gag atg	aag gct gcc aaa gag	aag ctg aag tac tgg cag		1763
Asn Asp Glu Glu Met	Lys Ala Ala Lys Glu	Lys Leu Lys Tyr Trp Gln		
511	516	521	526	
cgg ctg cgg cac gac	ctg gag cgc gct cgc	ctg ctg atc gag ctg ctg		1811
Arg Leu Arg His Asp	Leu Glu Arg Ala Arg	Leu Leu Ile Glu Leu Leu		
527	532	537	542	
cgc aag cgg gag aag	ctc aag cgt gag cag	gtg aag gtg gag cag gtc		1859
Arg Lys Arg Glu Lys	Leu Lys Arg Glu Gln	Val Lys Val Glu Gln Val		
543	548	553	558	
gcc atg gag ctg cgg	ctg acc ccg ctg acg	gtg ctg ctg cgc tca gtg		1907
Ala Met Glu Leu Arg	Leu Thr Pro Leu Thr	Val Leu Leu Arg Ser Val		
559	564	569	574	
ctg gac cag ctg caa	gac aag gac ccc gcc	agg ata ttt gcg cag ccc		1955
Leu Asp Gln Leu Gln	Asp Lys Asp Pro Ala	Arg Ile Phe Ala Gln Pro		
575	580	585	590	
gtg agt ctg aag gag	gta cca gat tat ttg	gat cac att aaa cat ccc		2003
Val Ser Leu Lys Glu	Val Pro Asp Tyr Leu	Asp His Ile Lys His Pro		
591	596	601	606	
atg gac ttt gcc aca	atg agg aaa cgg tta	gaa gct caa ggg tat aaa		2051
Met Asp Phe Ala Thr	Met Arg Lys Arg Leu	Glu Ala Gln Gly Tyr Lys		
607	612	617	622	
aac ctc cat gag ttt	gag gag gat ttt gat	ctc att ata gat aac tgc		2099
Asn Leu His Glu Phe	Glu Glu Asp Phe Asp	Leu Ile Ile Asp Asn Cys		
623	628	633	638	
atg aag tac aat gcc	agg gac acc gtg ttc	tat aga gcc gcg gtg agg		2147
Met Lys Tyr Asn Ala	Arg Asp Thr Val Phe	Tyr Arg Ala Ala Val Arg		
639	644	649	654	
ctg cgc gat cag gga	ggt gtt gtt ctg agg	cag gcc cgg cgc gag gtg		2195
Leu Arg Asp Gln Gly	Gly Val Val Leu Arg	Gln Ala Arg Arg Glu Val		
655	660	665	670	
gac agc atc gcc ttg	gaa gag gcc tcg ggg	atg cac ctg cct gag cgg		2243
Asp Ser Ile Gly Leu	Glu Glu Ala Ser Gly	Met His Leu Pro Glu Arg		
671	676	681	686	
cct gct gcg gca ccg	cgg cgg cct ttc tcc	tgg gaa gac gtg gac agg		2291
Pro Ala Ala Ala Pro	Arg Arg Pro Phe Ser	Trp Glu Asp Val Asp Arg		
687	692	697	702	

ttg ctg gac ccc gcc aac aga gcc cac ctg ggc ctg gag gag cag ctg	2339
Leu Leu Asp Pro Ala Asn Arg Ala His Leu Gly Leu Glu Glu Gln Leu	
703 708 713 718	
aga gag ctg ctg gac atg ctc gac ctc acc tgc gct atg aag tcc agc	2387
Arg Glu Leu Leu Asp Met Leu Asp Leu Thr Cys Ala Met Lys Ser Ser	
719 724 729 734	
ggc tcc cgg agc aag cgg gca aag ctg ctc aaa aag gaa att gcc ctt	2435
Gly Ser Arg Ser Lys Arg Ala Lys Leu Leu Lys Lys Glu Ile Ala Leu	
735 740 745 750	
ctc cga aac aag ctg agc cag cag cac agc cag ccc ctg ccc acg ggg	2483
Leu Arg Asn Lys Leu Ser Gln Gln His Ser Gln Pro Leu Pro Thr Gly	
751 756 761 766	
cca ggc ttg gaa ggc ttc gaa gag gac gga gct gcg ctg ggg ccg gag	2531
Pro Gly Leu Glu Gly Phe Glu Glu Asp Gly Ala Ala Leu Gly Pro Glu	
767 772 777 782	
gcg ggc gag gaa gga gat aaa tct ccc cct aaa ctt gaa cca tca gat	2579
Ala Gly Glu Glu Gly Asp Lys Ser Pro Pro Lys Leu Glu Pro Ser Asp	
783 788 793 798	
gca tta cct ctt cct tca aac tcg gag act aat tca gaa cca cca acc	2627
Ala Leu Pro Leu Pro Ser Asn Ser Glu Thr Asn Ser Glu Pro Pro Thr	
799 804 809 814	
ctc aaa cca gta gaa ctc aac cca gag cag agt aaa ctt ttc aaa aga	2675
Leu Lys Pro Val Glu Leu Asn Pro Glu Gln Ser Lys Leu Phe Lys Arg	
815 820 825 830	
gtc aca ttt gat aat gaa tca cat agc gct tgc act cag agc gca ctg	2723
Val Thr Phe Asp Asn Glu Ser His Ser Ala Cys Thr Gln Ser Ala Leu	
831 836 841 846	
gta agc gga cgc cct cca gag ccc acc cgc gcc agt agt ggc gat gtg	2771
Val Ser Gly Arg Pro Pro Glu Pro Thr Arg Ala Ser Ser Gly Asp Val	
847 852 857 862	
ccg gcg gcg gcg gcc tcc gcg gtg gcg gag cca gca agc gat gta aac	2819
Pro Ala Ala Ala Ala Ser Ala Val Ala Glu Pro Ala Ser Asp Val Asn	
863 868 873 878	
aga cgc act tct gtt ctc ttc tgc aaa tcg aaa agt gta agc ccc cca	2867
Arg Arg Thr Ser Val Leu Phe Cys Lys Ser Lys Ser Val Ser Pro Pro	
879 884 889 894	
aag tct gcc aag aac act gaa acc cag cca act tct cct cag cta ggg	2915
Lys Ser Ala Lys Asn Thr Glu Thr Gln Pro Thr Ser Pro Gln Leu Gly	
895 900 905 910	
acc aaa acc ttt ttg tct gta gtc ctt ccg agg ttg gag act ctt ctg	2963
Thr Lys Thr Phe Leu Ser Val Val Leu Pro Arg Leu Glu Thr Leu Leu	
911 916 921 926	

cag cca agg aaa agg tcg cgg agc aca tgc gga gac tcc gag gtg gag	3011
Gln Pro Arg Lys Arg Ser Arg Ser Thr Cys Gly Asp Ser Glu Val Glu	
927 932 937 942	
gag gag tcc cca gga aag cgc ctg gac gca ggt ctc acc aac ggc ttt	3059
Glu Glu Ser Pro Gly Lys Arg Leu Asp Ala Gly Leu Thr Asn Gly Phe	
943 948 953 958	
ggg ggt gcg agg agc gag cag gag ccg ggc ggc ggc ctg ggg agg aag	3107
Gly Gly Ala Arg Ser Glu Gln Glu Pro Gly Gly Leu Gly Arg Lys	
959 964 969 974	
gcc aca ccc cga cga cgc tgt gcc tcc gag tcc agc atc tcc tcc agc	3155
Ala Thr Pro Arg Arg Arg Cys Ala Ser Glu Ser Ser Ile Ser Ser Ser	
975 980 985 990	
aac agc ccg ctc tgc gac tcg agc ttt aat gcg ccc aaa tgt ggg cgg	3203
Asn Ser Pro Leu Cys Asp Ser Ser Phe Asn Ala Pro Lys Cys Gly Arg	
991 996 1001 1006	
ggc aaa ccg gct ctt gtg cga cgg cac acg ctg gag gac cgc agt gag	3251
Gly Lys Pro Ala Leu Val Arg Arg His Thr Leu Glu Asp Arg Ser Glu	
1007 1012 1017 1022	
ctg atc tcc tgc atc gag aat ggg aac tac gcc aag gcg gcc agg atc	3299
Leu Ile Ser Cys Ile Glu Asn Gly Asn Tyr Ala Lys Ala Ala Arg Ile	
1023 1028 1033 1038	
gca gcc gaa gtc ggc cag agc agc atg tgg atc tcc act gat gcc gcc	3347
Ala Ala Glu Val Gly Gln Ser Ser Met Trp Ile Ser Thr Asp Ala Ala	
1039 1044 1049 1054	
gcc tcg gtg ctg gag cct ctg aag gtg gtg tgg gcc aag tgc agc ggc	3395
Ala Ser Val Leu Glu Pro Leu Lys Val Val Trp Ala Lys Cys Ser Gly	
1055 1060 1065 1070	
tac ccc tcc tac ccg gca ctg atc atc gac ccc aag atg ccc cgt gtg	3443
Tyr Pro Ser Tyr Pro Ala Leu Ile Ile Asp Pro Lys Met Pro Arg Val	
1071 1076 1081 1086	
cct ggc cac cac aac ggc gtc acc atc ccg gcc cca ccc ctg gac gtg	3491
Pro Gly His His Asn Gly Val Thr Ile Pro Ala Pro Pro Leu Asp Val	
1087 1092 1097 1102	
ctg aag att ggg gag cac atg cag acc aag tct gat gag aag ctg ttc	3539
Leu Lys Ile Gly Glu His Met Gln Thr Lys Ser Asp Glu Lys Leu Phe	
1103 1108 1113 1118	
ctc gtt ctc ttt ttt gat aat aag aga agt tgg cag tgg ctt cct aag	3587
Leu Val Leu Phe Phe Asp Asn Lys Arg Ser Trp Gln Trp Leu Pro Lys	
1119 1124 1129 1134	
tcc aaa atg gtt ccc ctt ggt att gac gaa act ata gac aag tta aag	3635
Ser Lys Met Val Pro Leu Gly Ile Asp Glu Thr Ile Asp Lys Leu Lys	
1135 1140 1145 1150	
atg atg gaa ggg agg aat tcc agc atc cgg aag gcc gtg cgg atc gct	3683

Met Met Glu Gly Arg Asn Ser Ser Ile Arg Lys Ala Val Arg Ile Ala	
1151	1156 1161 1166
ttt gac cgc gcc atg aac cac ctg agc cgc gtc cac ggg gag ccg acc	3731
Phe Asp Arg Ala Met Asn His Leu Ser Arg Val His Gly Glu Pro Thr	
1167	1172 1177 1182
agc gac ctc agt gac att gac tga cggccccggc gccagcgcgg gtcttgtcca	3785
Ser Asp Leu Ser Asp Ile Asp *	
1183	1188
tagtggtgat aagctgtaca tgtttgtata ttgttcaaaa cttaacttat totgattttt	3845
agttatagct ctttaattct ttttccccgg ggagggggga ggttttattt ccaagttttc	3905
taggaaccca tctccgtctg ggcgctgtga gtgggggtggg cacgtccggg cagcccagtg	3965
cgtctgtcgc acgtccccag gccgtgctgc tggcgtcact ttctttgata tgtagctttt	4025
tcttaaagac ttttgaatgt ttaataattt tgtaaactcat gctctttaca cagagtacca	4085
cttatttaat aagacgggat gttaaatttac aatgacaaat gtgtatttta agaaagaaaa	4145
tgacattatt ttgaatggta ctttgtggaa agaggggaga ataaagttat gctgtgtaca	4205
tcacttgcag atcaccaaaa acactccgct gcccgtagcc gccggtgggt gtgtccccgc	4265
tcccgctcgc ccgcccacct caaacccgc aggtgtgcct cccagcggat tatttattgt	4325
agaaagtgtg ttcatattgt ttataatgaa aaatacattt gcaaaggat attgatatgc	4385
atttttatac aggcacataa aaattcaact tggcttggga gcagaatgca ttgcattgta	4445
taaatgactc tggcctgtgt gtactttgat tttataactt gtaatctttt gtttacaatg	4505
aggggctttc tgtaacttgt ttttaatttag aacactttgg tagcaataga aactttggat	4565
acatttttgt atggtacctg tgatgtatat agaattagta ctttattttt atttttaaga	4625
ggtaaagcat tatgttgggg aaagtagggg gggtttccaa atttgcattt tttatattaa	4685
aaataaagtc aagatttgga cgggtgtggc attttattcc tacagcccta gacggctagg	4745
tgagcccca ggacgggtgg ggtgctggct gcagggggcg gggacacgcc tttatcttga	4805
aaactgtcat gggatggcat tatttgttat ttcacctgat catattttta ttttaaaact	4865
tcagttacat aaaagtttta aatgcttttt ttaagcctac accgtttgta acatctccat	4925
agaaacttgg aaatcaa	4942

<210> 268
 <211> 1301
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (162)..(935)

<400> 268

taagcttgcg gccgccaact tttttttttt ttcaatgaac atgacttctg gagtcaaggt 60

tgttggggcca ttccccccgt tccactcact gggaatataa atagcaccga cagcgcagaa 120

cacagagcca gagagctgga agtgagagca gatccctaac c atg agc acc agc 173

Met Ser Thr Ser

1

caa cca ggg gcc tgc cca tgc cag gga gct gca agc cgc ccc gcc att 221

Gln Pro Gly Ala Cys Pro Cys Gln Gly Ala Ala Ser Arg Pro Ala Ile

5

10

15

20

ctc tac gca ctt ctg agc tcc agc ctc aag gct gtc ccc cga ccc cgt 269

Leu Tyr Ala Leu Leu Ser Ser Ser Leu Lys Ala Val Pro Arg Pro Arg

21

26

31

36

agc cgc tgc cta tgt agg cag cac cgg ccc gtc cag cta tgt gca cct 317

Ser Arg Cys Leu Cys Arg Gln His Arg Pro Val Gln Leu Cys Ala Pro

37

42

47

52

cat cgc acc tgc cgg gag gcc ttg gat gtt ctg gcc aag aca gtg gcc 365

His Arg Thr Cys Arg Glu Ala Leu Asp Val Leu Ala Lys Thr Val Ala

53

58

63

68

ttc ctc agg aac ctg cca tcc ttc tgg cag ctg cct ccc cag gac cag 413

Phe Leu Arg Asn Leu Pro Ser Phe Trp Gln Leu Pro Pro Gln Asp Gln

69

74

79

84

cgg cgg ctg ctg cag ggt tgc tgg ggc ccc ctc ttc ctg ctt ggg ttg 461

Arg Arg Leu Leu Gln Gly Cys Trp Gly Pro Leu Phe Leu Leu Gly Leu

85

90

95

100

gcc caa gat gct gtg acc ttt gag gtg gct gag gcc ccg gtg ccc agc 509

Ala Gln Asp Ala Val Thr Phe Glu Val Ala Glu Ala Pro Val Pro Ser

101

106

111

116

ata ctc aag aag att ctg ctg gag gag ccc agc agc agt gga ggc agt 557

Ile Leu Lys Lys Ile Leu Leu Glu Glu Pro Ser Ser Ser Gly Gly Ser

117

122

127

132

ggc caa ctg cca gac aga ccc cag ccc tcc ctg gct gcg gtg cag tgg 605

Gly Gln Leu Pro Asp Arg Pro Gln Pro Ser Leu Ala Ala Val Gln Trp

133

138

143

148

ctt caa tgc tgt ctg gag tcc ttc tgg agc ctg gag ctt agc ccc aag 653

Leu Gln Cys Cys Leu Glu Ser Phe Trp Ser Leu Gly Leu Ser Pro Lys

149

154

159

164

gaa tat gcc tgc ctg aaa ggg acc atc ctc ttc aac ccc gat gtg cca 701

Glu Tyr Ala Cys Leu Lys Gly Thr Ile Leu Phe Asn Pro Asp Val Pro

1

5

aag gag aca gta aaa tta tcc cat gaa gat gac cat att ctt gag gac	337
Lys Glu Thr Val Lys Leu Ser His Glu Asp Asp His Ile Leu Glu Asp	
12 17 22 27	
gct gga tct tct gat att tct agt gat gct gct tgt aca aat cca aat	385
Ala Gly Ser Ser Asp Ile Ser Ser Asp Ala Ala Cys Thr Asn Pro Asn	
28 33 38 43	
aag aca gaa aac agc ctt gta ggt ttg cct agt tgt gta gat gaa gtg	433
Lys Thr Glu Asn Ser Leu Val Gly Leu Pro Ser Cys Val Asp Glu Val	
44 49 54 59	
act gaa tgt aat ttg gaa ttg aag gat acc atg ggt att gct gat aaa	481
Thr Glu Cys Asn Leu Glu Leu Lys Asp Thr Met Gly Ile Ala Asp Lys	
60 65 70 75	
act gag aac acc ctt gaa aga aat aaa att gaa ccg ttg ggt tat tgt	529
Thr Glu Asn Thr Leu Glu Arg Asn Lys Ile Glu Pro Leu Gly Tyr Cys	
76 81 86 91	
gaa gat gcg gag tct aat agg cag ttg gag agc act gag ttt aat aaa	577
Glu Asp Ala Glu Ser Asn Arg Gln Leu Glu Ser Thr Glu Phe Asn Lys	
92 97 102 107	
tca aac tta gag gtg gtt gat act agt act ttt gga ccg gaa agt aat	625
Ser Asn Leu Glu Val Asp Thr Ser Thr Phe Gly Pro Glu Ser Asn	
108 113 118 123	
atc ttg gaa aat gct att tgt gat gtg cct gac caa aat tca aaa cag	673
Ile Leu Glu Asn Ala Ile Cys Asp Val Pro Asp Gln Asn Ser Lys Gln	
124 129 134 139	
ttg aat gct ata gaa agt act aaa ata gag tcc cat gaa aca gca aac	721
Leu Asn Ala Ile Glu Ser Thr Lys Ile Glu Ser His Glu Thr Ala Asn	
140 145 150 155	
ctt cag gat gac aga aac agc cag tca agt agc gtt tct tac tta gag	769
Leu Gln Asp Asp Arg Asn Ser Gln Ser Ser Ser Val Ser Tyr Leu Glu	
156 161 166 171	
tca aaa agt gta aaa tcc aaa cat aca aaa cct gta att cat tct aag	817
Ser Lys Ser Val Lys Ser Lys His Thr Lys Pro Val Ile His Ser Lys	
172 177 182 187	
caa aac atg acc aca gat gct ccg aag aaa att gtt gca gca aag tat	865
Gln Asn Met Thr Thr Asp Ala Pro Lys Lys Ile Val Ala Ala Lys Tyr	
188 193 198 203	
gaa gta ata cat agc aaa act aaa gtt aat gtc aaa agt gtg aaa cga	913
Glu Val Ile His Ser Lys Thr Lys Val Asn Val Lys Ser Val Lys Arg	
204 209 214 219	
aat act gat gta cca gaa tct cag caa aat ttt cat agg cca gtc aaa	961
Asn Thr Asp Val Pro Glu Ser Gln Gln Asn Phe His Arg Pro Val Lys	
220 225 230 235	

gtc aga aaa aaa caa att gat aag gag cca aag att cag agt tgc aat	1009
Val Arg Lys Lys Gln Ile Asp Lys Glu Pro Lys Ile Gln Ser Cys Asn	
236 241 246 251	
tct ggg gtt aaa tct gtg aaa aac caa gct cat tct gta ctg aaa aaa	1057
Ser Gly Val Lys Ser Val Lys Asn Gln Ala His Ser Val Leu Lys Lys	
252 257 262 267	
aca tta cag gat caa act tta gta caa att ttc aag ccc tta act cat	1105
Thr Leu Gln Asp Gln Thr Leu Val Gln Ile Phe Lys Pro Leu Thr His	
268 273 278 283	
tct ttg agt gat aag tca cac gct cat cct ggt tgc ttg aaa gaa cct	1153
Ser Leu Ser Asp Lys Ser His Ala His Pro Gly Cys Leu Lys Glu Pro	
284 289 294 299	
cat cat cct gca caa act gga cat gta tca cat tct agc cag aaa cag	1201
His His Pro Ala Gln Thr Gly His Val Ser His Ser Ser Gln Lys Gln	
300 305 310 315	
tgt cat aag cct cag caa cag gcc cca gca atg aaa acc aat agt cac	1249
Cys His Lys Pro Gln Gln Gln Ala Pro Ala Met Lys Thr Asn Ser His	
316 321 326 331	
gtg aag gaa gag ctt gaa cac cca ggc gtt gag cat ttt aag gaa gag	1297
Val Lys Glu Glu Leu Glu His Pro Gly Val Glu His Phe Lys Glu Glu	
332 337 342 347	
gat aaa ctg aaa ctg aaa aaa cct gag aag aac cta caa ccc cgc caa	1345
Asp Lys Leu Lys Leu Lys Lys Pro Glu Lys Asn Leu Gln Pro Arg Gln	
348 353 358 363	
aga aga agc agc aaa agt ttt tct tta gat gag cca cca ttg ttc att	1393
Arg Arg Ser Ser Lys Ser Phe Ser Leu Asp Glu Pro Pro Leu Phe Ile	
364 369 374 379	
cca gat aac ata gct acc ata aga aga gaa ggc tct gat cat agc tcc	1441
Pro Asp Asn Ile Ala Thr Ile Arg Arg Glu Gly Ser Asp His Ser Ser	
380 385 390 395	
tca ttt gaa agc aaa tat atg tgg act ccc agc aag cag tgt ggg ttt	1489
Ser Phe Glu Ser Lys Tyr Met Trp Thr Pro Ser Lys Gln Cys Gly Phe	
396 401 406 411	
tgc aaa aaa cca cat ggc aac agg ttt atg gtt ggc tgt ggg aga tgt	1537
Cys Lys Lys Pro His Gly Asn Arg Phe Met Val Gly Cys Gly Arg Cys	
412 417 422 427	
gat gac tgg ttt cat ggt gat tgt gtt ggg tta agt ctt tct caa gca	1585
Asp Asp Trp Phe His Gly Asp Cys Val Gly Leu Ser Leu Ser Gln Ala	
428 433 438 443	
cag cag atg ggc gag gaa gac aaa gaa tat gtc tgt gta aaa tgt tgt	1633
Gln Gln Met Gly Glu Glu Asp Lys Glu Tyr Val Cys Val Lys Cys Cys	
444 449 454 459	

gct gaa gaa gac aaa aag act gaa ata cta gat cca gat act ttg gaa	1681
Ala Glu Glu Asp Lys Lys Thr Glu Ile Leu Asp Pro Asp Thr Leu Glu	
460 465 470 475	
aac caa gct aca gtt gaa ttc cat agt gga gat aaa aca atg gag tgt	1729
Asn Gln Ala Thr Val Glu Phe His Ser Gly Asp Lys Thr Met Glu Cys	
476 481 486 491	
gaa aag ctt gga tta tca aaa cac aca aca aat gat aga acc aaa tat	1777
Glu Lys Leu Gly Leu Ser Lys His Thr Thr Asn Asp Arg Thr Lys Tyr	
492 497 502 507	
ata gat gat aca gtg aag cac aag gtc aaa att tta aaa cgg gag tct	1825
Ile Asp Asp Thr Val Lys His Lys Val Lys Ile Leu Lys Arg Glu Ser	
508 513 518 523	
ggt gaa ggc aga aat tca tca gac tgt aga gat aat gaa att aaa aaa	1873
Gly Glu Gly Arg Asn Ser Ser Asp Cys Arg Asp Asn Glu Ile Lys Lys	
524 529 534 539	
tgg cag cta gct cct ctt cgt aag atg gga caa cca gtt tta cct cgg	1921
Trp Gln Leu Ala Pro Leu Arg Lys Met Gly Gln Pro Val Leu Pro Arg	
540 545 550 555	
aga tcc tca gaa gaa aaa agt gaa aaa ata cgg aaa gag tct aca act	1969
Arg Ser Ser Glu Glu Lys Ser Glu Lys Ile Pro Lys Glu Ser Thr Thr	
556 561 566 571	
gtt act tgc aca gga gaa aaa gct tca aaa cca ggt act cat gag aag	2017
Val Thr Cys Thr Gly Glu Lys Ala Ser Lys Pro Gly Thr His Glu Lys	
572 577 582 587	
caa gag atg aaa aag aag aaa gtt gaa aaa gga gtg ctt aat gta cat	2065
Gln Glu Met Lys Lys Lys Lys Val Glu Lys Gly Val Leu Asn Val His	
588 593 598 603	
cct gct gct tct gct tcc aag cct tct gca gat cag atc agg caa agt	2113
Pro Ala Ala Ser Ala Ser Lys Pro Ser Ala Asp Gln Ile Arg Gln Ser	
604 609 614 619	
gtc aga cat tct ctc aaa gac att ctt atg aag aga ctt aca gac tca	2161
Val Arg His Ser Leu Lys Asp Ile Leu Met Lys Arg Leu Thr Asp Ser	
620 625 630 635	
aat ttg aag gta cca gag gaa aag gca gca aaa gtt gcc aca aaa att	2209
Asn Leu Lys Val Pro Glu Glu Lys Ala Ala Lys Val Ala Thr Lys Ile	
636 641 646 651	
gag aaa gag ctt ttc tct ttt ttt cgg gac aca gat gct aaa tat aag	2257
Glu Lys Glu Leu Phe Ser Phe Phe Arg Asp Thr Asp Ala Lys Tyr Lys	
652 657 662 667	
aac aaa tat aga agt ttg atg ttt aat ttg aaa gat cct aaa aac aat	2305
Asn Lys Tyr Arg Ser Leu Met Phe Asn Leu Lys Asp Pro Lys Asn Asn	
668 673 678 683	
ata tta ttt aaa aaa gta ctg aaa gga gaa gta act cct gat cat ctt	2353

Ile	Leu	Phe	Lys	Lys	Val	Leu	Lys	Gly	Glu	Val	Thr	Pro	Asp	His	Leu		
684					689					694					699		
atc	aga	atg	agt	cca	gaa	gaa	cta	gct	tct	aaa	gag	tta	gct	gct	tgg	2401	
Ile	Arg	Met	Ser	Pro	Glu	Glu	Leu	Ala	Ser	Lys	Glu	Leu	Ala	Ala	Trp		
700					705					710					715		
aga	cga	aga	gaa	aac	aga	cat	acc	ata	gaa	atg	att	gag	aaa	gag	cag	2449	
Arg	Arg	Arg	Glu	Asn	Arg	His	Thr	Ile	Glu	Met	Ile	Glu	Lys	Glu	Gln		
716					721					726					731		
aga	gaa	gtg	gaa	cga	cgg	cca	atc	acc	aaa	ata	act	cat	aaa	ggt	gaa	2497	
Arg	Glu	Val	Glu	Arg	Arg	Pro	Ile	Thr	Lys	Ile	Thr	His	Lys	Gly	Glu		
732					737					742					747		
ata	gaa	att	gag	agt	gat	gcc	cca	atg	aaa	gaa	cag	gaa	gca	gcc	atg	2545	
Ile	Glu	Ile	Glu	Ser	Asp	Ala	Pro	Met	Lys	Glu	Gln	Glu	Ala	Ala	Met		
748					753					758					763		
gag	att	cag	gaa	cca	gcc	gcc	aat	aag	tca	ttg	gag	aag	cca	gaa	gga	2593	
Glu	Ile	Gln	Glu	Pro	Ala	Ala	Asn	Lys	Ser	Leu	Glu	Lys	Pro	Glu	Gly		
764					769					774					779		
tct	gaa	aaa	caa	aaa	gag	gag	gtt	gac	tct	atg	tct	aaa	gat	acc	act	2641	
Ser	Glu	Lys	Gln	Lys	Glu	Glu	Val	Asp	Ser	Met	Ser	Lys	Asp	Thr	Thr		
780					785					790					795		
agt	caa	cac	aga	cag	cat	ctt	ttt	gat	ctc	aac	tgc	aaa	atc	tgc	ata	2689	
Ser	Gln	His	Arg	Gln	His	Leu	Phe	Asp	Leu	Asn	Cys	Lys	Ile	Cys	Ile		
796					801					806					811		
ggt	cga	atg	gca	cca	cct	gta	gat	gat	ctt	tct	cca	aaa	aaa	gta	aaa	2737	
Gly	Arg	Met	Ala	Pro	Pro	Val	Asp	Asp	Leu	Ser	Pro	Lys	Lys	Val	Lys		
812					817					822					827		
gtt	gtt	gta	gga	gta	gct	cgc	aaa	cat	tca	gac	aat	gaa	gca	gaa	agt	2785	
Val	Val	Val	Gly	Val	Ala	Arg	Lys	His	Ser	Asp	Asn	Glu	Ala	Glu	Ser		
828					833					838					843		
ata	gca	gat	gca	tta	tct	tca	acc	tca	aat	att	ttg	gct	tct	gaa	ttc	2833	
Ile	Ala	Asp	Ala	Leu	Ser	Ser	Thr	Ser	Asn	Ile	Leu	Ala	Ser	Glu	Phe		
844					849					854					859		
ttt	gag	gag	gag	aaa	cag	gag	tct	cca	aag	tca	acg	ttc	tct	cct	gct	2881	
Phe	Glu	Glu	Glu	Lys	Gln	Glu	Ser	Pro	Lys	Ser	Thr	Phe	Ser	Pro	Ala		
860					865					870					875		
cca	cgt	cca	gag	atg	cct	gga	act	gtt	gaa	gtt	gag	tct	acc	ttt	ctg	2929	
Pro	Arg	Pro	Glu	Met	Pro	Gly	Thr	Val	Glu	Val	Glu	Ser	Thr	Phe	Leu		
876					881					886					891		
gct	cga	ttg	aac	ttc	atc	tgg	aaa	ggt	ttt	atc	aac	atg	cct	tct	gtg	2977	
Ala	Arg	Leu	Asn	Phe	Ile	Trp	Lys	Gly	Phe	Ile	Asn	Met	Pro	Ser	Val		
892					897					902					907		
gca	aaa	ttt	gtt	acc	aaa	gcc	tat	cca	gta	tct	ggc	tcc	cca	gaa	tac	3025	
Ala	Lys	Phe	Val	Thr	Lys	Ala	Tyr	Pro	Val	Ser	Gly	Ser	Pro	Glu	Tyr		

908	913	918	923	
ctg aca gag gac cta cca gat agt att caa gta ggt ggc agg ata tca				3073
Leu Thr Glu Asp Leu Pro Asp Ser Ile Gln Val Gly Gly Arg Ile Ser				
924	929	934	939	
cct cag aca gtt tgg gat tat gtg gaa aaa ata aaa gca tca gga acc				3121
Pro Gln Thr Val Trp Asp Tyr Val Glu Lys Ile Lys Ala Ser Gly Thr				
940	945	950	955	
aag gaa att tgt gtg gtt cgc ttc aca cca gta act gaa gaa gat caa				3169
Lys Glu Ile Cys Val Val Arg Phe Thr Pro Val Thr Glu Glu Asp Gln				
956	961	966	971	
att tct tat act ttg ctc ttt gca tac ttc agt agc aga aag cgc tat				3217
Ile Ser Tyr Thr Leu Leu Phe Ala Tyr Phe Ser Ser Arg Lys Arg Tyr				
972	977	982	987	
gga gta gct gct aac aac atg aag cag gtt aaa gat atg tac ctt att				3265
Gly Val Ala Ala Asn Asn Met Lys Gln Val Lys Asp Met Tyr Leu Ile				
988	993	998	1003	
cct ttg ggt gcc aca gat aaa att cca cac cct ctt gtg cct ttt gat				3313
Pro Leu Gly Ala Thr Asp Lys Ile Pro His Pro Leu Val Pro Phe Asp				
1004	1009	1014	1019	
gga cct ggg ctt gaa ctg cat aga cct aat cta ttg ttg ggc tta att				3361
Gly Pro Gly Leu Glu Leu His Arg Pro Asn Leu Leu Leu Gly Leu Ile				
1020	1025	1030	1035	
att cgt cag aaa ctg aag cga cag cac agt gcc tgt gct agt act agt				3409
Ile Arg Gln Lys Leu Lys Arg Gln His Ser Ala Cys Ala Ser Thr Ser				
1036	1041	1046	1051	
cat ata gct gag act cct gaa agt gca cca cca ata gca ttg cca cct				3457
His Ile Ala Glu Thr Pro Glu Ser Ala Pro Pro Ile Ala Leu Pro Pro				
1052	1057	1062	1067	
gat aaa aaa agt aaa ata gaa gtt tct aca gaa gaa gca cca gag gaa				3505
Asp Lys Lys Ser Lys Ile Glu Val Ser Thr Glu Glu Ala Pro Glu Glu				
1068	1073	1078	1083	
gaa aat gac ttt ttt aat tct ttt aca act gta tta cac aag cag aga				3553
Glu Asn Asp Phe Phe Asn Ser Phe Thr Thr Val Leu His Lys Gln Arg				
1084	1089	1094	1099	
aat aaa cct cag cag aat ctt cag gaa gac ctt cca aca gca gtt gaa				3601
Asn Lys Pro Gln Gln Asn Leu Gln Glu Asp Leu Pro Thr Ala Val Glu				
1100	1105	1110	1115	
cct tta atg gaa gtc acc aaa cag gag cca cca aaa cct tta aga ttt				3649
Pro Leu Met Glu Val Thr Lys Gln Glu Pro Pro Lys Pro Leu Arg Phe				
1116	1121	1126	1131	
ctt cct ggc gtg ttg att ggc tgg gag aat caa cct act act ctg gaa				3697
Leu Pro Gly Val Leu Ile Gly Trp Glu Asn Gln Pro Thr Thr Leu Glu				
1132	1137	1142	1147	

tta gca aat aaa cct ctt cct gtg gat gat ata ctt caa agc ctt ttg	3745
Leu Ala Asn Lys Pro Leu Pro Val Asp Asp Ile Leu Gln Ser Leu Leu	
1148 1153 1158 1163	
ggc acc act ggt caa gta tat gac cag gcc cag tca gtg atg gaa caa	3793
Gly Thr Thr Gly Gln Val Tyr Asp Gln Ala Gln Ser Val Met Glu Gln	
1164 1169 1174 1179	
aac act gtt aaa gaa att cca ttt tta aat gag cag acc aac tca aaa	3841
Asn Thr Val Lys Glu Ile Pro Phe Leu Asn Glu Gln Thr Asn Ser Lys	
1180 1185 1190 1195	
ata gag aaa aca gat aat gtg gaa gta act gat ggt gaa aac aag gag	3889
Ile Glu Lys Thr Asp Asn Val Glu Val Thr Asp Gly Glu Asn Lys Glu	
1196 1201 1206 1211	
ata aaa gtt aaa gta gat aat att tca gaa tct aca gat aag tca gca	3937
Ile Lys Val Lys Val Asp Asn Ile Ser Glu Ser Thr Asp Lys Ser Ala	
1212 1217 1222 1227	
gaa ata gaa aca tca gta gta ggg tcc tct tcc att tct gca ggg tct	3985
Glu Ile Glu Thr Ser Val Val Gly Ser Ser Ser Ile Ser Ala Gly Ser	
1228 1233 1238 1243	
ttg acg agt ctt agt ctc aga ggt aag cca cca gat gtt tct aca gaa	4033
Leu Thr Ser Leu Ser Leu Arg Gly Lys Pro Pro Asp Val Ser Thr Glu	
1244 1249 1254 1259	
gca ttt tta aca aat tta tca att cag tca aaa caa gag gaa act gtg	4081
Ala Phe Leu Thr Asn Leu Ser Ile Gln Ser Lys Gln Glu Glu Thr Val	
1260 1265 1270 1275	
gag agt aaa gag aaa aca tta aaa aga cag ctt cag gaa gat caa gag	4129
Glu Ser Lys Glu Lys Thr Leu Lys Arg Gln Leu Gln Glu Asp Gln Glu	
1276 1281 1286 1291	
aat aat ttg caa gat aac cag act tca aat agt tct cca tgc aga tct	4177
Asn Asn Leu Gln Asp Asn Gln Thr Ser Asn Ser Ser Pro Cys Arg Ser	
1292 1297 1302 1307	
aat gta gga aaa gga aac ata gat ggt aat gtg agc tgt agt gaa aac	4225
Asn Val Gly Lys Gly Asn Ile Asp Gly Asn Val Ser Cys Ser Glu Asn	
1308 1313 1318 1323	
ctt gtt gct aat aca gcg agg tct cca cag ttt atc aac ctg aaa agg	4273
Leu Val Ala Asn Thr Ala Arg Ser Pro Gln Phe Ile Asn Leu Lys Arg	
1324 1329 1334 1339	
gat cct agg caa gca gca gga cga agt cag cct gta act act tca gaa	4321
Asp Pro Arg Gln Ala Ala Gly Arg Ser Gln Pro Val Thr Thr Ser Glu	
1340 1345 1350 1355	
agc aaa gat gga gat agt tgc cgg aat gga gaa aaa cac atg ctg cct	4369
Ser Lys Asp Gly Asp Ser Cys Arg Asn Gly Glu Lys His Met Leu Pro	
1356 1361 1366 1371	

ggc ctg tca cac aac aag gag cac tta aca gaa caa atc aat gta gag	4417
Gly Leu Ser His Asn Lys Glu His Leu Thr Glu Gln Ile Asn Val Glu	
1372 1377 1382 1387	
gaa aag ttg tgt tct gca gag aaa aac tcg tgt gtt cag cag agt gac	4465
Glu Lys Leu Cys Ser Ala Glu Lys Asn Ser Cys Val Gln Gln Ser Asp	
1388 1393 1398 1403	
aat tta aaa gtt gca caa aac tca cca tca gta gaa aac ata cag act	4513
Asn Leu Lys Val Ala Gln Asn Ser Pro Ser Val Glu Asn Ile Gln Thr	
1404 1409 1414 1419	
tct caa gca gaa caa gca aaa ccc tta cag gag gat att tta atg caa	4561
Ser Gln Ala Glu Gln Ala Lys Pro Leu Gln Glu Asp Ile Leu Met Gln	
1420 1425 1430 1435	
aat att gaa act gtg cac cca ttt cga aga gga tca gca gta gcg aca	4609
Asn Ile Glu Thr Val His Pro Phe Arg Arg Gly Ser Ala Val Ala Thr	
1436 1441 1446 1451	
tct cat ttt gaa gtt gga aac aca tgt cca tca gaa ttt cct tct aaa	4657
Ser His Phe Glu Val Gly Asn Thr Cys Pro Ser Glu Phe Pro Ser Lys	
1452 1457 1462 1467	
agc atc acc ttt act tcc aga agc acc agc ccc aga aca agt aca aac	4705
Ser Ile Thr Phe Thr Ser Arg Ser Thr Ser Pro Arg Thr Ser Thr Asn	
1468 1473 1478 1483	
ttt tca ccc atg agg cca cag cag ccc aac ctt cag cat ctc aag tct	4753
Phe Ser Pro Met Arg Pro Gln Gln Pro Asn Leu Gln His Leu Lys Ser	
1484 1489 1494 1499	
agc cca cct gga ttt cca ttt cca ggg cct cct aat ttt ccc cca caa	4801
Ser Pro Pro Gly Phe Pro Phe Pro Gly Pro Pro Asn Phe Pro Pro Gln	
1500 1505 1510 1515	
agc atg ttt gga ttt cca cca cat ttg cca cct cca tta ctt ccc cct	4849
Ser Met Phe Gly Phe Pro Pro His Leu Pro Pro Pro Leu Leu Pro Pro	
1516 1521 1526 1531	
cca ggc ttt ggc ttt gct caa aat ccc atg gtt ccc tgg cca cct gtt	4897
Pro Gly Phe Gly Phe Ala Gln Asn Pro Met Val Pro Trp Pro Pro Val	
1532 1537 1542 1547	
gtt cat ctc cca ggt cag cca cag cgt atg atg ggt cct ctc tca caa	4945
Val His Leu Pro Gly Gln Pro Gln Arg Met Met Gly Pro Leu Ser Gln	
1548 1553 1558 1563	
gca tca agg tat ata ggc ccg cag aat ttt tac cag gtt aaa gac att	4993
Ala Ser Arg Tyr Ile Gly Pro Gln Asn Phe Tyr Gln Val Lys Asp Ile	
1564 1569 1574 1579	
cgg agg cca gaa agg cgc cat agt gac cct tgg ggt agg caa gac caa	5041
Arg Arg Pro Glu Arg Arg His Ser Asp Pro Trp Gly Arg Gln Asp Gln	
1580 1585 1590 1595	
cag caa ctg gat agg cca ttt aat agg ggt aaa ggg gac cgc cag aga	5089

attttaaggg atattttgat tctaaatag ataaaaataat ttctcaccta ttttgtgtgt 6199
gtgacttgaa attcagtagt aaaagaattt cttctttaaa gctttaaaaa aaaaaaa 6256

<210> 270
<211> 4125
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (546)..(3089)

<220>
<221> misc_feature
<222> (1)...(4125)
<223> n = a,t,c or g

<400> 270
cataggccaa caataaatga ataggtcatc ttagcaccca gttttcactt atcttcggct 60
gtatgttggt ggattggacg gaaaccattt ccacagaaca gttatgacag attcgaatta 120
aaacgctcac tataggaatt ggcttcgag gccagatcgg gcacgagggg gagagggcct 180
taaagggtggc gtccgctgtt agaaacactt ggcgagggta aaggggtggc ggcgagagga 240
ggttcccacc cgtggctttc ttagagaaat gaagtcttaa gtcttaata gacaacaagg 300
agggccgacg ggtgtcnttt ggacgcgtct ggngccctc cctccgccaa aggaaaagcc 360
ccttgatga gaggcaggcg cttcagagaa gctaagaaaa gcacctctcc gcgcgccccca 420
cctcctcgc ctcgcgtcc tctgagcag cgggccaga ctgcgtccg gccgcggccc 480
tcgcccgcg gagccctcct accccggccc gacgctcggc ccgcgacctg ccccgagccc 540
tctcc atg gag gca gcc cgc ccc tcc ggc tcc tgg aac gga gcc ctc 587
Met Glu Ala Ala Arg Pro Ser Gly Ser Trp Asn Gly Ala Leu
1 5 10
tgc cgg ctg ctc ctg ctg acc ctc gcg atc tta ata ttt gcc agt gat 635
Cys Arg Leu Leu Leu Leu Thr Leu Ala Ile Leu Ile Phe Ala Ser Asp
15 20 25 30
gcc tgc aaa aat gtg aca tta cat gtt ccc tcc aaa cta gat gcc gag 683
Ala Cys Lys Asn Val Thr Leu His Val Pro Ser Lys Leu Asp Ala Glu
31 36 41 46
aaa ctt gtt ggt aga gtt aac ctg aaa gag tgc ttt aca gct gca aat 731
Lys Leu Val Gly Arg Val Asn Leu Lys Glu Cys Phe Thr Ala Ala Asn
47 52 57 62
cta att cat tca agt gat cct gac ttc caa att ttg gag gat ggt tca 779

Leu Ile His Ser Ser Asp Pro Asp Phe Gln Ile Leu Glu Asp Gly Ser	
63 68 73 78	
gtc tat aca aca aat act att cta ttg tcc tcg gag aag aga agt ttt	827
Val Tyr Thr Thr Asn Thr Ile Leu Leu Ser Ser Glu Lys Arg Ser Phe	
79 84 89 94	
acc ata tta ctt tcc aac act gag aac caa gaa aag aag aaa ata ttt	875
Thr Ile Leu Leu Ser Asn Thr Glu Asn Gln Glu Lys Lys Lys Ile Phe	
95 100 105 110	
gtc ttt ttg gag cat caa aca aag gtc cta aag aaa aga cat act aaa	923
Val Phe Leu Glu His Gln Thr Lys Val Leu Lys Lys Arg His Thr Lys	
111 116 121 126	
gaa aaa gtt cta agg cgc gcc aag aga aga tgg gct cca att cct tgt	971
Glu Lys Val Leu Arg Arg Ala Lys Arg Arg Trp Ala Pro Ile Pro Cys	
127 132 137 142	
tcg atg cta gaa aac tcc ttg ggt cct ttt cca ctt ttc ctt caa cag	1019
Ser Met Leu Glu Asn Ser Leu Gly Pro Phe Pro Leu Phe Leu Gln Gln	
143 148 153 158	
gtt caa tct gac acg gcc caa aac tat acc ata tac tat tcc ata aga	1067
Val Gln Ser Asp Thr Ala Gln Asn Tyr Thr Ile Tyr Tyr Ser Ile Arg	
159 164 169 174	
ggg cct gga gtt gac caa gaa cct cgg aat tta ttt tat gtg gag aga	1115
Gly Pro Gly Val Asp Gln Glu Pro Arg Asn Leu Phe Tyr Val Glu Arg	
175 180 185 190	
gac act gga aac ttg tat tgt act cgt cct gta gat cgt gag cag tat	1163
Asp Thr Gly Asn Leu Tyr Cys Thr Arg Pro Val Asp Arg Glu Gln Tyr	
191 196 201 206	
gaa tct ttt gag ata att gcc ttt gca aca act cca gat ggg tat act	1211
Glu Ser Phe Glu Ile Ile Ala Phe Ala Thr Thr Pro Asp Gly Tyr Thr	
207 212 217 222	
cca gaa ctt cca ctg ccc cta ata atc aaa ata gag gat gaa aat gat	1259
Pro Glu Leu Pro Leu Pro Leu Ile Ile Lys Ile Glu Asp Glu Asn Asp	
223 228 233 238	
aac tac cca att ttt aca gaa gaa act tat act ttt aca att ttt gaa	1307
Asn Tyr Pro Ile Phe Thr Glu Glu Thr Tyr Thr Phe Thr Ile Phe Glu	
239 244 249 254	
aat tgc aga gtg ggc act act gtg gga caa gtg tgt gct act gac aaa	1355
Asn Cys Arg Val Gly Thr Thr Val Gly Gln Val Cys Ala Thr Asp Lys	
255 260 265 270	
gat gag cct gac acg atg cac aca cgc ctg aag tac tcc atc att ggg	1403
Asp Glu Pro Asp Thr Met His Thr Arg Leu Lys Tyr Ser Ile Ile Gly	
271 276 281 286	
cag gtg cca cca tca ccc acc cta ttt tct atg cat cca act aca ggc	1451
Gln Val Pro Pro Ser Pro Thr Leu Phe Ser Met His Pro Thr Thr Gly	

287	292	297	302	
gtg atc acc aca aca tca tct cag cta gac aga gag tta att gac aag				1499
Val Ile Thr Thr Thr Ser Ser Gln Leu Asp Arg Glu Leu Ile Asp Lys				
303	308	313	318	
tac cag ttg aaa ata aaa gta caa gac atg gat ggt cag tat ttt ggt				1547
Tyr Gln Leu Lys Ile Lys Val Gln Asp Met Asp Gly Gln Tyr Phe Gly				
319	324	329	334	
cta cag aca act tca act tgt atc att aac att gat gat gta aat gac				1595
Leu Gln Thr Thr Ser Thr Cys Ile Ile Asn Ile Asp Asp Val Asn Asp				
335	340	345	350	
cac ttg cca aca ttt act cgt act tct tat gtg aca tca gtg gaa gaa				1643
His Leu Pro Thr Phe Thr Arg Thr Ser Tyr Val Thr Ser Val Glu Glu				
351	356	361	366	
aat aca gtt gat gtg gaa atc tta cga gtt act gtt gag gat aag gac				1691
Asn Thr Val Asp Val Glu Ile Leu Arg Val Thr Val Glu Asp Lys Asp				
367	372	377	382	
tta gtg aat act gct aac tgg aga gct aat tat acc att tta aag ggc				1739
Leu Val Asn Thr Ala Asn Trp Arg Ala Asn Tyr Thr Ile Leu Lys Gly				
383	388	393	398	
aat gaa aat ggc aat ttt aaa att gta aca gat gcc aaa acc aat gaa				1787
Asn Glu Asn Gly Asn Phe Lys Ile Val Thr Asp Ala Lys Thr Asn Glu				
399	404	409	414	
gga gtt ctt tgt gta gtt aag cct ttg aat tat gaa gaa aag caa cag				1835
Gly Val Leu Cys Val Val Lys Pro Leu Asn Tyr Glu Glu Lys Gln Gln				
415	420	425	430	
atg atc ttg caa att ggt gta gtt aat gaa gct cca ttt tcc aga gag				1883
Met Ile Leu Gln Ile Gly Val Val Asn Glu Ala Pro Phe Ser Arg Glu				
431	436	441	446	
gct agt cca aga tca gcc atg agc aca gca aca gtt act gtt aat gta				1931
Ala Ser Pro Arg Ser Ala Met Ser Thr Ala Thr Val Thr Val Asn Val				
447	452	457	462	
gaa gat cag gat gag ggc cct gag tgt aac cct cca ata cag act gtt				1979
Glu Asp Gln Asp Glu Gly Pro Glu Cys Asn Pro Pro Ile Gln Thr Val				
463	468	473	478	
cgc atg aaa gaa aat gca gaa gtg gga aca aca agc aat gga tat aaa				2027
Arg Met Lys Glu Asn Ala Glu Val Gly Thr Thr Ser Asn Gly Tyr Lys				
479	484	489	494	
gca tat gac cca gaa aca aga agt agc agt ggc ata agg tat aag aaa				2075
Ala Tyr Asp Pro Glu Thr Arg Ser Ser Ser Gly Ile Arg Tyr Lys Lys				
495	500	505	510	
tta act gat cca aca ggg tgg gtc acc att gat gaa aat aca gga tca				2123
Leu Thr Asp Pro Thr Gly Trp Val Thr Ile Asp Glu Asn Thr Gly Ser				
511	516	521	526	

atc aaa gtt ttc aga agc ctg gat aga gag gca gag acc atc aaa aat Ile Lys Val Phe Arg Ser Leu Asp Arg Glu Ala Glu Thr Ile Lys Asn 527 532 537 542	2171
ggc ata tat aat att aca gtc ctt gca tca gac caa gga ggg aga aca Gly Ile Tyr Asn Ile Thr Val Leu Ala Ser Asp Gln Gly Gly Arg Thr 543 548 553 558	2219
tgt acg ggg aca ctg ggc att ata ctt caa gac gtg aat gat aac agc Cys Thr Gly Thr Leu Gly Ile Ile Leu Gln Asp Val Asn Asp Asn Ser 559 564 569 574	2267
cca ttc ata cct aaa aag aca gtg atc atc tgc aaa ccc acc atg tca Pro Phe Ile Pro Lys Lys Thr Val Ile Ile Cys Lys Pro Thr Met Ser 575 580 585 590	2315
tct gcg gag att gtt gcg gtt gat cct gat gag cct atc cat ggc cca Ser Ala Glu Ile Val Ala Val Asp Pro Asp Glu Pro Ile His Gly Pro 591 596 601 606	2363
ccc ttt gac ttt agt ctg gag agt tct act tca gaa gta cag aga atg Pro Phe Asp Phe Ser Leu Glu Ser Ser Thr Ser Glu Val Gln Arg Met 607 612 617 622	2411
tgg aga ctg aaa gca att aat gat aca gca gca cgt ctt tcc tat cag Trp Arg Leu Lys Ala Ile Asn Asp Thr Ala Ala Arg Leu Ser Tyr Gln 623 628 633 638	2459
aat gat cct cca ttt ggc tca tat gta gta cct ata aca gtg aga gat Asn Asp Pro Pro Phe Gly Ser Tyr Val Val Pro Ile Thr Val Arg Asp 639 644 649 654	2507
aga ctt ggc atg tct agt gtc act tca ttg gat gtt aca ctg tgt gac Arg Leu Gly Met Ser Ser Val Thr Ser Leu Asp Val Thr Leu Cys Asp 655 660 665 670	2555
tgc att acc gaa aat gac tgc aca cat cgt gta gat cca agg att ggc Cys Ile Thr Glu Asn Asp Cys Thr His Arg Val Asp Pro Arg Ile Gly 671 676 681 686	2603
ggg gga gga gta caa ctt gga aag tgg gcc atc ctt gca ata ttg ttg Gly Gly Gly Val Gln Leu Gly Lys Trp Ala Ile Leu Ala Ile Leu Leu 687 692 697 702	2651
ggc ata gca ttg ctc ttt tgc atc ctg ttt acg ctg gtc tgt ggg gct Gly Ile Ala Leu Leu Phe Cys Ile Leu Phe Thr Leu Val Cys Gly Ala 703 708 713 718	2699
tct ggg acg tct aaa caa cca aaa gta att cct gat gat tta gcc cag Ser Gly Thr Ser Lys Gln Pro Lys Val Ile Pro Asp Asp Leu Ala Gln 719 724 729 734	2747
cag aac cta att gta tca aac aca gaa gct cct gga gat gac aaa gtg Gln Asn Leu Ile Val Ser Asn Thr Glu Ala Pro Gly Asp Asp Lys Val 735 740 745 750	2795

tat tct gcg aat ggc ttc aca acc caa act gtg ggc gct tct gct cag	2843
Tyr Ser Ala Asn Gly Phe Thr Thr Gln Thr Val Gly Ala Ser Ala Gln	
751 756 761 766	
gga gtt tgt ggc acc gtg gga tca gga atc aaa aac gga ggt cag gag	2891
Gly Val Cys Gly Thr Val Gly Ser Gly Ile Lys Asn Gly Gly Gln Glu	
767 772 777 782	
acc atc gaa atg gtg aaa gga gga cac cag acc tcg gaa tcc tgc cgg	2939
Thr Ile Glu Met Val Lys Gly Gly His Gln Thr Ser Glu Ser Cys Arg	
783 788 793 798	
ggg gct ggc cac cat cac acc ctg gac tcc tgc agg gga gga cac acg	2987
Gly Ala Gly His His His Thr Leu Asp Ser Cys Arg Gly Gly His Thr	
799 804 809 814	
gag gtg gac aac tgc aga tac act tac tcg gag tgg cac agt ttt act	3035
Glu Val Asp Asn Cys Arg Tyr Thr Tyr Ser Glu Trp His Ser Phe Thr	
815 820 825 830	
cag ccc cgt ctt ggt gaa gaa tcc att aga gga cac act ctg att aaa	3083
Gln Pro Arg Leu Gly Glu Glu Ser Ile Arg Gly His Thr Leu Ile Lys	
831 836 841 846	
aat taa acaatgaaag aaagtgtatc tgtgtaatca agatgaaaat cacaagcatg	3139
Asn *	
847	
cccaagacta tgtcctgaca tataactatg aaggaagagg atcgggtggct gggctctgtag	3199
gttgttgacag tgaacgacaa gaagaagatg ggcttgaatt tttggataat ttggagccca	3259
aatttaggac actagcagaa gcatgcatga agagatgagt gtgttctaata aagtctctga	3319
aagccagtgg ctttatgact tttaaaaaaa attacaaacc aagaatTTTT taaagcagaa	3379
gatgctatTT gtggggggtt ttctctcatt atttggatgg aatctctttg gtcaaagtga	3439
catttacaga gagacactat aaacaagtac acaaattttt caatttttac atatttttaa	3499
attacttata ttctatccaa ggaggtctac agagaaatta aagtctgcct tatttgttac	3559
atttgggtat aatgacaaca gccaatTTat agtgcaataa aatgtaatta attcaagttc	3619
ttattataga ctatttgaag cacaacctaa tggaaaattg tagagacctt gctttaacat	3679
tatctccagt taattaagtg ttcattgtgg gcttggaac tggtgttttc ctgaacatct	3739
aaagtgtgta gactgcattc ttgtattat tttattgttg taatgtgacc ttttcaactgt	3799
gcaaaggag atttctagcc aggcattgac tattacaatt tcattttggg ggagtttagt	3859
tttaggtttt attgtatata agatcctgca ctgaatctgt gtctcctctg ttacctactt	3919
ttgccagtga aatttaagtt ttaaaataact ttcagaatgt atttttacta ctgcaagttt	3979
ttgggtcttta aaatgtcaag tagcatctct ctctttctct ctgtctcttt ctgtttctct	4039

ctccagtttt tttttttttt aatttccata tgggctaaga atcagaatat ttgaaatctg 4099
tctggctttc tccctcataa gtgagg 4125

<210> 271
<211> 1865
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (107)..(1558)

<400> 271
gaaagaaatt gagatggtgc acgatgcaca gttgaagtga acttgcgggg tttttcagta 60
tctacgattc atagatctgg aattcgcggc cgcgtcgacc cgcacc atg ggg tcc 115
Met Gly Ser
1
cgc cac ttc gag ggg att tat gac cac gtg ggg cac ttc ggc aga ttc 163
Arg His Phe Glu Gly Ile Tyr Asp His Val Gly His Phe Gly Arg Phe
4 9 14 19
cag aga gtc ctc tat ttc ata tgt gcc ttc cag aac atc tct tgt ggt 211
Gln Arg Val Leu Tyr Phe Ile Cys Ala Phe Gln Asn Ile Ser Cys Gly
20 25 30 35
att cac tac ttg gct tct gtg ttc atg gga gtc acc cct cat cat gtc 259
Ile His Tyr Leu Ala Ser Val Phe Met Gly Val Thr Pro His His Val
36 41 46 51
tgc agg ccc cca ggc aat tgt cat ctg gac tca ttg tgg gac ttg ggg 307
Cys Arg Pro Pro Gly Asn Cys His Leu Asp Ser Leu Trp Asp Leu Gly
52 57 62 67
att aga gga cct gag aca aag atg ctg ctg ccc tac tgc ttg cta acg 355
Ile Arg Gly Pro Glu Thr Lys Met Leu Leu Pro Tyr Cys Leu Leu Thr
68 73 78 83
aag cta gga cgc cgg gtg gtc ttg tgg gcc aca agc agt agc atg ttt 403
Lys Leu Gly Arg Arg Val Val Leu Trp Ala Thr Ser Ser Ser Met Phe
84 89 94 99
ttg ttt gga ata gca gcg gcg ttt gca gtt gat tat tac acc ttc atg 451
Leu Phe Gly Ile Ala Ala Ala Phe Ala Val Asp Tyr Tyr Thr Phe Met
100 105 110 115
gct gct cgc ttt ttt ctt gcc atg gtt gca agt ggc tat ctt gtg gtg 499
Ala Ala Arg Phe Phe Leu Ala Met Val Ala Ser Gly Tyr Leu Val Val
116 121 126 131
ggg ttt gtc tat gtg atg gaa ttc att ggc atg aag tct cgg aca tgg 547

Gly Phe Val Tyr Val Met Glu Phe Ile Gly Met Lys Ser Arg Thr Trp	
132 137 142 147	
gcg tct gtc cat ttg cat tcc ttt ttt gca gtt gga acc ctg ctg gtg	595
Ala Ser Val His Leu His Ser Phe Phe Ala Val Gly Thr Leu Leu Val	
148 153 158 163	
gct ttg aca gga tac ttg gtc agg acc tgg tgg ctt tac cag atg atc	643
Ala Leu Thr Gly Tyr Leu Val Arg Thr Trp Trp Leu Tyr Gln Met Ile	
164 169 174 179	
ctc tcc aca gtg act gtc ccc ttt atc ctg tgc tgt tgg gtg ctc cca	691
Leu Ser Thr Val Thr Val Pro Phe Ile Leu Cys Cys Trp Val Leu Pro	
180 185 190 195	
gag aca cct ttt tgg ctt ctc tca gag gga cga tat gaa gaa gca caa	739
Glu Thr Pro Phe Trp Leu Leu Ser Glu Gly Arg Tyr Glu Glu Ala Gln	
196 201 206 211	
aaa ata gtt gac atc atg gcc aag tgg aac agg gca agc tcc tgt aaa	787
Lys Ile Val Asp Ile Met Ala Lys Trp Asn Arg Ala Ser Ser Cys Lys	
212 217 222 227	
ctg tca gaa ctt tta tca ctg gac cta caa ggt cct gtt agt aat agc	835
Leu Ser Glu Leu Leu Ser Leu Asp Leu Gln Gly Pro Val Ser Asn Ser	
228 233 238 243	
ccc act gaa gtt cag aag cac aac cta tca tat ctg ttt tat aac tgg	883
Pro Thr Glu Val Gln Lys His Asn Leu Ser Tyr Leu Phe Tyr Asn Trp	
244 249 254 259	
agc att acg aaa agg aca ctt acc gtt tgg cta atc tgg ttc act gga	931
Ser Ile Thr Lys Arg Thr Leu Thr Val Trp Leu Ile Trp Phe Thr Gly	
260 265 270 275	
agt ttg gga ttc tac tgc ttt tcc ttg aat tct gtt aac tta gga ggc	979
Ser Leu Gly Phe Tyr Ser Phe Ser Leu Asn Ser Val Asn Leu Gly Gly	
276 281 286 291	
aat gaa tac tta aac ctc ttc ctc ctg ggt gta gtg gaa att ccc gcc	1027
Asn Glu Tyr Leu Asn Leu Phe Leu Leu Gly Val Val Glu Ile Pro Ala	
292 297 302 307	
tac acc ttc gtg tgc atc gcc atg gac aag gtc ggg agg aga aca gtc	1075
Tyr Thr Phe Val Cys Ile Ala Met Asp Lys Val Gly Arg Arg Thr Val	
308 313 318 323	
ctg gcc tac tct ctt ttc tgc agt gca ctg gcc tgt ggt gtc gtt atg	1123
Leu Ala Tyr Ser Leu Phe Cys Ser Ala Leu Ala Cys Gly Val Val Met	
324 329 334 339	
gtg atc ccc cag aaa cat tat att ttg ggt gtg gtg aca gct atg gtt	1171
Val Ile Pro Gln Lys His Tyr Ile Leu Gly Val Val Thr Ala Met Val	
340 345 350 355	
gga aaa ttt gcc atc ggg gca gca ttt ggc ctc att tat ctt tat aca	1219
Gly Lys Phe Ala Ile Gly Ala Ala Phe Gly Leu Ile Tyr Leu Tyr Thr	

356	361	366	371	
gct gag ctg tat cca acc att gta aga tgc ctg gct gtg gga agc ggc				1267
Ala Glu Leu Tyr Pro Thr Ile Val Arg Ser Leu Ala Val Gly Ser Gly				
372	377	382	387	
agc atg gtg tgt cgc ctg gcc agc atc ctg gcg ccg ttc tct gtg gac				1315
Ser Met Val Cys Arg Leu Ala Ser Ile Leu Ala Pro Phe Ser Val Asp				
388	393	398	403	
ctc agc agc att tgg atc ttc ata cca cag ttg ttt gtt ggg act atg				1363
Leu Ser Ser Ile Trp Ile Phe Ile Pro Gln Leu Phe Val Gly Thr Met				
404	409	414	419	
gcc ctc ctg agt gga gtg tta aca cta aag ctt cca gaa acc ctt ggg				1411
Ala Leu Leu Ser Gly Val Leu Thr Leu Lys Leu Pro Glu Thr Leu Gly				
420	425	430	435	
aaa cgg cta gca act act tgg gag gag gct gca aaa ctg gag tca gag				1459
Lys Arg Leu Ala Thr Thr Trp Glu Glu Ala Ala Lys Leu Glu Ser Glu				
436	441	446	451	
aat gaa agc aag tca agc aaa tta ctt ctc aca act aat aat agt ggg				1507
Asn Glu Ser Lys Ser Ser Lys Leu Leu Leu Thr Thr Asn Asn Ser Gly				
452	457	462	467	
ctg gaa aaa acg gaa gcg att acc ccc agg gat tct ggt ctt ggt gaa				1555
Leu Glu Lys Thr Glu Ala Ile Thr Pro Arg Asp Ser Gly Leu Gly Glu				
468	473	478	483	
taa atgt gccatgcctg ctgtctagca cctgaaatat tatttaccct aatgcctttg				1612
*				
484				
tattagagga atcttattct catctcccat atgttgtttg tatgtctttt taataaattt				1672
tgtaagaaaa ttttaaagca aatatgttat aaaagaaata aaaactaaga tgaaaattct				1732
cagttttaaa aactgctttc ttattgctgc aaaatatttt tcaacatttg tttttctatg				1792
tagttgattc tcaacctttc cccaccaccc ccctaccatg ctcggtgccga attcttggcc				1852
tcgagggcca aat				1865

<210> 272
 <211> 2495
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (411)..(812)

 <400> 272

taggggacta gtggatctta tcatagtttt ggctgactat gcagggctta aaaggccagc	1095
gtctgtttga gggggaatga cctctaaccat ctgtaaaatt tgtctcatct ttttaatttct	1155
tttaacttatt tcaaaatcat ctcatgaccc ttgtgtgcct ctttgtgaag ccctatttag	1215
caatttcagg ggagtcaaaa accttgcaac ttcctttctcc actaaccag gactaaaaat	1275
ggacaggctg acctcagtgt ttacaaattc agaattttga taggggtaga tatggagaaa	1335
gacctatttc ctgggtctct gctgtgtagt ctccttcagg cttattgtgc tcagtgaaca	1395
tccagtgtg ggtgcagctc catcacctc ttgtgtgtt acatgtctct ttctatgata	1455
agagggttgt gttggtggca cctccactac tcttttctgt ttgttgagtt tgaattgtgt	1515
aacatctttg atcagtgggt gtatctgtaa tgaaggaggt tcaaggaggt gtgctttcca	1575
agtgatagtc tataggagtg ttttaatttct tgcagctcca tctggttgct gcatttgaag	1635
catggcatta atttgtattt gcctgttct ttgacctaaa gttgaagggt ttagagtttt	1695
taacctgac tgtagagcag agaggttgaa agcacttaac tcttgtttag tatcctcatt	1755
gccttgctgc ctgggtatct ggcccccttc cataaacatt tcttttcagt tcatgtagtt	1815
ctttaataga aagctgctat tatgtatatt gtcatttgtg aaggaagttg gagagtcaca	1875
gctttactgt gacaggtttt gcccaaggct ttgataacctg tccccagggt tatcttaaaa	1935
gcaagttgtt cccccactac tttcctttcc ctctgccctg ccattcctat tacaatgctg	1995
tgaaaaaagt totgottctt aggtgaatgg gtactttcta ttttgtttct aaacgagcaa	2055
ttttgaggat gaaatgggaa gatatcattg cttccttttt gcacctattg ggtatgtaca	2115
ctctggccga agggagtctt tatgttttagt ttcaaaatat attactttcc tggattctct	2175
tcttcacttt ttctgacttt ggggtccattt tcttttcatt gcctcctttt ccaggcagct	2235
ctattcttgc agagccatag caggacatgt taaaattcca atagaaaaca ctaaaaggaa	2295
agtctgtgga atcactagtg actaaatact gggaacctat tttctcaatc ttctccatg	2355
ttgtgttctt tgtattcttg agatgataat atattatgta tttgaattcc tgaaaaatgg	2415
aaaatgttta agatatatgt atataaagtg tatgctgtat tggtgcaata atggtaatta	2475
aaaatatgaa aaaaaaaaaa	2495

<210> 273
 <211> 2362
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (62)..(2128)

<400> 273

cgggcgcgcg tcccggtccag gtccggagta accgccgccg ccgccgccaa agctcgccaa 60

c atg gcg gac ctg gag gct gtg ctg gcc gat gtc agt tac ctg atg 106
Met Ala Asp Leu Glu Ala Val Leu Ala Asp Val Ser Tyr Leu Met
1 5 10

gcc atg gag aag agc aag gcg acc ccg gcc gcc cgc gcc agc aag agg 154
Ala Met Glu Lys Ser Lys Ala Thr Pro Ala Ala Arg Ala Ser Lys Arg
16 21 26 31

atc gtc ctg ccg gag ccc agt atc cgg agt gtg atg cag aag tac ctt 202
Ile Val Leu Pro Glu Pro Ser Ile Arg Ser Val Met Gln Lys Tyr Leu
32 37 42 47

gca gag aga aat gaa ata acc ttt gac aag att ttc aat cag aaa att 250
Ala Glu Arg Asn Glu Ile Thr Phe Asp Lys Ile Phe Asn Gln Lys Ile
48 53 58 63

ggg ttc ttg cta ttt aaa gat ttt tgt ttg aat gaa att aat gaa gct 298
Gly Phe Leu Leu Phe Lys Asp Phe Cys Leu Asn Glu Ile Asn Glu Ala
64 69 74 79

gta cct cag gtg aag ttt tat gaa gag ata aag gaa tat gaa aaa ctt 346
Val Pro Gln Val Lys Phe Tyr Glu Glu Ile Lys Glu Tyr Glu Lys Leu
80 85 90 95

gat aat gag gaa gac cgc ctt tgc aga agt cga caa att tat gat gcc 394
Asp Asn Glu Glu Asp Arg Leu Cys Arg Ser Arg Gln Ile Tyr Asp Ala
96 101 106 111

tac atc atg aag gaa ctt ctt tcc tgt tca cat cct ttc tca aag caa 442
Tyr Ile Met Lys Glu Leu Leu Ser Cys Ser His Pro Phe Ser Lys Gln
112 117 122 127

gct gta gaa cac gta caa agt cat tta tcc aag aaa caa gtg aca tca 490
Ala Val Glu His Val Gln Ser His Leu Ser Lys Lys Gln Val Thr Ser
128 133 138 143

act ctt ttt cag cca tac ata gaa gaa att tgt gaa agc ctt cga ggt 538
Thr Leu Phe Gln Pro Tyr Ile Glu Glu Ile Cys Glu Ser Leu Arg Gly
144 149 154 159

gac att ttt caa aaa ttt atg gaa agt gac aag ttc act aga ttt tgt 586
Asp Ile Phe Gln Lys Phe Met Glu Ser Asp Lys Phe Thr Arg Phe Cys
160 165 170 175

cag tgg aaa aac gtt gaa tta aat atc cat ttg acc atg aat gag ttc 634
Gln Trp Lys Asn Val Glu Leu Asn Ile His Leu Thr Met Asn Glu Phe
176 181 186 191

agt gtg cat agg att att gga cga gga gga ttc ggg gaa gtt tat ggt	682
Ser Val His Arg Ile Ile Gly Arg Gly Gly Phe Gly Glu Val Tyr Gly	
192 197 202 207	
tgC agg aaa gca gac act gga aaa atg tat gca atg aaa tgc tta gat	730
Cys Arg Lys Ala Asp Thr Gly Lys Met Tyr Ala Met Lys Cys Leu Asp	
208 213 218 223	
aag aag agg atc aaa atg aaa caa gga gaa aca tta gcc tta aat gaa	778
Lys Lys Arg Ile Lys Met Lys Gln Gly Glu Thr Leu Ala Leu Asn Glu	
224 229 234 239	
aga atc atg ttg tct ctt gtc agc aca gga gac tgt cct ttc att gta	826
Arg Ile Met Leu Ser Leu Val Ser Thr Gly Asp Cys Pro Phe Ile Val	
240 245 250 255	
tgt atg acc tat gcc ttc cat acc cca gat aaa ctc tgc ttc atc ctg	874
Cys Met Thr Tyr Ala Phe His Thr Pro Asp Lys Leu Cys Phe Ile Leu	
256 261 266 271	
gat ctg atg aac ggg ggc gat ttg cac tac cac ctt tca caa cac ggt	922
Asp Leu Met Asn Gly Gly Asp Leu His Tyr His Leu Ser Gln His Gly	
272 277 282 287	
gtg ttc tct gag aag gag atg cgg ttt tat gcc act gaa atc att ctg	970
Val Phe Ser Glu Lys Glu Met Arg Phe Tyr Ala Thr Glu Ile Ile Leu	
288 293 298 303	
ggg ctg gaa cac atg cac aat cgg ttt gtt gtc tac aga gat ttg aag	1018
Gly Leu Glu His Met His Asn Arg Phe Val Val Tyr Arg Asp Leu Lys	
304 309 314 319	
cca gca aat att ctc ttg gat gaa cat gga cac gca aga ata tca gat	1066
Pro Ala Asn Ile Leu Leu Asp Glu His Gly His Ala Arg Ile Ser Asp	
320 325 330 335	
ctt ggt ctt gcc tgc gat ttt tcc aaa aag aag cct cat gcg agt gtg	1114
Leu Gly Leu Ala Cys Asp Phe Ser Lys Lys Lys Pro His Ala Ser Val	
336 341 346 351	
ggc acc cat ggg tac atg gct ccc gag gtg ctg cag aag ggg acg gcc	1162
Gly Thr His Gly Tyr Met Ala Pro Glu Val Leu Gln Lys Gly Thr Ala	
352 357 362 367	
tat gac agc agt gcc gac tgg ttc tcc ctg ggc tgc atg ctt ttc aaa	1210
Tyr Asp Ser Ser Ala Asp Trp Phe Ser Leu Gly Cys Met Leu Phe Lys	
368 373 378 383	
ctt ctg aga ggg cac agc cct ttc aga caa cat aaa acc aaa gac aag	1258
Leu Leu Arg Gly His Ser Pro Phe Arg Gln His Lys Thr Lys Asp Lys	
384 389 394 399	
cat gaa att/gac cga atg aca ctc acc gtg aat gtg gaa ctt cca gac	1306
His Glu Ile Asp Arg Met Thr Leu Thr Val Asn Val Glu Leu Pro Asp	
400 405 410 415	
acc ttc tct cct gaa ctg aag tcc ctt ttg gag ggc ttg ctt cag cga	1354

Thr Phe Ser Pro Glu Leu Lys Ser Leu Leu Glu Gly Leu Leu Gln Arg	
416 421 426 431	
gac gtt agc aag cgg ctg ggc tgt cac gga ggc ggc tca cag gaa gta	1402
Asp Val Ser Lys Arg Leu Gly Cys His Gly Gly Gly Ser Gln Glu Val	
432 437 442 447	
aaa gag cac agc ttt ttc aaa ggt gtt gac tgg cag cat gtc tac tta	1450
Lys Glu His Ser Phe Phe Lys Gly Val Asp Trp Gln His Val Tyr Leu	
448 453 458 463	
caa aag tac cca cca ccc ttg att cct ccc cgg gga gaa gtc aat gct	1498
Gln Lys Tyr Pro Pro Pro Leu Ile Pro Pro Arg Gly Glu Val Asn Ala	
464 469 474 479	
gct gat gcc ttt gat att ggc tca ttt gat gaa gag gat acc aaa ggg	1546
Ala Asp Ala Phe Asp Ile Gly Ser Phe Asp Glu Glu Asp Thr Lys Gly	
480 485 490 495	
att aag cta ctt gat tgc gac caa gaa ctc tac aag aac ttc cct ttg	1594
Ile Lys Leu Leu Asp Cys Asp Gln Glu Leu Tyr Lys Asn Phe Pro Leu	
496 501 506 511	
gtc atc tct gaa cgc tgg cag caa gaa gta acg gaa aca gtt tat gaa	1642
Val Ile Ser Glu Arg Trp Gln Gln Glu Val Thr Glu Thr Val Tyr Glu	
512 517 522 527	
gca gta aat gca gac aca gat aaa atc gag gcc agg aag aga gct aaa	1690
Ala Val Asn Ala Asp Thr Asp Lys Ile Glu Ala Arg Lys Arg Ala Lys	
528 533 538 543	
aat aag caa ctt ggc cac gaa gaa gat tac gct ctg ggg aag gac tgt	1738
Asn Lys Gln Leu Gly His Glu Glu Asp Tyr Ala Leu Gly Lys Asp Cys	
544 549 554 559	
att atg cac ggg tac atg ctg aaa ctg gga aac cca ttt ctg act cag	1786
Ile Met His Gly Tyr Met Leu Lys Leu Gly Asn Pro Phe Leu Thr Gln	
560 565 570 575	
tgg cag cgt cgc tat ttt tac ctc ttt cca aat aga ctt gaa tgg aga	1834
Trp Gln Arg Arg Tyr Phe Tyr Leu Phe Pro Asn Arg Leu Glu Trp Arg	
576 581 586 591	
gga gag gga gag tcc cgg caa aat tta ctg aca atg gaa cag att ctc	1882
Gly Glu Gly Glu Ser Arg Gln Asn Leu Leu Thr Met Glu Gln Ile Leu	
592 597 602 607	
tct gtg gaa gaa act caa att aaa gac aaa aaa tgc att ttg ttc aga	1930
Ser Val Glu Glu Thr Gln Ile Lys Asp Lys Lys Cys Ile Leu Phe Arg	
608 613 618 623	
ata aaa gga ggg aaa caa ttt gtc ttg caa tgt gag agt gat cca gag	1978
Ile Lys Gly Gly Lys Gln Phe Val Leu Gln Cys Glu Ser Asp Pro Glu	
624 629 634 639	
ttt gtg cag tgg aag aaa gag ttg aac gaa acc ttc aag gag gcc cag	2026
Phe Val Gln Trp Lys Lys Glu Leu Asn Glu Thr Phe Lys Glu Ala Gln	

640	645	650	655	
cgg cta ttg cgt cgt gcc ccg aag ttc ctc aac aaa cct cgg tca ggt				2074
Arg Leu Leu Arg Arg Ala Pro Lys Phe Leu Asn Lys Pro Arg Ser Gly				
656	661	666	671	
act gtg gag ctc cca aag cca tcc ctc tgt cac aga aac agc aac ggc				2122
Thr Val Glu Leu Pro Lys Pro Ser Leu Cys His Arg Asn Ser Asn Gly				
672	677	682	687	
ctc tag caccagaaa cagggagggt cctcgaggag gacacaccag ggtctcagcc				2178
Leu *				
688				
ttttggggtg aacgaggatg aggcattctga tctattcgct accgggactc ctccaggctc				2238
ccgagaggag tcgggaccct tcggcttggg gtcagctcag ctccctgcct tgtcacattt				2298
gtctgcatta gaaactactg aagaaataaa agttcttttt ctttgctaca aaaaaaaaaa				2358
aaaa				2362

<210> 274
 <211> 1829
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (146)..(1390)

<400> 274	
attacgccaa gcttggcacg aggcgtttgt cccttgccgt acccgactta ataccaatgt	60
agccccgggaa ccgagttgcg ggagtgcggt ctgtgccgtt ccggccagga gtttgccgac	120
tgcagacgtc ctgcgaaccg gcaag atg tgc tct ctg ggg ttg ttc cct cct	172
Met Cys Ser Leu Gly Leu Phe Pro Pro	
1 5	
cca ccg cct cgg ggt caa gtc acc cta tat gag cac aat aac gag ctg	220
Pro Pro Pro Arg Gly Gln Val Thr Leu Tyr Glu His Asn Asn Glu Leu	
10 15 20 25	
gtg acg ggc agt agc tat gag agc ccg ccc ccc gac ttc cgg ggc cag	268
Val Thr Gly Ser Ser Tyr Glu Ser Pro Pro Pro Asp Phe Arg Gly Gln	
26 31 36 41	
tgg atc aat ctt cct gtc cta caa ctg aca aag gat ccc cta aag acc	316
Trp Ile Asn Leu Pro Val Leu Gln Leu Thr Lys Asp Pro Leu Lys Thr	
42 47 52 57	
cct gga agg ctg gac cat ggc aca aga act gcc ttc atc cat cac cgg	364
Pro Gly Arg Leu Asp His Gly Thr Arg Thr Ala Phe Ile His His Arg	

58	63	68	73	
gag caa gtg tgg aag aga tgc atc aac att tgg cgt gat gtg ggc ctt				412
Glu Gln Val Trp Lys Arg Cys Ile Asn Ile Trp Arg Asp Val Gly Leu				
74	79	84	89	
ttt ggg gtg cta aat gaa att gca aac tca gaa gaa gag gtg ttt gag				460
Phe Gly Val Leu Asn Glu Ile Ala Asn Ser Glu Glu Glu Val Phe Glu				
90	95	100	105	
tgg gtg aag acg gca tcc ggc tgg gcc ctg gca ctc tgt cga tgg gcc				508
Trp Val Lys Thr Ala Ser Gly Trp Ala Leu Ala Leu Cys Arg Trp Ala				
106	111	116	121	
tct tcc ctc cat ggg tcc ctg ttc ccc cat ctg tct ctc agg agc gaa				556
Ser Ser Leu His Gly Ser Leu Phe Pro His Leu Ser Leu Arg Ser Glu				
122	127	132	137	
gat ctg atc gct gaa ttt gcc caa gtc aca aat tgg tcc agc tgc tgc				604
Asp Leu Ile Ala Glu Phe Ala Gln Val Thr Asn Trp Ser Ser Cys Cys				
138	143	148	153	
ttg cgt gtc ttt gca tgg cac ccc cac acc aac aag ttt gca gtg gcc				652
Leu Arg Val Phe Ala Trp His Pro His Thr Asn Lys Phe Ala Val Ala				
154	159	164	169	
ctg cta gat gac tca gtc cgt gtg tat aat gcc agc agc acc ata gtc				700
Leu Leu Asp Asp Ser Val Arg Val Tyr Asn Ala Ser Ser Thr Ile Val				
170	175	180	185	
ccc tcc ctg aag cac cgg ctg cag cga aat gtg gcg tct ctg gcc tgg				748
Pro Ser Leu Lys His Arg Leu Gln Arg Asn Val Ala Ser Leu Ala Trp				
186	191	196	201	
aag ccc ctt agt gcc tct gtc ttg gct gtg gcc tgc cag agc tgc att				796
Lys Pro Leu Ser Ala Ser Val Leu Ala Val Ala Cys Gln Ser Cys Ile				
202	207	212	217	
ctt atc tgg acc ctg gac cct acc tcc ttg tct acc cga ccc tct tct				844
Leu Ile Trp Thr Leu Asp Pro Thr Ser Leu Ser Thr Arg Pro Ser Ser				
218	223	228	233	
ggc tgt gcc caa gtg ctg tct cac cct ggg cat aca cct gtt acc agc				892
Gly Cys Ala Gln Val Leu Ser His Pro Gly His Thr Pro Val Thr Ser				
234	239	244	249	
ttg gcc tgg gcc ccc agt ggg ggg cgg ctg ctc tca gct tca ccc gtg				940
Leu Ala Trp Ala Pro Ser Gly Gly Arg Leu Leu Ser Ala Ser Pro Val				
250	255	260	265	
gat gct gct atc cgg gta tgg gat gtc tca aca gag acc tgt gtc ccc				988
Asp Ala Ala Ile Arg Val Trp Asp Val Ser Thr Glu Thr Cys Val Pro				
266	271	276	281	
ctt ccc tgg ttt cga gga ggt ggg gtg acc aac ctg ctc tgg tcc cca				1036
Leu Pro Trp Phe Arg Gly Gly Gly Val Thr Asn Leu Leu Trp Ser Pro				
282	287	292	297	

gac ggc agc aaa atc ctg gct acc act cct tca gct gtc ttt cga gtc	1084
Asp Gly Ser Lys Ile Leu Ala Thr Thr Pro Ser Ala Val Phe Arg Val	
298 303 308 313	
tgg gag gcc cag atg tgg act tgt gag agg tgg cct act cta tca ggg	1132
Trp Glu Ala Gln Met Trp Thr Cys Glu Arg Trp Pro Thr Leu Ser Gly	
314 319 324 329	
cgc tgt cag act ggc tgc tgg agc cca gat ggc agc cga ctg ctg ttc	1180
Arg Cys Gln Thr Gly Cys Trp Ser Pro Asp Gly Ser Arg Leu Leu Phe	
330 335 340 345	
act gta ttg gga gag cca ctg att tac tcc ctg tct ttt cca gaa cgt	1228
Thr Val Leu Gly Glu Pro Leu Ile Tyr Ser Leu Ser Phe Pro Glu Arg	
346 351 356 361	
tgt ggt gag gga aag ggt gcg ttg gag gtg caa agt cag caa cga ttg	1276
Cys Gly Glu Gly Lys Gly Ala Leu Glu Val Gln Ser Gln Gln Arg Leu	
362 367 372 377	
tgg cag atc tgt ctg aga caa caa tac aga cac cag atg gtg agg aga	1324
Trp Gln Ile Cys Leu Arg Gln Gln Tyr Arg His Gln Met Val Arg Arg	
378 383 388 393	
ggc ttg ggg gag agg ctc act cca tgg tct ggg acc cca gtg ggg aac	1372
Gly Leu Gly Glu Arg Leu Thr Pro Trp Ser Gly Thr Pro Val Gly Asn	
394 399 404 409	
gtc tgg ctg tgc tta tga aaggaa agccaagggt acaggatggt aaaccagtca	1426
Val Trp Leu Cys Leu *	
410 415	
tcctcctttt tcgcactcga aacagccctg tgtttgagct ccttcctgt ggcattatcc	1486
agggggagcc aggagcccag cccagctca tcactttcca tccttccttc aacaaagggg	1546
ccctgctcag tgtgggctgg tccacaggcc gaattgccca catcccgctg tactttgtca	1606
atgcccagtt tccacgtttt agcccagtgc ttgggcgggc ccaggaaccc cctgctgggg	1666
gtggaggctc tattcatgac ctgcccctct ttactgagac atccccaacc tctgcccctt	1726
gggaccctct cccagggccca ccacctgttc tgcccactc cccacattcc cacctctaag	1786
aataaataag ttttcctttt gttttccact caaaaaaaaaaaa aaa	1829

<210> 275

<211> 1708

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (36)..(1571)

<400> 275

gcacaggagg agttggcgtc cggggagcaa gggcc atg gcc acc gtg cag gag 53
Met Ala Thr Val Gln Glu
1

aag gct gct gcg ctg aac ctc tcg gct ctc cac agc ccc gcg cac agg 101
Lys Ala Ala Ala Leu Asn Leu Ser Ala Leu His Ser Pro Ala His Arg
7 12 17 22

cct ccg ggt ttc agt gta gct cag aag cca ttt gga gcc acg tat gta 149
Pro Pro Gly Phe Ser Val Ala Gln Lys Pro Phe Gly Ala Thr Tyr Val
23 28 33 38

tgg agc agc atc ata aac act ctt caa aca caa gtg gaa gtg aaa aaa 197
Trp Ser Ser Ile Ile Asn Thr Leu Gln Thr Gln Val Glu Val Lys Lys
39 44 49 54

cga agg cac cgt tta aaa cga cat aat gac tgc ttt gtt ggt tca gaa 245
Arg Arg His Arg Leu Lys Arg His Asn Asp Cys Phe Val Gly Ser Glu
55 60 65 70

gct gtg gat gtc att ttt tct cac cta att cag aat aag tat ttt ggt 293
Ala Val Asp Val Ile Phe Ser His Leu Ile Gln Asn Lys Tyr Phe Gly
71 76 81 86

gat gta gat att cct cga gcc aaa gtg gtg aga gtg tgt caa gcg ctt 341
Asp Val Asp Ile Pro Arg Ala Lys Val Val Arg Val Cys Gln Ala Leu
87 92 97 102

atg gac tac aaa gta ttt gaa gca gtt cca acc aaa gtc ttt gga aaa 389
Met Asp Tyr Lys Val Phe Glu Ala Val Pro Thr Lys Val Phe Gly Lys
103 108 113 118

gac aaa aaa cct aca ttt gaa gat agt agt tgc agc ctt tat aga ttc 437
Asp Lys Lys Pro Thr Phe Glu Asp Ser Ser Cys Ser Leu Tyr Arg Phe
119 124 129 134

acc aca ata cct aac caa gac agt cag tta ggc aaa gag aac aaa cta 485
Thr Thr Ile Pro Asn Gln Asp Ser Gln Leu Gly Lys Glu Asn Lys Leu
135 140 145 150

tat tca cct gcc agg tat gca gat gca tta ttt aag tca tcc gat atc 533
Tyr Ser Pro Ala Arg Tyr Ala Asp Ala Leu Phe Lys Ser Ser Asp Ile
151 156 161 166

aga tca gcc agt tta gag gac ctg tgg gaa aat ctg agt tta aag cct 581
Arg Ser Ala Ser Leu Glu Asp Leu Trp Glu Asn Leu Ser Leu Lys Pro
167 172 177 182

gcc aac tcc cct cat gta aat atc tct aca acc ttg tct cca caa gtt 629
Ala Asn Ser Pro His Val Asn Ile Ser Thr Thr Leu Ser Pro Gln Val
183 188 193 198

att aat gaa gtg tgg caa gaa gaa aca att ggg cgt cta cta caa ctt 677
Ile Asn Glu Val Trp Gln Glu Glu Thr Ile Gly Arg Leu Leu Gln Leu

199	204	209	214	
gta gac ctt cca ctt ctt gac tcc tta ctg aaa cag caa gag gct gta				725
Val Asp Leu Pro Leu Leu Asp Ser Leu Leu Lys Gln Gln Glu Ala Val				
215	220	225	230	
cct aaa att cct caa cct aag agg cag tcc acc atg gtc aac agc agt				773
Pro Lys Ile Pro Gln Pro Lys Arg Gln Ser Thr Met Val Asn Ser Ser				
231	236	241	246	
aac tat ctg gat cga ggg att ctc aag gct tat agt gac tct cag gaa				821
Asn Tyr Leu Asp Arg Gly Ile Leu Lys Ala Tyr Ser Asp Ser Gln Glu				
247	252	257	262	
gat gag tgg ctc tcg gca gca att gac tgt tta gaa tac ctt cca gac				869
Asp Glu Trp Leu Ser Ala Ala Ile Asp Cys Leu Glu Tyr Leu Pro Asp				
263	268	273	278	
caa atg gtg gtg gaa ata agc aga agc ttt cct gag caa cca gac cga				917
Gln Met Val Val Glu Ile Ser Arg Ser Phe Pro Glu Gln Pro Asp Arg				
279	284	289	294	
aca gac tta gtg aaa gaa ctt ctg ttt gat gcc att ggc aga tat tac				965
Thr Asp Leu Val Lys Glu Leu Leu Phe Asp Ala Ile Gly Arg Tyr Tyr				
295	300	305	310	
agt agt agg gaa cct ctg tta aat cac tta tct gac gtt cat aat gga				1013
Ser Ser Arg Glu Pro Leu Leu Asn His Leu Ser Asp Val His Asn Gly				
311	316	321	326	
att gca gaa ctc tta gtg aat ggg aag acg gaa ata gct tta gaa gct				1061
Ile Ala Glu Leu Leu Val Asn Gly Lys Thr Glu Ile Ala Leu Glu Ala				
327	332	337	342	
acc cag ctc ctt cta aag ctt tta gat ttc caa aat aga gaa gaa ttt				1109
Thr Gln Leu Leu Leu Lys Leu Leu Asp Phe Gln Asn Arg Glu Glu Phe				
343	348	353	358	
aga aga cta ctg tat ttc atg gct gtt gca gca aat cct tct gag ttt				1157
Arg Arg Leu Leu Tyr Phe Met Ala Val Ala Ala Asn Pro Ser Glu Phe				
359	364	369	374	
aaa tta cag aaa gaa agt gac aac cga atg gtt gtg aaa agg ata ttc				1205
Lys Leu Gln Lys Glu Ser Asp Asn Arg Met Val Val Lys Arg Ile Phe				
375	380	385	390	
tca aaa gct att gtt gac aat aaa aat tta tcc aaa ggc aaa aca gat				1253
Ser Lys Ala Ile Val Asp Asn Lys Asn Leu Ser Lys Gly Lys Thr Asp				
391	396	401	406	
ctt ctg gta ctc ttt tta atg gat cat cag aaa gat gtt ttt aag att				1301
Leu Leu Val Leu Phe Leu Met Asp His Gln Lys Asp Val Phe Lys Ile				
407	412	417	422	
cct gga act cta cat aaa att gta agt gtt aag ctt atg gcc ata cag				1349
Pro Gly Thr Leu His Lys Ile Val Ser Val Lys Leu Met Ala Ile Gln				
423	428	433	438	

aac gga aga gat cca aat aga gat gca gga tat att tat tgc cag aga	1397
Asn Gly Arg Asp Pro Asn Arg Asp Ala Gly Tyr Ile Tyr Cys Gln Arg	
439 444 449 454	
att gat caa cgt gac tat tcc aac aat aca gag aag aca acc aaa gat	1445
Ile Asp Gln Arg Asp Tyr Ser Asn Asn Thr Glu Lys Thr Thr Lys Asp	
455 460 465 470	
gag ctg ttg aat tta cta aaa act ctt gat gag gat tca aaa ctt tct	1493
Glu Leu Leu Asn Leu Leu Lys Thr Leu Asp Glu Asp Ser Lys Leu Ser	
471 476 481 486	
gcc aaa gag aag aaa aaa ttg cta ggt caa ttc tat aag tgt cac cca	1541
Ala Lys Glu Lys Lys Lys Leu Leu Gly Gln Phe Tyr Lys Cys His Pro	
487 492 497 502	
gac atc ttt att gag cat ttt gga gac tga g tttttaatat ctgtatataa	1592
Asp Ile Phe Ile Glu His Phe Gly Asp *	
503 508	
gttgtgtatt ttaagaataa attatgtatc ctaaatatcc aatcacattt gtaagtgtgg	1652
aagctctaaa tttgaaactg tacttaataa aaattttttt gtataaaaaa aaaaaa	1708

<210> 276
 <211> 1582
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (132)..(1052)

<400> 276	
ccactttgta caagaaagct gggtacgcgt aagcttgggc ccctcgaggg atactctaga	60
gcggccgctc gcgatctaga gccgagggca cgtgcatgcc ccctgggttaa gagttgcagg	120
tagcggtagc g atg gac act ctg gat cga gta gta aag ccc aaa acg aaa	170
Met Asp Thr Leu Asp Arg Val Val Lys Pro Lys Thr Lys	
1 5 10	
aga gcc aag aga ttc ctt gag aag aga gaa ccg aaa ctc aat gaa aat	218
Arg Ala Lys Arg Phe Leu Glu Lys Arg Glu Pro Lys Leu Asn Glu Asn	
14 19 24 29	
att aaa aat gcc atg ctg att aaa ggg gga aat gca aat gca aca gtg	266
Ile Lys Asn Ala Met Leu Ile Lys Gly Gly Asn Ala Asn Ala Thr Val	
30 35 40 45	
aca aaa gta ctt aaa gat gtg tat gca ctg aaa aaa cca tac agt gta	314
Thr Lys Val Leu Lys Asp Val Tyr Ala Leu Lys Lys Pro Tyr Ser Val	
46 51 56 61	

cta tat aaa aag aaa aat att aca aga cct ttt gag gat cag aca tca	362
Leu Tyr Lys Lys Lys Asn Ile Thr Arg Pro Phe Glu Asp Gln Thr Ser	
62 67 72 77	
ctg gaa ttc ttt tca aag aag tca gat tgt tct tta ttc atg ttt ggc	410
Leu Glu Phe Phe Ser Lys Lys Ser Asp Cys Ser Leu Phe Met Phe Gly	
78 83 88 93	
tcc cat aat aag aag cgg cca aat aat cta gta ata ggt cgt atg tat	458
Ser His Asn Lys Lys Arg Pro Asn Asn Leu Val Ile Gly Arg Met Tyr	
94 99 104 109	
gac tac cat gtg ctg gat atg att gaa tta ggt att gag aat ttt gtc	506
Asp Tyr His Val Leu Asp Met Ile Glu Leu Gly Ile Glu Asn Phe Val	
110 115 120 125	
tct cta aaa gac att aag aac agt aaa tgt cct gag gga aca aaa ccc	554
Ser Leu Lys Asp Ile Lys Asn Ser Lys Cys Pro Glu Gly Thr Lys Pro	
126 131 136 141	
atg ctg ata ttt gct ggc gat gat ttc gat gta aca gaa gat tat aga	602
Met Leu Ile Phe Ala Gly Asp Asp Phe Asp Val Thr Glu Asp Tyr Arg	
142 147 152 157	
aga cta aaa agt ctt ctt att gat ttc ttc aga ggc ccc aca gta tca	650
Arg Leu Lys Ser Leu Leu Ile Asp Phe Phe Arg Gly Pro Thr Val Ser	
158 163 168 173	
aat atc cgc ctg gct gga tta gag tat gtt ctg cac ttc act gca ctg	698
Asn Ile Arg Leu Ala Gly Leu Glu Tyr Val Leu His Phe Thr Ala Leu	
174 179 184 189	
aat ggg aag att tac ttt cga agc tat aag ttg ctg ttg aag aaa tct	746
Asn Gly Lys Ile Tyr Phe Arg Ser Tyr Lys Leu Leu Leu Lys Lys Ser	
190 195 200 205	
ggc tgc aga aca cca cgg att gaa ttg gaa gag atg gga ccc tca ttg	794
Gly Cys Arg Thr Pro Arg Ile Glu Leu Glu Glu Met Gly Pro Ser Leu	
206 211 216 221	
gat ctg gtt ctg agg agg aca cac ctg gca tcg gat gac ctt tat aaa	842
Asp Leu Val Leu Arg Arg Thr His Leu Ala Ser Asp Asp Leu Tyr Lys	
222 227 232 237	
tta tct atg aaa atg cca aaa gct ctc aag cca aag aag aag aaa aat	890
Leu Ser Met Lys Met Pro Lys Ala Leu Lys Pro Lys Lys Lys Lys Asn	
238 243 248 253	
att tcc cat gat act ttt ggt aca act tat gga agg att cat atg cag	938
Ile Ser His Asp Thr Phe Gly Thr Thr Tyr Gly Arg Ile His Met Gln	
254 259 264 269	
aag caa gac cta agc aaa cta caa acc agg aaa atg aag ggg ttg aag	986
Lys Gln Asp Leu Ser Lys Leu Gln Thr Arg Lys Met Lys Gly Leu Lys	
270 275 280 285	

[illegible]

1

1

1

59	64	69	74	
tct gcg cag tgc agg	cag ata ccg ttt gac	acc acc aac aac aga aag		292
Ser Ala Gln Cys Arg	Gln Ile Pro Phe Asp	Thr Thr Asn Asn Arg Lys		
75	80	85	90	
atc aga gtt aat gga	acc aaa gaa cct atc	gag ttc aaa tcc aat cag		340
Ile Arg Val Asn Gly	Thr Lys Glu Pro Ile	Glu Phe Lys Ser Asn Gln		
91	96	101	106	
tgg ttt gga gca aca	gtg aaa gct cac aaa	gga aaa gtt gtg gcc tgt		388
Trp Phe Gly Ala Thr	Val Lys Ala His Lys	Gly Lys Val Val Ala Cys		
107	112	117	122	
gct cct tta tat cac	tgg aga act ctt aaa	ccg aca cca gaa aaa gga		436
Ala Pro Leu Tyr His	Trp Arg Thr Leu Lys	Pro Thr Pro Glu Lys Gly		
123	128	133	138	
cca gtt ggc acc tgc	tat gta gca att cag	aac ttc agc gct tat gcc		484
Pro Val Gly Thr Cys	Tyr Val Ala Ile Gln	Asn Phe Ser Ala Tyr Ala		
139	144	149	154	
gag ttc tct cct tgc	gga aac agc aat gct	gat ccg gaa ggc cag ggt		532
Glu Phe Ser Pro Cys	Gly Asn Ser Asn Ala	Asp Pro Glu Gly Gln Gly		
155	160	165	170	
tac tgc caa gca gga	ttt agt ctg gat ttt	tat aag aat gga gac ctt		580
Tyr Cys Gln Ala Gly	Phe Ser Leu Asp Phe	Tyr Lys Asn Gly Asp Leu		
171	176	181	186	
att gtg gga gga cct	ggg agt ttc tac tgg	caa gga caa gtg atc act		628
Ile Val Gly Gly Pro	Gly Ser Phe Tyr Trp	Gln Gly Gln Val Ile Thr		
187	192	197	202	
gcc agt gtt gca gat	atc att gca aat tac	tca ttc aag gat atc ctc		676
Ala Ser Val Ala Asp	Ile Ile Ala Asn Tyr	Ser Phe Lys Asp Ile Leu		
203	208	213	218	
agg aaa ctg gca gga	gaa aag cag acg gaa	gtg gct cca gct tcc tat		724
Arg Lys Leu Ala Gly	Glu Lys Gln Thr Glu	Val Ala Pro Ala Ser Tyr		
219	224	229	234	
gat gac agt tac ctt	gga tac tca gtt gct	gct ggg gag ttt act ggg		772
Asp Asp Ser Tyr Leu	Gly Tyr Ser Val Ala	Ala Gly Glu Phe Thr Gly		
235	240	245	250	
gat tct cag caa gaa	ttg gtt gct gga att	cca aga gga gca cag aat		820
Asp Ser Gln Gln Glu	Leu Val Ala Gly Ile	Pro Arg Gly Ala Gln Asn		
251	256	261	266	
ttt gga tat gtt tcc	atc att aac tcc tac	gat atg acg ttt att cag		868
Phe Gly Tyr Val Ser	Ile Ile Asn Ser Tyr	Asp Met Thr Phe Ile Gln		
267	272	277	282	
aat ttc acg gga gaa	cag atg gca tct tat	ttt gga tat acc gtt gtc		916
Asn Phe Thr Gly Glu	Gln Met Ala Ser Tyr	Phe Gly Tyr Thr Val Val		
283	288	293	298	

gta tca gat gtt aac agt gat gga ctg gat gat gtc ctg gtt ggg gca	964
Val Ser Asp Val Asn Ser Asp Gly Leu Asp Asp Val Leu Val Gly Ala	
299 304 309 314	
cct ctc ttt atg gaa cgt gaa ttt gag agc aac ccc aga gaa gta ggg	1012
Pro Leu Phe Met Glu Arg Glu Phe Glu Ser Asn Pro Arg Glu Val Gly	
315 320 325 330	
caa atc tac ctg tat ttg caa gtg agc tct ctc ctc ttc aga gac ccc	1060
Gln Ile Tyr Leu Tyr Leu Gln Val Ser Ser Leu Leu Phe Arg Asp Pro	
331 336 341 346	
cag atc ctc act ggc acc gag acg ttt ggg aga ttc ggt agt gct atg	1108
Gln Ile Leu Thr Gly Thr Glu Thr Phe Gly Arg Phe Gly Ser Ala Met	
347 352 357 362	
gca cac tta gga gac ctg aac caa gat ggc tac aat gac att gcc atc	1156
Ala His Leu Gly Asp Leu Asn Gln Asp Gly Tyr Asn Asp Ile Ala Ile	
363 368 373 378	
gga gtg cct ttt gca ggc aag gat caa aga ggc aaa gtg ctc att tat	1204
Gly Val Pro Phe Ala Gly Lys Asp Gln Arg Gly Lys Val Leu Ile Tyr	
379 384 389 394	
aat ggg aac aaa gat ggc tta aac acc aag cct tcc caa gtt ctg caa	1252
Asn Gly Asn Lys Asp Gly Leu Asn Thr Lys Pro Ser Gln Val Leu Gln	
395 400 405 410	
gga gtg tgg gcc tca cat gct gtc cct tcc gga ttt ggc ttt act tta	1300
Gly Val Trp Ala Ser His Ala Val Pro Ser Gly Phe Gly Phe Thr Leu	
411 416 421 426	
aga gga gat tca gac ata gac aag aat gat tac cca gat ttg att gtg	1348
Arg Gly Asp Ser Asp Ile Asp Lys Asn Asp Tyr Pro Asp Leu Ile Val	
427 432 437 442	
ggg gca ttt gga aca gga aaa gtc gct gtt tac aga gca aga ccg gtt	1396
Gly Ala Phe Gly Thr Gly Lys Val Ala Val Tyr Arg Ala Arg Pro Val	
443 448 453 458	
gtg act gta gat gcc cag ctt ctg ctg cac cca atg att atc aat ctt	1444
Val Thr Val Asp Ala Gln Leu Leu Leu His Pro Met Ile Ile Asn Leu	
459 464 469 474	
gaa aat aaa act tgc cag gtt cca gac tct atg aca tct gct gcc tgc	1492
Glu Asn Lys Thr Cys Gln Val Pro Asp Ser Met Thr Ser Ala Ala Cys	
475 480 485 490	
ttt tct tta aga gta tgt gca tct gtc aca ggc cag agc att gca aac	1540
Phe Ser Leu Arg Val Cys Ala Ser Val Thr Gly Gln Ser Ile Ala Asn	
491 496 501 506	
aca ata gtc ttg atg gca gag gtg caa tta gat tcc ctg aaa cag aaa	1588
Thr Ile Val Leu Met Ala Glu Val Gln Leu Asp Ser Leu Lys Gln Lys	
507 512 517 522	

gga gct att aaa cgg acg ctc ttc ctt gat aac cat cag gct cat cgc	1636
Gly Ala Ile Lys Arg Thr Leu Phe Leu Asp Asn His Gln Ala His Arg	
523 528 533 538	
gtc ttc cct ctt gtg ata aaa agg cag aaa tcc cac cag tgc cag gat	1684
Val Phe Pro Leu Val Ile Lys Arg Gln Lys Ser His Gln Cys Gln Asp	
539 544 549 554	
ttc atc gtt tac ctt cga gat gaa act gaa ttc cga gat aaa tta tct	1732
Phe Ile Val Tyr Leu Arg Asp Glu Thr Glu Phe Arg Asp Lys Leu Ser	
555 560 565 570	
cca atc aac att agt ttg aat tac agt ttg gac gaa tcc acc ttt aaa	1780
Pro Ile Asn Ile Ser Leu Asn Tyr Ser Leu Asp Glu Ser Thr Phe Lys	
571 576 581 586	
gaa ggc ctg gaa gtg aaa cca ata ttg aac tac tac aga gaa aac att	1828
Glu Gly Leu Glu Val Lys Pro Ile Leu Asn Tyr Tyr Arg Glu Asn Ile	
587 592 597 602	
gtt agt gaa cag gct cac att ctg gtg gac tgt gga gaa gac aat ctg	1876
Val Ser Glu Gln Ala His Ile Leu Val Asp Cys Gly Glu Asp Asn Leu	
603 608 613 618	
tgt gtt cct gac ttg aag ctg tcg gct aga cca gat aag cat cag gta	1924
Cys Val Pro Asp Leu Lys Leu Ser Ala Arg Pro Asp Lys His Gln Val	
619 624 629 634	
atc att gga gat gaa aat cac ctt atg ctc ata ata aat gca aga aat	1972
Ile Ile Gly Asp Glu Asn His Leu Met Leu Ile Ile Asn Ala Arg Asn	
635 640 645 650	
gaa ggg gaa gga gca tat gaa gct gaa ctc ttt gta atg ata cca gaa	2020
Glu Gly Glu Gly Ala Tyr Glu Ala Glu Leu Phe Val Met Ile Pro Glu	
651 656 661 666	
gag gca gat tat gtt gga atc gaa cgc aac aac aag gga ttt cga cca	2068
Glu Ala Asp Tyr Val Gly Ile Glu Arg Asn Asn Lys Gly Phe Arg Pro	
667 672 677 682	
ctg agc tgt gag tac aag atg gaa aat gta acc agg atg gtg gtg tgt	2116
Leu Ser Cys Glu Tyr Lys Met Glu Asn Val Thr Arg Met Val Val Cys	
683 688 693 698	
gac ctt ggg aac cct atg gtg tct gga aca aat tat tcc ctg ggc ctc	2164
Asp Leu Gly Asn Pro Met Val Ser Gly Thr Asn Tyr Ser Leu Gly Leu	
699 704 709 714	
cga ttt gca gtt cca cgt ctt gag aaa aca aac atg agc att aac ttc	2212
Arg Phe Ala Val Pro Arg Leu Glu Lys Thr Asn Met Ser Ile Asn Phe	
715 720 725 730	
gat ctc caa atc aga agt tcc aac aag gac aat cca gac agc aat ttt	2260
Asp Leu Gln Ile Arg Ser Ser Asn Lys Asp Asn Pro Asp Ser Asn Phe	
731 736 741 746	
gtg agc ctg caa atc aac atc act gct gta gcg cag gtg gaa ata aga	2308

Val	Ser	Leu	Gln	Ile	Asn	Ile	Thr	Ala	Val	Ala	Gln	Val	Glu	Ile	Arg	
747					752					757					762	
gga	gtg	tca	cac	cct	ccg	cag	att	gtt	ctg	ccc	att	cat	aac	tgg	gaa	2356
Gly	Val	Ser	His	Pro	Pro	Gln	Ile	Val	Leu	Pro	Ile	His	Asn	Trp	Glu	
763					768					773					778	
cca	gaa	gag	gag	ccc	cac	aaa	gag	gag	gag	ggt	gga	cca	ttg	gtg	gaa	2404
Pro	Glu	Glu	Glu	Pro	His	Lys	Glu	Glu	Glu	Val	Gly	Pro	Leu	Val	Glu	
779					784					789					794	
cat	att	tat	gag	ctg	cac	aat	att	gga	cca	agt	acc	atc	agt	gac	acc	2452
His	Ile	Tyr	Glu	Leu	His	Asn	Ile	Gly	Pro	Ser	Thr	Ile	Ser	Asp	Thr	
795					800					805					810	
atc	ctg	gag	gtg	ggc	tgg	cct	ttc	tct	gcc	cgg	gat	gaa	ttt	ctt	ctc	2500
Ile	Leu	Glu	Val	Gly	Trp	Pro	Phe	Ser	Ala	Arg	Asp	Glu	Phe	Leu	Leu	
811					816					821					826	
tat	att	ttc	cat	att	caa	act	ctg	gga	cct	ctg	cag	tgc	caa	cca	aat	2548
Tyr	Ile	Phe	His	Ile	Gln	Thr	Leu	Gly	Pro	Leu	Gln	Cys	Gln	Pro	Asn	
827					832					837					842	
cct	aat	atc	aat	cca	cag	gat	ata	aag	cct	gct	gcc	tcc	cca	gag	gac	2596
Pro	Asn	Ile	Asn	Pro	Gln	Asp	Ile	Lys	Pro	Ala	Ala	Ser	Pro	Glu	Asp	
843					848					853					858	
acc	cct	gag	ctc	agc	gcc	ttt	ttg	cga	aac	tct	act	att	cct	cat	ctt	2644
Thr	Pro	Glu	Leu	Ser	Ala	Phe	Leu	Arg	Asn	Ser	Thr	Ile	Pro	His	Leu	
859					864					869					874	
gtc	agg	aag	agg	gat	gta	cat	gtg	gtc	gaa	ttc	cac	aga	cag	agc	cct	2692
Val	Arg	Lys	Arg	Asp	Val	His	Val	Val	Glu	Phe	His	Arg	Gln	Ser	Pro	
875					880					885					890	
gca	aaa	ata	ctg	aat	tgt	aca	aat	atc	gag	tgt	tta	caa	atc	tcc	tgt	2740
Ala	Lys	Ile	Leu	Asn	Cys	Thr	Asn	Ile	Glu	Cys	Leu	Gln	Ile	Ser	Cys	
891					896					901					906	
gca	gtg	gga	cga	ctc	gaa	gga	gga	gaa	agc	gca	gtc	ctg	aaa	gtc	agg	2788
Ala	Val	Gly	Arg	Leu	Glu	Gly	Gly	Glu	Ser	Ala	Val	Leu	Lys	Val	Arg	
907					912					917					922	
tca	cga	tta	tgg	gcc	cac	acc	ttc	ctc	cag	aga	aaa	aat	gat	ccc	tat	2836
Ser	Arg	Leu	Trp	Ala	His	Thr	Phe	Leu	Gln	Arg	Lys	Asn	Asp	Pro	Tyr	
923					928					933					938	
gct	ctt	gca	tcc	ctg	gtg	tcc	ttt	gaa	gtt	aag	aag	atg	cct	tat	aca	2884
Ala	Leu	Ala	Ser	Leu	Val	Ser	Phe	Glu	Val	Lys	Lys	Met	Pro	Tyr	Thr	
939					944					949					954	
gat	cag	cca	gca	aaa	ctc	cca	gaa	gga	agc	ata	gca	att	aag	aca	tca	2932
Asp	Gln	Pro	Ala	Lys	Leu	Pro	Glu	Gly	Ser	Ile	Ala	Ile	Lys	Thr	Ser	
955					960					965					970	
gtt	att	tgg	gca	act	ccg	aat	gtt	tcc	ttc	tca	atc	cca	tta	tgg	gta	2980
Val	Ile	Trp	Ala	Thr	Pro	Asn	Val	Ser	Phe	Ser	Ile	Pro	Leu	Trp	Val	

971	976	981	986	
ata ata cta gca ata ctt ctt gga ttg ttg gtt ctc gcc att tta acc				3028
Ile Ile Leu Ala Ile Leu Leu Gly Leu Leu Val Leu Ala Ile Leu Thr				
987	992	997	1002	
tta gct tta tgg aag tgt gga ttc ttt gac aga gcc aga cct cct cag				3076
Leu Ala Leu Trp Lys Cys Gly Phe Phe Asp Arg Ala Arg Pro Pro Gln				
1003	1008	1013	1018	
gag gac atg acc gac agg gaa cag ctg aca aat gac aag acc cct gag				3124
Glu Asp Met Thr Asp Arg Glu Gln Leu Thr Asn Asp Lys Thr Pro Glu				
1019	1024	1029	1034	
gca tga caagaaaaaa aaaaaa				3146
Ala *				
1035				

<210> 278
 <211> 3524
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (184)..(1545)

<400> 278	
taagcttgcg gccgccaatt tttttttttt tttttttct gctgccgctc cgggtccggg	60
ccattttccg ggccggggcgc actaagggtgc ggggccccgg ggcccagtat atgaccgcgc	120
gtcctgctat ccttcgcttc ccccgcccca tgtggctgcg gggccgcggc ggcgctgccc	180
act atg gcc cgg aaa gta gtt agc agg aag cgg aaa gcg ccc gcc tcg	228
Met Ala Arg Lys Val Val Ser Arg Lys Arg Lys Ala Pro Ala Ser	
1 5 10	
ccg gga gct ggg agc gac gct cag ggc ccg cag ttt ggc tgg gat cac	276
Pro Gly Ala Gly Ser Asp Ala Gln Gly Pro Gln Phe Gly Trp Asp His	
16 21 26 31	
tcg ctt cac aaa agg aaa aga ctt cct cct gtg aag aga tcc tta gta	324
Ser Leu His Lys Arg Lys Arg Leu Pro Pro Val Lys Arg Ser Leu Val	
32 37 42 47	
tac tac ttg aag aac cgg gaa gtc agg cta cag aat gaa acc agc tac	372
Tyr Tyr Leu Lys Asn Arg Glu Val Arg Leu Gln Asn Glu Thr Ser Tyr	
48 53 58 63	
tct cga gtg ttg cat ggt tat gca gca cag caa ctt ccc agt ctc ctg	420
Ser Arg Val Leu His Gly Tyr Ala Ala Gln Gln Leu Pro Ser Leu Leu	
64 69 74 79	

aag gag aga gag ttt cac ctt ggg acc ctt aat aaa gtg ttt gca tct	468
Lys Glu Arg Glu Phe His Leu Gly Thr Leu Asn Lys Val Phe Ala Ser	
80 85 90 95	
cag tgg ttg aat cat agg caa gtg gtg tgt ggc aca aaa tgc aac acg	516
Gln Trp Leu Asn His Arg Gln Val Val Cys Gly Thr Lys Cys Asn Thr	
96 101 106 111	
cta ttt gtc gta gat gtc cag aca agc cag atc acc aag atc ccc att	564
Leu Phe Val Val Asp Val Gln Thr Ser Gln Ile Thr Lys Ile Pro Ile	
112 117 122 127	
ctg aaa gac cgg gag cct gga ggt gtg acc cag cag ggc tgt ggt atc	612
Leu Lys Asp Arg Glu Pro Gly Gly Val Thr Gln Gln Gly Cys Gly Ile	
128 133 138 143	
cat gcc atc gag ctg aat cct tct aga aca ctg cta gcc act gga gga	660
His Ala Ile Glu Leu Asn Pro Ser Arg Thr Leu Leu Ala Thr Gly Gly	
144 149 154 159	
gac aac ccc aac agt ctt gcc atc tat cga cta cct acg ctg gat cct	708
Asp Asn Pro Asn Ser Leu Ala Ile Tyr Arg Leu Pro Thr Leu Asp Pro	
160 165 170 175	
gtg tgt gta gga gat gat gga cac aag gac tgg atc ttt tcc atc gca	756
Val Cys Val Gly Asp Asp Gly His Lys Asp Trp Ile Phe Ser Ile Ala	
176 181 186 191	
tgg atc agc gac act atg gca gtg tct ggc tca cgt gat ggt tct atg	804
Trp Ile Ser Asp Thr Met Ala Val Ser Gly Ser Arg Asp Gly Ser Met	
192 197 202 207	
gga ctc tgg gag gtg aca gat gat gtt ttg acc aaa agt gat gcg aga	852
Gly Leu Trp Glu Val Thr Asp Asp Val Leu Thr Lys Ser Asp Ala Arg	
208 213 218 223	
cac aat gtg tca cgg gtc cct gtg tat gca cac atc act cac aag gcc	900
His Asn Val Ser Arg Val Pro Val Tyr Ala His Ile Thr His Lys Ala	
224 229 234 239	
tta aag gac atc ccc aaa gaa gac aca aac cct gac aac tgc aag gtt	948
Leu Lys Asp Ile Pro Lys Glu Asp Thr Asn Pro Asp Asn Cys Lys Val	
240 245 250 255	
cgg gct ctg gcc ttc aac aac aag aac aag gaa ctg gga gca gtg tct	996
Arg Ala Leu Ala Phe Asn Asn Lys Asn Lys Glu Leu Gly Ala Val Ser	
256 261 266 271	
ctg gat ggc tac ttt cat ctc tgg aag gct gaa aat aca cta tct aag	1044
Leu Asp Gly Tyr Phe His Leu Trp Lys Ala Glu Asn Thr Leu Ser Lys	
272 277 282 287	
ctc ctc tcc acc aaa ctg cca tat tgc cgt gag aat gtg tgt ctg gct	1092
Leu Leu Ser Thr Lys Leu Pro Tyr Cys Arg Glu Asn Val Cys Leu Ala	
288 293 298 303	

tat ggt agt gaa tgg tca gtt tat gca gtg ggc tcc caa gct cat gtc	1140
Tyr Gly Ser Glu Trp Ser Val Tyr Ala Val Gly Ser Gln Ala His Val	
304 309 314 319	

tcc ttc ttg gat cca cgg cag cca tca tac aac gtc aag tct gtc tgt	1188
Ser Phe Leu Asp Pro Arg Gln Pro Ser Tyr Asn Val Lys Ser Val Cys	
320 325 330 335	

tcc agg gag cga ggc agt gga atc cgg tca gtg agt ttc tac gag cac	1236
Ser Arg Glu Arg Gly Ser Gly Ile Arg Ser Val Ser Phe Tyr Glu His	
336 341 346 351	

atc atc act gtg gga aca ggg cag ggc tcc ctg ctg ttc tat gac atc	1284
Ile Ile Thr Val Gly Thr Gly Gln Gly Ser Leu Leu Phe Tyr Asp Ile	
352 357 362 367	

cga gct cag aga ttt ctg gaa gag agg ctc tca gct tgt tat ggg tcc	1332
Arg Ala Gln Arg Phe Leu Glu Glu Arg Leu Ser Ala Cys Tyr Gly Ser	
368 373 378 383	

aag ccc aga cta gca ggg gag aat ctg aaa cta acc act ggc aaa ggc	1380
Lys Pro Arg Leu Ala Gly Glu Asn Leu Lys Leu Thr Thr Gly Lys Gly	
384 389 394 399	

tgg ctg aat cat gat gaa acc tgg agg aat tac ttt tca gac att gac	1428
Trp Leu Asn His Asp Glu Thr Trp Arg Asn Tyr Phe Ser Asp Ile Asp	
400 405 410 415	

ttc ttc ccc aat gct gtt tac acc cac tgc tac gac tcg tct gga acg	1476
Phe Phe Pro Asn Ala Val Tyr Thr His Cys Tyr Asp Ser Ser Gly Thr	
416 421 426 431	

aaa ctc ttt gtg gca gga ggt ccc ctc cct tca ggg ctc cat gga aac	1524
Lys Leu Phe Val Ala Gly Gly Pro Leu Pro Ser Gly Leu His Gly Asn	
432 437 442 447	

tat gct ggg ctc tgg agt taa tg acaactcccc aaatgcagag atttacacta	1577
Tyr Ala Gly Leu Trp Ser *	
448 453	

acttccattc tcagtttctt tggtttctttt gattttttttt ttcttaattg tgtgaggctc	1637
---	------

ttgtgtttta gtgggaacac caaagtttgc ctatagtta ggcacttaat aggaagaagc	1697
--	------

tctgtacaga aatctgaaag ttgttttgct tttgttttc ccctttggta atcaaaattt	1757
--	------

tactatcttt tattatttct ggcttttcaa ccaaacattg ttgctaattc ctatttttct	1817
---	------

ttaagtgaca cacattctcc tgtctctggc ttcttcaggc tgaaatgaca tagtctttct	1877
---	------

cacccttact tcactcttga gaggtagggc tcctttataa ttacatgggt gctctcagac	1937
---	------

tttctgtgaa agtttgggag ctgtgtgtgt ctgtgtgtgt gtgagagaga gatcttgtct	1997
---	------

gcgtgtgtgt gtgtgatctt gtgtgcctgt aggtactgtg tgtcactgaa attacctgga	2057
---	------

gtgaggatta cttgtaatta aaatatttat aaaagaaaca actttattca cagagtccag	2117
---	------

ctttgggact agtctgtatc ttgtttttta agtctaacaa cactgataat aggaagtaaa	2177
aacagaaagg aaaagaaatt accactggga aaatcttttt agtttagattg taggcttcct	2237
ggggcctccc atgccaggac tgcaaagtga tccagcccta cctgtcttcc cacctgtgtg	2297
tccccctgtg gggaagttgg tgtcacttcc ccttcccacc ctcacatctg cttagccagt	2357
agccacaccc ctaaaacatc agactcacca tccaggtgca gctccagagg ctacaaaagg	2417
cttcatggga cttgaatccc catcctagct tctctctcct tcccccaag acctgatctg	2477
gttttaaggg gcctggagct gggagtctca agtctgctaa gattcacatc catagcccc	2537
atggctttga ggagaatcct ctctgccatt cttccaatct ccccagtggg ttttgctatt	2597
attttctaaa ttgggttaag tctaagaagg tgggggtgag cagggggttt atctgtgtgt	2657
agtgagtgtc tcatgtgtgg aatattcatt ttcttactgc agtgggactt ggggttgaag	2717
ccacccctcc tactctgttg gcttagccct gagatgggta caggctggcc tgcagtcagc	2777
atcattgtgc atgtgacagc atcaatgtga ttagtaattt gtctgttctc cccttgaact	2837
gtctgttttag tctgaggttt ttaaacttgc aggcagctga ctgtgatgtc caattgttcc	2897
ctgattttta cacatcatgt caaagataac agctgttccc acccaccagt tcctctaagc	2957
acatactctg cttttctgtc aacatcccat tttggggaaa ggaaaagtca tatttattcc	3017
tgcaccccag ttttttaact tgttctccca gttgtcccc tcttctctgg gtgtaagaag	3077
ggaaattgga aaaaaaatta tatatatatt ctctttttaa tgggtgggggg ctactggaga	3137
ggagagacag caagtcaccc ctaacttggt acacagcaca taccacaggt tctggaattc	3197
tcatcttoga acctagagaa ataggtgcta taaacagga attaagcaaa atgctggatg	3257
ctatagatct ttttaattgtc ttaatttttt ttctattatt aaactacagg ctgtagattt	3317
cttagttctc acagaacttc tatcatttta aactgacttg tatatttaaa aaaaaaatct	3377
tcagtaggat gttttgtact attgctagac cctcttctgt aatgggtaat gcgtttgatt	3437
gtttgagatt ttctgttttt aaaaatgtag cacttgactt tttgccaagg aaaaaataa	3497
aaattattcc agtgcaaaaa aaaaaaa	3524

<210> 279
 <211> 3073
 <212> DNA
 <213> Homo sapiens

```
<220>
<221> misc_feature
<222> (1)...(3073)
<223> n = a,t,c or g
```

ttgaaancta gtaagtcgta cgcctgcggt accggtccgg aannnggggt cgacgatttc 60

gtgcccgcg atg gag ccg gag act ctg gag gcg cga atc aat aga gcc 168
Met Glu Pro Glu Thr Leu Glu Ala Arg Ile Asn Arg Ala
 1 5 10

tgc	gag	cag	ctc	aac	gag	gac	ttt	gag	ggg	cct	cca	ctc	gcc	acc	cgg	264
Cys	Glu	Gln	Leu	Asn	Glu	Asp	Phe	Glu	Gly	Pro	Pro	Leu	Ala	Thr	Arg	
30					35					40					45	

gcc ttg acg gtg ctg gaa aca tgc atg aag agc tgc ggc aag cgg ttc 360
Ala Leu Thr Val Leu Glu Thr Cys Met Lys Ser Cys Gly Lys Arg Phe
62 67 72 77

gtg tct ccc aag tat ctg ggc tct cgg aca tcg gag aag gtg aag aac 456
Val Ser Pro Lys Tyr Leu Gly Ser Arg Thr Ser Glu Lys Val Lys Asn
94 99 104 109

gtg aaa atc gca gag gcc tac cag atg cta aag aag cag ggg att gta 552
Val Lys Ile Ala Glu Ala Tyr Gln Met Leu Lys Lys Gln Gly Ile Val
126 131 136 141

cca cgg cgg aag aat gtg atc ttt gaa gat gag gag aaa tcc aag atg 648
Pro Arg Pro Lys Asn Val Ile Phe Glu Asp Glu Glu Lys Ser Lys Met
158 163 168 173

ctg gcc cgc ctg ctg aag agc tcc cat ccc gaa gac ctc cgc gca gcc Leu Ala Arg Leu Leu Lys Ser Ser His Pro Glu Asp Leu Arg Ala Ala 174 179 184 189	696
aat aag ctc atc aaa gag atg gtg cag gag gac cag aag cgg atg gag Asn Lys Leu Ile Lys Glu Met Val Gln Glu Asp Gln Lys Arg Met Glu 190 195 200 205	744
aag atc tcg aag agg gtg aat gcc atc gag gag gtg aac aac aat gtg Lys Ile Ser Lys Arg Val Asn Ala Ile Glu Glu Val Asn Asn Asn Val 206 211 216 221	792
aaa ctg ctc acg gag atg gtg atg agc cac agc cag ggc ggc gca gca Lys Leu Leu Thr Glu Met Val Met Ser His Ser Gln Gly Gly Ala Ala 222 227 232 237	840
gct ggc agc agc gag gac ctc atg aag gaa ctg tac cag cgc tgt gag Ala Gly Ser Ser Glu Asp Leu Met Lys Glu Leu Tyr Gln Arg Cys Glu 238 243 248 253	888
cgg atg cgg ccc acg ctc ttc cga ctg gcg agt gac aca gag gac aat Arg Met Arg Pro Thr Leu Phe Arg Leu Ala Ser Asp Thr Glu Asp Asn 254 259 264 269	936
gat gag gcc tta gcg gag atc ctg cag gcc aat gac aac ctc acc cag Asp Glu Ala Leu Ala Glu Ile Leu Gln Ala Asn Asp Asn Leu Thr Gln 270 275 280 285	984
gtg atc aac ctg tat aag cag ctg gtg cgg ggt gag gag gtc aac ggt Val Ile Asn Leu Tyr Lys Gln Leu Val Arg Gly Glu Glu Val Asn Gly 286 291 296 301	1032
gat gcc aca gcc ggc tcc atc cct ggg agc acc tcg gcc ctg ctg gat Asp Ala Thr Ala Gly Ser Ile Pro Gly Ser Thr Ser Ala Leu Leu Asp 302 307 312 317	1080
ctc tca ggc ctg gat ctc ccg cct gcg ggc acc acc tac cca gct atg Leu Ser Gly Leu Asp Leu Pro Pro Ala Gly Thr Thr Tyr Pro Ala Met 318 323 328 333	1128
ccc acc cgc oct ggc gag cag gcc agc cct gag cag ccc agt gcc tca Pro Thr Arg Pro Gly Glu Gln Ala Ser Pro Glu Gln Pro Ser Ala Ser 334 339 344 349	1176
gtt tcc ctg ctt gac gac gag ctc atg tct ctg ggc ctc agt gac ccc Val Ser Leu Leu Asp Asp Glu Leu Met Ser Leu Gly Leu Ser Asp Pro 350 355 360 365	1224
aca ccc cct tca ggc cca agc ctg gat ggt acc gga tgg aac agc ttc Thr Pro Pro Ser Gly Pro Ser Leu Asp Gly Thr Gly Trp Asn Ser Phe 366 371 376 381	1272
cag tcg tcg gat gcc act gag ccc cca gcc cct gct ctg gcc cag gcc Gln Ser Ser Asp Ala Thr Glu Pro Pro Ala Pro Ala Leu Ala Gln Ala 382 387 392 397	1320

ccc agt atg gaa agc cga ccc cca gcg cag aca tcc ctg cca gca agc	1368
Pro Ser Met Glu Ser Arg Pro Pro Ala Gln Thr Ser Leu Pro Ala Ser	
398 403 408 413	
agc ggt ctg gac gac cta gac ctc ctg ggg aag acc ctc ctg cag cag	1416
Ser Gly Leu Asp Asp Leu Asp Leu Leu Gly Lys Thr Leu Leu Gln Gln	
414 419 424 429	
tcg ctg ccc ccg gaa tcc cag caa gtg cgg tgg gag aag cag cag cca	1464
Ser Leu Pro Pro Glu Ser Gln Gln Val Arg Trp Glu Lys Gln Gln Pro	
430 435 440 445	
acc ccc cgg ctc aca ctc cgg gac ctg cag aat aag agc agc agc tgc	1512
Thr Pro Arg Leu Thr Leu Arg Asp Leu Gln Asn Lys Ser Ser Ser Cys	
446 451 456 461	
agc tcc ccc agc tcc agc gcc acc agc ctt ctc cac acc gtg tcc cca	1560
Ser Ser Pro Ser Ser Ser Ala Thr Ser Leu Leu His Thr Val Ser Pro	
462 467 472 477	
gag ccc ccc agg cct ccg cag cag ccc gta cca acc gag ctc tca ctg	1608
Glu Pro Pro Arg Pro Pro Gln Gln Pro Val Pro Thr Glu Leu Ser Leu	
478 483 488 493	
gcc agc atc act gtg ccc ctg gag tcc atc aaa ccc agc aac atc ctg	1656
Ala Ser Ile Thr Val Pro Leu Glu Ser Ile Lys Pro Ser Asn Ile Leu	
494 499 504 509	
ccc gtg act gtg tat gac cag cac ggc ttc cgc atc ctc ttc cat ttt	1704
Pro Val Thr Val Tyr Asp Gln His Gly Phe Arg Ile Leu Phe His Phe	
510 515 520 525	
gcc cgg gac cca ctg cca ggg cgc tcc gac gtg ctg gtg gtg gtt	1752
Ala Arg Asp Pro Leu Pro Gly Arg Ser Asp Val Leu Val Val Val	
526 531 536 541	
tcc atg ctg agc acc gcc ccc cag ccc atc cgc aac atc gtg ttc cag	1800
Ser Met Leu Ser Thr Ala Pro Gln Pro Ile Arg Asn Ile Val Phe Gln	
542 547 552 557	
tca gct gtc ccc aag gtt atg aag gtg aag ctg cag cca ccc tcg ggc	1848
Ser Ala Val Pro Lys Val Met Lys Val Lys Leu Gln Pro Pro Ser Gly	
558 563 568 573	
acg gag ctg cca gct ttt aac ccc atc gtc cac ccc tca gca atc acc	1896
Thr Glu Leu Pro Ala Phe Asn Pro Ile Val His Pro Ser Ala Ile Thr	
574 579 584 589	
cag gtc ctg ctg ctt gcc aac ccc cag aag gag aag gtt cgc ctc cgc	1944
Gln Val Leu Leu Leu Ala Asn Pro Gln Lys Glu Lys Val Arg Leu Arg	
590 595 600 605	
tac aag ctc acc ttc acc atg ggt gac cag acc tac aac gag atg ggg	1992
Tyr Lys Leu Thr Phe Thr Met Gly Asp Gln Thr Tyr Asn Glu Met Gly	
606 611 616 621	
gat gtg gac cag ttc ccc cca cct gaa acc tgg ggt agc ctc tag aac	2040

Asp Val Asp Gln Phe Pro Pro Pro Glu Thr Trp Gly Ser Leu *

622

627

632

agaggggctg gggagaggaa ggggcagagg gaccggtcac tgtccagcct ggagggagggc 2100
attggtggcc aaggacaccc tttgttgccc atggccattc acccccagggc ctggtgcttc 2160
tccccacacc cctgtaggcc tcaagtgact cttccccctc ctgctccggc cccgcccctg 2220
ctgagccaaa ccagtagga ggctgggcct gggtttgtgc cgctgggggc tccatcacgg 2280
ggacctggag agggaggggc tgtgtagcct tggagaact tgggtcatgg ggaggaagca 2340
cagctgttgg ggaagggcca ggacctcagg cccagcccca accccagctg ggggtggggc 2400
ttccccacct gtctcttatg ccttatggga aggccagcc ataactcggg ggccatgctg 2460
gagctgggga ccagcttagg cctcctccat aggaaccag tgactggggg gtgacgccta 2520
cacccccagc tatttgact ctggtgtgtg gtttgactct gcttttcttc cggattggcc 2580
ctgtggtcac agcctcaggg ggccaggctg ggggaacctc acctggcccg tactcctggg 2640
ggtttccctt tgccattggg cccctgagg gactgtgggg gctcaagggt aatgccagag 2700
gcccattggc ccagcgaggg gctgtggggc acctagagtt ctgggtgtgt ctccctcatt 2760
cattggcctc tgctggggcc tcctatgggt gtcttacgtc tgtccatcca tctgtccgtg 2820
gtcagaagtg gggtcagtgt gtgagtgaga gcaggagtat ttatgaaaat aaaacgtcgt 2880
ttttcctgga aaaaaaaaaa aaaaaaaaaa aaaggggggg ccccttttaa aaaaaccaat 2940
tttaccctcc cgggctggca aaataaaatt ttttttaagg ggccccaaa aaaaaatccc 3000
gggccccggt tttaaaaacg ggggaagggg aaaaaccgga gggaccccca aaaaaacccc 3060
cttgaaaaaa aaa 3073

<210> 280

<211> 3937

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (334) .. (3246)

<400> 280

atcggaactc ggaatgpcgt tataactatc tattcgatga tgaagatacc ccaccaaacc 60
caaaaaaaga gatctctcga ggatccgaat tcgcgccgc gtcgaccgga cggcaagcgg 120
cgggagatct tcaaaatggg agcccagagg caccgcccag gcctcggaag gtgtcagggg 180

atg ttt tat aca tta ctt atc ggg aga cca ccc ttc gac act gac aca	978
Met Phe Tyr Thr Leu Leu Ile Gly Arg Pro Pro Phe Asp Thr Asp Thr	
200 205 210 215	
gtc aag aac aca tta aat aaa gta gta ttg gca gat tat gaa atg cca	1026
Val Lys Asn Thr Leu Asn Lys Val Val Leu Ala Asp Tyr Glu Met Pro	
216 221 226 231	
act ttt ttg tca ata gag gcc aag gac ctt att cac cag tta ctt cgt	1074
Thr Phe Leu Ser Ile Glu Ala Lys Asp Leu Ile His Gln Leu Leu Arg	
232 237 242 247	
aga aat cca gca gat cgt tta agt ctg tct tca gta ttg gac cat cct	1122
Arg Asn Pro Ala Asp Arg Leu Ser Leu Ser Ser Val Leu Asp His Pro	
248 253 258 263	
ttt atg tcc cga aat tct tca aca aaa agt aaa gat tta gga act gtg	1170
Phe Met Ser Arg Asn Ser Ser Thr Lys Ser Lys Asp Leu Gly Thr Val	
264 269 274 279	
gaa gac tca att gat agt ggg cat gcc aca att tct act gca att aca	1218
Glu Asp Ser Ile Asp Ser Gly His Ala Thr Ile Ser Thr Ala Ile Thr	
280 285 290 295	
gct tct tcc agt acc agt ata agt ggt agt tta ttt gac aaa aga aga	1266
Ala Ser Ser Ser Thr Ser Ile Ser Gly Ser Leu Phe Asp Lys Arg Arg	
296 301 306 311	
ctt ttg att ggt cag cca ctc cca aat aaa atg act gta ttt cca aag	1314
Leu Leu Ile Gly Gln Pro Leu Pro Asn Lys Met Thr Val Phe Pro Lys	
312 317 322 327	
aat aaa agt tca act gat ttt tct tct tca gga gat gga aac agt ttt	1362
Asn Lys Ser Ser Thr Asp Phe Ser Ser Ser Gly Asp Gly Asn Ser Phe	
328 333 338 343	
tat act cag tgg gga aat caa gaa acc agt aat agt gga agg gga aga	1410
Tyr Thr Gln Trp Gly Asn Gln Glu Thr Ser Asn Ser Gly Arg Gly Arg	
344 349 354 359	
gta att caa gat gca gaa gaa agg cca cat tct cga tac ctt cgt aga	1458
Val Ile Gln Asp Ala Glu Glu Arg Pro His Ser Arg Tyr Leu Arg Arg	
360 365 370 375	
gct tat tcc tct gat aga tct ggc act tct aat agt cag tct caa gca	1506
Ala Tyr Ser Ser Asp Arg Ser Gly Thr Ser Asn Ser Gln Ser Gln Ala	
376 381 386 391	
aaa aca tat aca atg gaa cga tgt cac tca gca gaa atg ctt tca gtg	1554
Lys Thr Tyr Thr Met Glu Arg Cys His Ser Ala Glu Met Leu Ser Val	
392 397 402 407	
tcc aaa aga tca gga gga ggt gaa aat gaa gag agg tac tca ccc aca	1602
Ser Lys Arg Ser Gly Gly Gly Glu Asn Glu Glu Arg Tyr Ser Pro Thr	
408 413 418 423	
gac aac aat gcc aac att ttt aac ttc ttt aaa gaa aag aca tcc agt	1650

Asp	Asn	Asn	Ala	Asn	Ile	Phe	Asn	Phe	Phe	Lys	Glu	Lys	Thr	Ser	Ser		
424					429					434					439		
agt	tct	gga	tct	ttt	gaa	aga	cct	gat	aac	aat	caa	gca	ctc	tcc	aat		1698
Ser	Ser	Gly	Ser	Phe	Glu	Arg	Pro	Asp	Asn	Asn	Gln	Ala	Leu	Ser	Asn		
440					445					450					455		
cat	ctt	tgt	cca	gga	aaa	act	cct	ttt	cca	ttt	gca	gac	ccg	aca	cct		1746
His	Leu	Cys	Pro	Gly	Lys	Thr	Pro	Phe	Pro	Phe	Ala	Asp	Pro	Thr	Pro		
456					461					466					471		
cag	act	gaa	acc	gta	caa	cag	tgg	ttt	ggg	aat	ctg	caa	ata	aat	gct		1794
Gln	Thr	Glu	Thr	Val	Gln	Gln	Trp	Phe	Gly	Asn	Leu	Gln	Ile	Asn	Ala		
472					477					482					487		
cat	tta	aga	aaa	act	act	gaa	tat	gac	agc	atc	agc	cca	aac	cgg	gac		1842
His	Leu	Arg	Lys	Thr	Thr	Glu	Tyr	Asp	Ser	Ile	Ser	Pro	Asn	Arg	Asp		
488					493					498					503		
ttc	cag	ggc	cat	cca	gat	ttg	cag	aag	gac	aca	tca	aaa	aat	gcc	tgg		1890
Phe	Gln	Gly	His	Pro	Asp	Leu	Gln	Lys	Asp	Thr	Ser	Lys	Asn	Ala	Trp		
504					509					514					519		
act	gat	aca	aaa	gtc	aaa	aag	aac	tct	gat	gct	tct	gat	aat	gca	cat		1938
Thr	Asp	Thr	Lys	Val	Lys	Lys	Asn	Ser	Asp	Ala	Ser	Asp	Asn	Ala	His		
520					525					530					535		
tct	gta	aaa	cag	caa	aat	acc	atg	aaa	tat	atg	act	gca	ctt	cac	agt		1986
Ser	Val	Lys	Gln	Gln	Asn	Thr	Met	Lys	Tyr	Met	Thr	Ala	Leu	His	Ser		
536					541					546					551		
aaa	cct	gag	ata	atc	caa	caa	gaa	tgt	gtt	ttt	ggc	tca	gat	cct	ctt		2034
Lys	Pro	Glu	Ile	Ile	Gln	Gln	Glu	Cys	Val	Phe	Gly	Ser	Asp	Pro	Leu		
552					557					562					567		
tct	gaa	cag	agc	aag	act	agg	ggt	atg	gag	cca	cca	tgg	ggt	tat	cag		2082
Ser	Glu	Gln	Ser	Lys	Thr	Arg	Gly	Met	Glu	Pro	Pro	Trp	Gly	Tyr	Gln		
568					573					578					583		
aat	cgt	aca	tta	aga	agc	att	aca	tct	ccg	ttg	gtt	gct	cac	agg	tta		2130
Asn	Arg	Thr	Leu	Arg	Ser	Ile	Thr	Ser	Pro	Leu	Val	Ala	His	Arg	Leu		
584					589					594					599		
aaa	cca	atc	aga	cag	aaa	acc	aaa	aag	gct	gtg	gtg	agc	ata	ctt	gat		2178
Lys	Pro	Ile	Arg	Gln	Lys	Thr	Lys	Lys	Ala	Val	Val	Ser	Ile	Leu	Asp		
600					605					610					615		
tca	gag	gag	gtg	tgt	gtg	gag	ctt	gta	aag	gag	tat	gca	tct	caa	gaa		2226
Ser	Glu	Glu	Val	Cys	Val	Glu	Leu	Val	Lys	Glu	Tyr	Ala	Ser	Gln	Glu		
616					621					626					631		
tat	gtg	aaa	gaa	gtt	ctt	cag	ata	tct	agt	gat	gga	aat	acg	atc	act		2274
Tyr	Val	Lys	Glu	Val	Leu	Gln	Ile	Ser	Ser	Asp	Gly	Asn	Thr	Ile	Thr		
632					637					642					647		
att	tat	tat	cca	aat	ggt	ggt	aga	ggt	ttt	cct	ctt	gct	gat	aga	cca		2322
Ile	Tyr	Tyr	Pro	Asn	Gly	Gly	Arg	Gly	Phe	Pro	Leu	Ala	Asp	Arg	Pro		

648	653	658	663	
ccc tca cct act gac aac atc agt agg tac agc ttt gac aat tta cca				2370
Pro Ser Pro Thr Asp Asn Ile Ser Arg Tyr Ser Phe Asp Asn Leu Pro				
664	669	674	679	
gaa aaa tac tgg cga aaa tat caa tat gct tcc agg ttt gta cag ctt				2418
Glu Lys Tyr Trp Arg Lys Tyr Gln Tyr Ala Ser Arg Phe Val Gln Leu				
680	685	690	695	
gta aga tct aaa tct ccc aaa atc act tat ttt aca aga tat gct aaa				2466
Val Arg Ser Lys Ser Pro Lys Ile Thr Tyr Phe Thr Arg Tyr Ala Lys				
696	701	706	711	
tgc att ttg atg gag aat tct cct ggt gct gat ttt gag gtt tgg ttt				2514
Cys Ile Leu Met Glu Asn Ser Pro Gly Ala Asp Phe Glu Val Trp Phe				
712	717	722	727	
tat gat ggg gta aaa ata cac aaa aca gaa gat ttc att cag gtg att				2562
Tyr Asp Gly Val Lys Ile His Lys Thr Glu Asp Phe Ile Gln Val Ile				
728	733	738	743	
gaa aag aca ggg aag tct tac act tta aaa agt gaa agt gaa gtt aat				2610
Glu Lys Thr Gly Lys Ser Tyr Thr Leu Lys Ser Glu Ser Glu Val Asn				
744	749	754	759	
agc ttg aaa gag gag ata aaa atg tat atg gac cat gct aat gag ggt				2658
Ser Leu Lys Glu Glu Ile Lys Met Tyr Met Asp His Ala Asn Glu Gly				
760	765	770	775	
cat cgt att tgt tta gca ctg gaa tcc ata att tca gaa gag gaa agg				2706
His Arg Ile Cys Leu Ala Leu Glu Ser Ile Ile Ser Glu Glu Glu Arg				
776	781	786	791	
aaa act agg agt gct ccc ttt ttc cca ata atc ata gga aga aaa cct				2754
Lys Thr Arg Ser Ala Pro Phe Phe Pro Ile Ile Ile Gly Arg Lys Pro				
792	797	802	807	
ggg agt act agt tca cct aag gcc tta tca cct cct cct tct gtg gat				2802
Gly Ser Thr Ser Ser Pro Lys Ala Leu Ser Pro Pro Pro Ser Val Asp				
808	813	818	823	
tca aat tac cca acg aga gat aga gca tct ttc aac aga atg gtc atg				2850
Ser Asn Tyr Pro Thr Arg Asp Arg Ala Ser Phe Asn Arg Met Val Met				
824	829	834	839	
cat agt gct gct tct cca aca cag gca cca atc ctt aat ccc tct atg				2898
His Ser Ala Ala Ser Pro Thr Gln Ala Pro Ile Leu Asn Pro Ser Met				
840	845	850	855	
gtt aca aat gaa gga ctt ggt ctt aca act aca gct tct gga aca gac				2946
Val Thr Asn Glu Gly Leu Gly Leu Thr Thr Thr Ala Ser Gly Thr Asp				
856	861	866	871	
atc tct tct aat agt cta aaa gat tgt ctt cct aaa tca gca caa ctt				2994
Ile Ser Ser Asn Ser Leu Lys Asp Cys Leu Pro Lys Ser Ala Gln Leu				
872	877	882	887	

ttg aaa tct gtt ttt gtg aaa aat gtt ggt tgg gct aca cag tta act	3042
Leu Lys Ser Val Phe Val Lys Asn Val Gly Trp Ala Thr Gln Leu Thr	
888 893 898 903	
agt gga gct gtg tgg gtt cag ttt aat gat ggg tcc cag ttg gtt gtg	3090
Ser Gly Ala Val Trp Val Gln Phe Asn Asp Gly Ser Gln Leu Val Val	
904 909 914 919	
cag gca gga gtg tct tct atc agt tat acc tca cca aat ggt caa aca	3138
Gln Ala Gly Val Ser Ser Ile Ser Tyr Thr Ser Pro Asn Gly Gln Thr	
920 925 930 935	
act agg tat gga gaa aat gaa aaa tta cca gac tac atc aaa cag aaa	3186
Thr Arg Tyr Gly Glu Asn Glu Lys Leu Pro Asp Tyr Ile Lys Gln Lys	
936 941 946 951	
tta cag tgt ctg tct tcc atc ctt ttg atg ttt tct aat ccg act cct	3234
Leu Gln Cys Leu Ser Ser Ile Leu Leu Met Phe Ser Asn Pro Thr Pro	
952 957 962 967	
aat ttt cat tga tta aaactccttt cagacatata agtttaataa ataacttttt	3289
Asn Phe His *	
968	
tggtgacttt caagtaaagt gatttttttt aatttacata aaagtcttca gaaagccttt	3349
ctatgaaaga attttaacct ataatgtaaa ggatgtattc tgagagaaca aagcagaatg	3409
aaacttgagt cacttactaa atatagtgga tataaaatag aacacctgac tttgctctta	3469
gaccataacc ccogaactta ctatgttcat atatttgtat tgaacaatct tttaaaagca	3529
aaaatgtaaa tgatgtgtag tttatttgtg cttttattgt tttccctgcg tctcagacat	3589
gttgagaatc atggacaaaa cctgctggaa ttttggaatt tttgaagatg taaataatgt	3649
gtatttatgt tataagtaac atatgtaaac atgtatatatt gttttatatt tattttttgta	3709
acaccagtgt ctgatgaaac atttttgcaa atgcatttta taaaaaata aatatagtga	3769
taagttacat tatcttttga ttcatttaat taaatactta tttttaaata acttaccagt	3829
aaactcactt tttaaatttt gttgcctgtt gaggagccaa tttaaatttta aatattaatt	3889
ttgcaaatgt taaatacatt gtttctctat tatctgaaaa aaaaaaaa	3937

<210> 281
 <211> 4382
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (92)..(2476)

<400> 281

gggtaccggtc	cggaattccc	gggtcgacga	tttcgtgcct	gtcgggtgac	gtgtctgcag	60
ttcctccgcg	tctactgoga	gtcaggccgt	g	atg gcg gac gcc tgg gaa gag		112
				Met Ala Asp Ala Trp Glu Glu		
			1		5	
att agg cgg ttg gcg gcc gac ttc cag cgg gcg cag ttc gcc gag gcc						160
Ile Arg Arg Leu Ala Ala Asp Phe Gln Arg Ala Gln Phe Ala Glu Ala						
8	13		18		23	
acg cag agg ttg tcc gag cgg aac tgc att gag att gtt aat aaa ttg						208
Thr Gln Arg Leu Ser Glu Arg Asn Cys Ile Glu Ile Val Asn Lys Leu						
24	29		34		39	
att gct cag aaa cag cta gaa gta gtt cat aca ctc gat gga aag gaa						256
Ile Ala Gln Lys Gln Leu Glu Val Val His Thr Leu Asp Gly Lys Glu						
40	45		50		55	
tat att act cca gcc caa att agt aaa gaa atg aga gat gag cta cat						304
Tyr Ile Thr Pro Ala Gln Ile Ser Lys Glu Met Arg Asp Glu Leu His						
56	61		66		71	
gtc cga ggt ggt cga gta aac att gtt gat cta caa cag gta att aat						352
Val Arg Gly Gly Arg Val Asn Ile Val Asp Leu Gln Gln Val Ile Asn						
72	77		82		87	
gtg gac ctg att cat att gaa aat aga att ggt gac att att aaa tca						400
Val Asp Leu Ile His Ile Glu Asn Arg Ile Gly Asp Ile Ile Lys Ser						
88	93		98		103	
gaa aag cat gtt cag tta gtg ttg gga caa ctg ata gat gag aat tat						448
Glu Lys His Val Gln Leu Val Leu Gly Gln Leu Ile Asp Glu Asn Tyr						
104	109		114		119	
ttg gat cgg ttg gca gaa gag gtc aat gat aaa ttg caa gaa agt ggt						496
Leu Asp Arg Leu Ala Glu Glu Val Asn Asp Lys Leu Gln Glu Ser Gly						
120	125		130		135	
cag gtc acc ata tca gaa ctg tgt aaa act tat gat ctt cct ggg aac						544
Gln Val Thr Ile Ser Glu Leu Cys Lys Thr Tyr Asp Leu Pro Gly Asn						
136	141		146		151	
ttt ctg aca cag gca cta act cag cga ctt ggt aga att atc agt gga						592
Phe Leu Thr Gln Ala Leu Thr Gln Arg Leu Gly Arg Ile Ile Ser Gly						
152	157		162		167	
cat att gat ctt gat aat aga gga gta att ttt acg gaa gct ttt gta						640
His Ile Asp Leu Asp Asn Arg Gly Val Ile Phe Thr Glu Ala Phe Val						
168	173		178		183	
gct cga cat aaa gca cgt atc cgt gga cta ttc agt gct att acc cgg						688
Ala Arg His Lys Ala Arg Ile Arg Gly/Leu Phe Ser Ala Ile Thr Arg						
184	189		194		199	

cct	aca	gct	gtg	aat	tct	ttg	att	tca	aaa	tat	gga	ttt	cag	gag	cag	736
Pro	Thr	Ala	Val	Asn	Ser	Leu	Ile	Ser	Lys	Tyr	Gly	Phe	Gln	Glu	Gln	
200					205					210					215	
ctt	ctt	tac	tct	gtg	ctt	gag	gaa	ctt	gtt	aat	agc	gga	cgc	tta	cga	784
Leu	Leu	Tyr	Ser	Val	Leu	Glu	Glu	Leu	Val	Asn	Ser	Gly	Arg	Leu	Arg	
216					221					226					231	
ggc	act	gtg	gtt	ggg	ggg	aga	cag	gat	aaa	gct	gtg	ttt	gtc	cct	gac	832
Gly	Thr	Val	Val	Gly	Gly	Arg	Gln	Asp	Lys	Ala	Val	Phe	Val	Pro	Asp	
232					237					242					247	
atc	tac	tcc	agg	aca	cag	agt	act	tgg	gtg	gat	tcc	ttt	ttc	agg	cag	880
Ile	Tyr	Ser	Arg	Thr	Gln	Ser	Thr	Trp	Val	Asp	Ser	Phe	Phe	Arg	Gln	
248					253					258					263	
aat	ggc	tat	cta	gaa	ttt	gat	gct	ttg	tcc	aga	ctt	gga	atc	cca	gat	928
Asn	Gly	Tyr	Leu	Glu	Phe	Asp	Ala	Leu	Ser	Arg	Leu	Gly	Ile	Pro	Asp	
264					269					274					279	
gct	gta	agc	tac	ata	aag	aaa	aga	tat	aag	act	aca	caa	ctc	ttg	ttt	976
Ala	Val	Ser	Tyr	Ile	Lys	Lys	Arg	Tyr	Lys	Thr	Thr	Gln	Leu	Leu	Phe	
280					285					290					295	
ttg	aaa	gca	gct	tgt	gtt	ggg	caa	gga	ctt	gtg	gat	caa	gtg	gaa	gca	1024
Leu	Lys	Ala	Ala	Cys	Val	Gly	Gln	Gly	Leu	Val	Asp	Gln	Val	Glu	Ala	
296					301					306					311	
tca	gta	gaa	gaa	gcc	atc	agc	tct	gga	aca	tgg	gtt	gat	att	gca	cct	1072
Ser	Val	Glu	Glu	Ala	Ile	Ser	Ser	Gly	Thr	Trp	Val	Asp	Ile	Ala	Pro	
312					317					322					327	
ctg	cta	ccc	act	tct	tta	tca	gtt	gaa	gat	gct	gcc	ata	ttg	ctt	cag	1120
Leu	Leu	Pro	Thr	Ser	Leu	Ser	Val	Glu	Asp	Ala	Ala	Ile	Leu	Leu	Gln	
328					333					338					343	
cag	gtg	atg	agg	gca	ttc	agc	aaa	cag	gcc	tca	act	gta	gtc	ttt	agc	1168
Gln	Val	Met	Arg	Ala	Phe	Ser	Lys	Gln	Ala	Ser	Thr	Val	Val	Phe	Ser	
344					349					354					359	
gac	act	gtt	gta	gtc	agt	gaa	aaa	ttt	ata	aat	gac	tgt	aca	gaa	ctg	1216
Asp	Thr	Val	Val	Val	Ser	Glu	Lys	Phe	Ile	Asn	Asp	Cys	Thr	Glu	Leu	
360					365					370					375	
ttc	cgt	gag	ctg	atg	cac	cag	aaa	gct	gaa	aag	gaa	atg	aaa	aat	aat	1264
Phe	Arg	Glu	Leu	Met	His	Gln	Lys	Ala	Glu	Lys	Glu	Met	Lys	Asn	Asn	
376					381					386					391	
cct	gtg	cat	tta	atc	act	gaa	gaa	gat	ctg	aaa	caa	atc	tcc	act	tta	1312
Pro	Val	His	Leu	Ile	Thr	Glu	Glu	Asp	Leu	Lys	Gln	Ile	Ser	Thr	Leu	
392					397					402					407	
gaa	agc	gtt	agt	aca	agt	aaa	aaa	aaa	aaa	aaa	aat	gag	cga	aga	agg	1360
Glu	Ser	Val	Ser	Thr	Ser	Lys	Lys	Lys	Lys	Lys	Asn	Glu	Arg	Arg	Arg	
408					413					418					423	
aaa	gca	aca	gag	ggc	agt	gga	agc	atg	aga	gga	gga	ggg	ggg	ggc	aat	1408

Lys	Ala	Thr	Glu	Gly	Ser	Gly	Ser	Met	Arg	Gly	Gly	Gly	Gly	Gly	Asn	
424					429					434					439	
gcc	aga	gag	tac	aaa	att	aaa	aaa	gtc	aag	aag	aaa	gga	aga	aaa	gat	1456
Ala	Arg	Glu	Tyr	Lys	Ile	Lys	Lys	Val	Lys	Lys	Lys	Gly	Arg	Lys	Asp	
440					445					450					455	
gat	gat	agt	gat	gat	gaa	tct	caa	tca	tcc	cac	act	gga	aag	aag	aag	1504
Asp	Asp	Ser	Asp	Asp	Glu	Ser	Gln	Ser	Ser	His	Thr	Gly	Lys	Lys	Lys	
456					461					466					471	
cca	gag	atc	agt	ttt	atg	ttc	cag	gat	gag	att	gaa	gat	ttt	tta	aga	1552
Pro	Glu	Ile	Ser	Phe	Met	Phe	Gln	Asp	Glu	Ile	Glu	Asp	Phe	Leu	Arg	
472					477					482					487	
aaa	cac	ata	caa	gat	gcc	cct	gag	gag	ttt	att	tcg	gaa	ctt	gct	gag	1600
Lys	His	Ile	Gln	Asp	Ala	Pro	Glu	Glu	Phe	Ile	Ser	Glu	Leu	Ala	Glu	
488					493					498					503	
tac	tta	ata	aaa	cct	ctt	aat	aaa	act	tat	ctc	gag	gtg	gta	cgt	tca	1648
Tyr	Leu	Ile	Lys	Pro	Leu	Asn	Lys	Thr	Tyr	Leu	Glu	Val	Val	Arg	Ser	
504					509					514					519	
gta	ttc	atg	tct	tca	aca	act	tct	gct	tct	ggg	acg	ggc	aga	aaa	cgc	1696
Val	Phe	Met	Ser	Ser	Thr	Thr	Ser	Ala	Ser	Gly	Thr	Gly	Arg	Lys	Arg	
520					525					530					535	
aca	atc	aag	gac	ttg	caa	gaa	gaa	gtt	tca	aac	ctg	tac	aat	aac	att	1744
Thr	Ile	Lys	Asp	Leu	Gln	Glu	Glu	Val	Ser	Asn	Leu	Tyr	Asn	Asn	Ile	
536					541					546					551	
agg	tta	ttt	gaa	aaa	ggg	atg	aag	ttt	ttt	gca	gat	gac	aca	cag	gct	1792
Arg	Leu	Phe	Glu	Lys	Gly	Met	Lys	Phe	Phe	Ala	Asp	Asp	Thr	Gln	Ala	
552					557					562					567	
gct	ctt	acc	aaa	cac	ttg	ctg	aag	tca	gtg	tgt	act	gat	atc	act	aac	1840
Ala	Leu	Thr	Lys	His	Leu	Leu	Lys	Ser	Val	Cys	Thr	Asp	Ile	Thr	Asn	
568					573					578					583	
ctc	att	ttc	aac	ttc	tta	gct	tcg	gat	tta	atg	atg	gca	gta	gac	gat	1888
Leu	Ile	Phe	Asn	Phe	Leu	Ala	Ser	Asp	Leu	Met	Met	Ala	Val	Asp	Asp	
584					589					594					599	
cct	gca	gcc	att	aca	agt	gaa	ata	aga	aag	aaa	att	tta	agt	aaa	tta	1936
Pro	Ala	Ala	Ile	Thr	Ser	Glu	Ile	Arg	Lys	Lys	Ile	Leu	Ser	Lys	Leu	
600					605					610					615	
tca	gaa	gaa	acc	aaa	gta	gct	ctt	aca	aaa	ctc	cat	aac	tct	ctg	aat	1984
Ser	Glu	Glu	Thr	Lys	Val	Ala	Leu	Thr	Lys	Leu	His	Asn	Ser	Leu	Asn	
616					621					626					631	
gaa	aag	agc	ata	gaa	gat	ttt	att	tct	tgt	ctg	gat	tct	gca	gca	gaa	2032
Glu	Lys	Ser	Ile	Glu	Asp	Phe	Ile	Ser	Cys	Leu	Asp	Ser	Ala	Ala	Glu	
632					637					642					647	
gct	tgt	gat	att	atg	gtg	aaa	agg	gga	gac	aaa	aaa	agg	gaa	aga	cag	2080
Ala	Cys	Asp	Ile	Met	Val	Lys	Arg	Gly	Asp	Lys	Lys	Arg	Glu	Arg	Gln	

648	653	658	663	
ata ctg ttc caa cat cga caa gca ctg gct gaa cag cta aag gtc aca				2128
Ile Leu Phe Gln His Arg Gln Ala Leu Ala Glu Gln Leu Lys Val Thr				
664	669	674	679	
gaa gac cct gct ctt att ctg cac ctc aca tca gtc ctg ttg ttt cag				2176
Glu Asp Pro Ala Leu Ile Leu His Leu Thr Ser Val Leu Leu Phe Gln				
680	685	690	695	
ttt tca acc cac agc atg ctc cat gca cct gga aga tgt gtc cca cag				2224
Phe Ser Thr His Ser Met Leu His Ala Pro Gly Arg Cys Val Pro Gln				
696	701	706	711	
atc att gct ttt ctt aat agt aaa att cca gag gat cag cat gct ctt				2272
Ile Ile Ala Phe Leu Asn Ser Lys Ile Pro Glu Asp Gln His Ala Leu				
712	717	722	727	
ttg gta aag tat caa ggt ttg gtt gta aag cag cta gtc agt caa agt				2320
Leu Val Lys Tyr Gln Gly Leu Val Val Lys Gln Leu Val Ser Gln Ser				
728	733	738	743	
aag aag act ggg cag gga gat tat ccc ttg aat aat gaa tta gac aaa				2368
Lys Lys Thr Gly Gln Gly Asp Tyr Pro Leu Asn Asn Glu Leu Asp Lys				
744	749	754	759	
gaa caa gaa gat gtt gcc agt act act cgt aaa gag ctt caa gaa ctt				2416
Glu Gln Glu Asp Val Ala Ser Thr Thr Arg Lys Glu Leu Gln Glu Leu				
760	765	770	775	
tct tca tcc att aaa gac ctt gtt ctc aaa tct agg aaa tca tot gtg				2464
Ser Ser Ser Ile Lys Asp Leu Val Leu Lys Ser Arg Lys Ser Ser Val				
776	781	786	791	
acg gaa gag taa tga tcttaattta catttgctcat atagtaagca ttttccccca				2519
Thr Glu Glu *				
792				
aggttgaagg tgagtgggtca caaaaaagta gtcactatac aactccccctc tccctgcaaa				2579
aaccacctca tacacacaca attcagttaa aacagtagta ttgtattaaa tgtaaattctt				2639
aaaaagatgt gaatttttgt aaattgggtt cttcatggaa gtttttttcc acctgatttt				2699
cacacaaata ctatatgaaa tttttcacat tattttcaca taattttaaa aattacatat				2759
ttcaggtttg ttctctttcc aaatggtgaa tgaaaaacaa attttccaat ccatttatcc				2819
ctggggaagg attcatttgt tgcgagtgcc agtatactta aatgtatact ttatatacat				2879
ttaagcagaa atttaaaatg tgggtcttttt tttttaaaag aaacacttct gtgtcagaaa				2939
tgaaaaataaa tcatgttttt tattttttaa tagaaagcac ttcaaaaacta aaatacagaa				2999
atttacaaaa aagaaaaatt attactaagc ccttgctctt atttttggca gaataaacat				3059
tgatttttgg tggggctgca aggatgcctt tacagggtgca caagaacgct agagtggccc				3119

atgcattgct gtgttctctt ctaaaacaag ctactaaca gagagagaac acatgcaatt	3179
tattaccagt aagcataagt catattttaac attggaataa ctaagcattt tatacaaaga	3239
tttttctttg acccagtttg catttgtaca ttttattttt ttagttcaac agctgctctg	3299
tcacataata ctttgtaaact actagtgtga aaaacagata ggatgccttt tccagtggta	3359
ggagcatctg taagtgcatt taaatcatta gaagcttttt tccaaaacta gaaaccctta	3419
ttaaaaaata gacatttttt tctaaagatt attagttaaa aataactaaa agagttcctt	3479
agagtaatca tttcaaccaa atgaatttca agcaacaact tacttactat ttatcaaaaa	3539
gggatttaatt tattttgaat ataattataa attaaatttc aaatatttaa aaatactatt	3599
ttatataatt ccttatgaca ttttaaactt tatattttta aatatttgaa tacgaaaaga	3659
tcagtctacc tctactccat tctagacaaa gtattaatcc ttagtgaaaag taattaatta	3719
aattgccaac ttggcattat tattaaactt gataggaacg caacattaaa tttaaaaatg	3779
ttttcccgctg ggtaattttc tattatatat tttcatatgg gcaaagggaa aaaatgataa	3839
atcctctgta atcacaaacc ccaatttcgt tttgtttatt cagcttctaa aatattgaac	3899
accagactt ttaattcaac ctttaagaac cttatcattt atgtttcagt agatatcaaa	3959
gtaatccatg tttgtgtcaa atgatcatag aaaataaata gaagagacag tgaagcaagt	4019
aaaaagaaaa gcattgtttt aatttgtttg cattaatttt tttcatttgt caaaatgctt	4079
cttttgttgc cacagtaaag aacagttttt attgttttgt aagtaaaatt acgtagctga	4139
ttttgtatgt aaagattaat ttccataata aaaattattg tatgtttact gtgatcttaa	4199
tgggcagggt taagaaagtt atttaaaata aagttaccta ttctactaaa ttttatagta	4259
ctttgaagct tctattaatt aacacaaaga ttaattggtg catataattt atatatatac	4319
attttgaatt ctcattttga acattattaa aggattttat ttttcttaca caaaaaaaaa	4379
aaa	4382

<210> 282
 <211> 2230
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS /
 <222> (85)..(1152)

<400> 282

gtaggcaggg actgggttct actgtgagct gagatccctg gagctccatg aaaaggagaa 60

aagaatgccg tgtttctctgg atct atg gag gga atc cca gga ttt cct gga 111
Met Glu Gly Ile Pro Gly Phe Pro Gly
1 5

aac cga gga tta atg ggc caa aag gga gaa att ggg cct cca gga cag 159
Asn Arg Gly Leu Met Gly Gln Lys Gly Glu Ile Gly Pro Pro Gly Gln
10 15 20 25

caa gga aaa aaa gga gcc cca ggg atg cct ggt tta atg gga agc aat 207
Gln Gly Lys Lys Gly Ala Pro Gly Met Pro Gly Leu Met Gly Ser Asn
26 31 36 41

ggc tca cca ggc cag cct gga aca ccg gga tct aag gga agc aaa ggt 255
Gly Ser Pro Gly Gln Pro Gly Thr Pro Gly Ser Lys Gly Ser Lys Gly
42 47 52 57

gaa cct gga att caa ggg atg cct ggg gct tct ggg ctc aag gga gaa 303
Glu Pro Gly Ile Gln Gly Met Pro Gly Ala Ser Gly Leu Lys Gly Glu
58 63 68 73

cca gga gca acg ggt tcc cca gga gaa cca gga tac atg ggt tta ccc 351
Pro Gly Ala Thr Gly Ser Pro Gly Glu Pro Gly Tyr Met Gly Leu Pro
74 79 84 89

ggg att caa gga aaa aag ggg gac aaa gga aat caa ggt gaa aaa ggt 399
Gly Ile Gln Gly Lys Lys Gly Asp Lys Gly Asn Gln Gly Glu Lys Gly
90 95 100 105

att cag ggt caa aag gga gaa aat gga aga cag gga att cca ggg caa 447
Ile Gln Gly Gln Lys Gly Glu Asn Gly Arg Gln Gly Ile Pro Gly Gln
106 111 116 121

cag gga att caa ggc cat cat ggt gca aaa gga gag aga ggt gaa aag 495
Gln Gly Ile Gln Gly His His Gly Ala Lys Gly Glu Arg Gly Glu Lys
122 127 132 137

gga gaa cct ggt gtc cga ggt gcc att gga tca aaa gga gaa tct ggg 543
Gly Glu Pro Gly Val Arg Gly Ala Ile Gly Ser Lys Gly Glu Ser Gly
138 143 148 153

gtg gat ggc ttg atg ggg ccc gca ggt cct aag ggg caa cct ggg gat 591
Val Asp Gly Leu Met Gly Pro Ala Gly Pro Lys Gly Gln Pro Gly Asp
154 159 164 169

cca ggt cct cag gga ccc cca ggt ttg gat ggg aag ccc gga aga gag 639
Pro Gly Pro Gln Gly Pro Pro Gly Leu Asp Gly Lys Pro Gly Arg Glu
170 175 180 185

ttt tca gaa caa ttt att cga caa gtt tgc aca gat gta ata aga gcc 687
Phe Ser Glu Gln Phe Ile Arg Gln Val Cys Thr Asp Val Ile Arg Ala
186 191 196 201

cag cta cca gtc tta ctt cag agt gga aga att aga aat tgt gat cat 735
Gln Leu Pro Val Leu Leu Gln Ser Gly Arg Ile Arg Asn Cys Asp His

202	207	212	217	
tgc ctg tcc caa cat ggc tcc ccg ggt att cct ggg cca cct ggt ccg				783
Cys Leu Ser Gln His Gly Ser Pro Gly Ile Pro Gly Pro Pro Gly Pro				
218	223	228	233	
ata ggc cca gag ggt ccc aga gga tta cct ggt ttg cca gga aga gat				831
Ile Gly Pro Glu Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Arg Asp				
234	239	244	249	
ggg gtt cct gga tta gtg ggt gtc cct gga cgt cca ggt gtc aga gga				879
Gly Val Pro Gly Leu Val Gly Val Pro Gly Arg Pro Gly Val Arg Gly				
250	255	260	265	
tta aaa ggc cta cca gga aga aat ggg gaa aaa ggg agc caa ggg ttt				927
Leu Lys Gly Leu Pro Gly Arg Asn Gly Glu Lys Gly Ser Gln Gly Phe				
266	271	276	281	
ggg tat cct gga gaa caa ggt cct cct ggt ccc cca ggt cca gag ggc				975
Gly Tyr Pro Gly Glu Gln Gly Pro Pro Gly Pro Pro Gly Pro Glu Gly				
282	287	292	297	
cct cct gga ata agc aaa gaa ggt cct cca gga gac cca ggt ctc cct				1023
Pro Pro Gly Ile Ser Lys Glu Gly Pro Pro Gly Asp Pro Gly Leu Pro				
298	303	308	313	
ggc aaa gat gga gac cat gga aaa cct gga atc caa ggg caa cca ggc				1071
Gly Lys Asp Gly Asp His Gly Lys Pro Gly Ile Gln Gly Gln Pro Gly				
314	319	324	329	
ccc cca ggc atc tgc gac cca tca cta tgt ttt agt gta att gcc aga				1119
Pro Pro Gly Ile Cys Asp Pro Ser Leu Cys Phe Ser Val Ile Ala Arg				
330	335	340	345	
aga gat ccg ttc aga aaa gga cca aac tat tag tgtctgat gcctcattca				1170
Arg Asp Pro Phe Arg Lys Gly Pro Asn Tyr *				
346	351	356		
gcagcctagg catggtgctt tttctgtggt cttttgcatc tcaggaagat aaccaacagt				1230
aatcccttga aaagaaactt aagtacctcg gcgtttttat tttttttttc ttatggaaaa				1290
aaatataaaa gatcacatat actgatttta aaggctcctc agtcatttgg agcccttgga				1350
ttagcagcat taattaaatc tcaagggttt cttgtaaagt ccatttatgt taatcaaagt				1410
tgaatataaa aatccaccat tgctgttag ccagtcagtt ttagtcactg tgaaatattt				1470
cacattcagc ctccatgcag tagagatttg agtttaattt catgtccatg tgactttcat				1530
gtttcctatc tcatagctca tgctactaca taagccaaaa catgtatctc atcattggaa				1590
gtaagatcag ggctgatatt cacctgggat agacagtatt ggtgaactac tcatttafta				1650
cagtgtctca gccttgataa ggggcagtgg attgcctgtt gttcgggtgt gtgaatagca				1710
cctctgaata agattagagt gtttcttaat tcatttcaaa ctctaaaatt agattaatgg				1770

tgggtgctaag aaagagtatt aattactttg ggaatgggtca aaattaacat taaaaacatt 1830
 ttagacaaaa agtttcattg tacattcaaa gaaaatgtaa gtttggaagt actaaaagac 1890
 tattttatac ttgttgatta atcggaatgt ttgttgatg ccttcatttt ccatttcact 1950
 tatatgtgta tgtccatata tgtaattttt cattgtagca aagctaattg aaataaagct 2010
 aatgctctag ttgaaagaaa aggaaaactc ctgaaatcct agaatgtctt gttattttta 2070
 gctgactgta aaatattatg aacagtcttt gtgtattgtg cttaatgctt ttgtaagaaa 2130
 cagaatttga aatattttcat ccttgctatg ctcaaaattt tgttacatgc ttgttattca 2190
 gagtataata aagtttttga caggcctgaa aaaaaaaaaa 2230

<210> 283
 <211> 2663
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (115)..(2157)

<400> 283
 cggaattccc gggtcgacga tttogtgcg gccggctgag tcctctccag ccgcgagagg 60
 cgtttctcca tccgcggctc gcgcgctgc tctgagcccc cgcgccccagg tggg atg 117
 Met
 1
 gaa gaa gcc tgt cag gtg cag aca act aag cga ggg gat cct cat gag 165
 Glu Glu Ala Cys Gln Val Gln Thr Thr Lys Arg Gly Asp Pro His Glu
 2 7 12 17
 tta aga aac ata ttt cta cag tat gcc agt act gag gtt gat gga gag 213
 Leu Arg Asn Ile Phe Leu Gln Tyr Ala Ser Thr Glu Val Asp Gly Glu
 18 23 28 33
 cgt tac atg acc cca gaa gac ttt gtt cag cgc tat ctt gga ctg tat 261
 Arg Tyr Met Thr Pro Glu Asp Phe Val Gln Arg Tyr Leu Gly Leu Tyr
 34 39 44 49
 aat gat cca aat agt aac cca aag atc gtg cag ctc ttg gca gga gta 309
 Asn Asp Pro Asn Ser Asn Pro Lys Ile Val Gln Leu Leu Ala Gly Val
 50 55 60 65
 gct gat caa acc aag gat ggg ttg atc tcc tat caa gag ttt ttg gca 357
 Ala Asp Gln Thr Lys Asp Gly Leu Ile Ser Tyr Gln Glu Phe Leu Ala
 66 71 76 81
 ttt gaa tct gtt tta tgt gct cca gat tcc atg ttc ata gtg gct ttc 405

Phe Glu Ser Val Leu Cys Ala Pro Asp Ser Met Phe Ile Val Ala Phe
82 87 92 97

cag ttg ttt gac aag agt gga aat gga gag gtg aca ttt gaa aat gtc 453
Gln Leu Phe Asp Lys Ser Gly Asn Gly Glu Val Thr Phe Glu Asn Val
98 103 108 113

aaa gaa att ttt gga cag act att att cat cat cat atc cct ttt aac 501
Lys Glu Ile Phe Gly Gln Thr Ile Ile His His His Ile Pro Phe Asn
114 119 124 129

tgg gat tgt gaa ttt atc cga ctg cat ttt ggg cat aac cgg aag aag 549
Trp Asp Cys Glu Phe Ile Arg Leu His Phe Gly His Asn Arg Lys Lys
130 135 140 145

cat ctt aac tac aca gaa ttc acg cag ttt ctc cag gag ctg caa ttg 597
His Leu Asn Tyr Thr Glu Phe Thr Gln Phe Leu Gln Glu Leu Gln Leu
146 151 156 161

gaa cat gca aga caa gcc ttt gca ctc aaa gac aaa agc aaa agt ggc 645
Glu His Ala Arg Gln Ala Phe Ala Leu Lys Asp Lys Ser Lys Ser Gly
162 167 172 177

atg att tct ggt ctg gat ttc agt gac atc atg gtt acc att aga tct 693
Met Ile Ser Gly Leu Asp Phe Ser Asp Ile Met Val Thr Ile Arg Ser
178 183 188 193

cac atg ctt act cct ttt gtg gag gag aac tta gtt tca gca gct gga 741
His Met Leu Thr Pro Phe Val Glu Glu Asn Leu Val Ser Ala Ala Gly
194 199 204 209

gga agt atc tca cac cag gtt agc ttc tcc tac ttc aat gca ttt aac 789
Gly Ser Ile Ser His Gln Val Ser Phe Ser Tyr Phe Asn Ala Phe Asn
210 215 220 225

tcg tta ctg aat aac atg gag ctt gtt cgt aag ata tat agc act cta 837
Ser Leu Leu Asn Asn Met Glu Leu Val Arg Lys Ile Tyr Ser Thr Leu
226 231 236 241

gct ggc aca agg aaa gat gtt gaa gtc aca aag gag gaa ttt gcc cag 885
Ala Gly Thr Arg Lys Asp Val Glu Val Thr Lys Glu Glu Phe Ala Gln
242 247 252 257

agt gcc ata cgc tat gga caa gtc aca cca cta gaa att gat att cta 933
Ser Ala Ile Arg Tyr Gly Gln Val Thr Pro Leu Glu Ile Asp Ile Leu
258 263 268 273

tat cag ctt gca gac tta tat aat gct tca ggg cgc ttg act ttg gca 981
Tyr Gln Leu Ala Asp Leu Tyr Asn Ala Ser Gly Arg Leu Thr Leu Ala
274 279 284 289

gat att gag aga ata gcc cca ttg gct gag ggg gcc tta cct tac aac 1029
Asp Ile Glu Arg Ile Ala Pro Leu Ala Glu Gly Ala Leu Pro Tyr Asn
290 295 300 305

ctg gca gaa ctt cag aga cag cag tct cct ggg tta ggc agg cct atc 1077
Leu Ala Glu Leu Gln Arg Gln Gln Ser Pro Gly Leu Gly Arg Pro Ile

306	311	316	321	
tgg ctc cag att gcc gag tct gct tac aga ttc act ctg ggc tca gtt				1125
Trp Leu Gln Ile Ala Glu Ser Ala Tyr Arg Phe Thr Leu Gly Ser Val				
322	327	332	337	
gct gga gct gtg gga gcc act gca gtg tat cct ata gat ctg gtg aag				1173
Ala Gly Ala Val Gly Ala Thr Ala Val Tyr Pro Ile Asp Leu Val Lys				
338	343	348	353	
acc cga atg caa aac cag cgt ggc tct ggc tct gtt gtt ggg gag cta				1221
Thr Arg Met Gln Asn Gln Arg Gly Ser Gly Ser Val Val Gly Glu Leu				
354	359	364	369	
atg tac aaa aac agc ttt gac tgt ttt aag aaa gtc ttg cgt tat gag				1269
Met Tyr Lys Asn Ser Phe Asp Cys Phe Lys Lys Val Leu Arg Tyr Glu				
370	375	380	385	
ggc ttc ttt gga ctc tac agg ggt ctg ata cca caa ctt ata ggg gtt				1317
Gly Phe Phe Gly Leu Tyr Arg Gly Leu Ile Pro Gln Leu Ile Gly Val				
386	391	396	401	
gct cca gaa aag gcc att aaa ctg act gtt aat gat ttt gtt cgg gac				1365
Ala Pro Glu Lys Ala Ile Lys Leu Thr Val Asn Asp Phe Val Arg Asp				
402	407	412	417	
aaa ttt acc aga aga gat ggc tct gtt cca ctt cca gca gaa gtt ctt				1413
Lys Phe Thr Arg Arg Asp Gly Ser Val Pro Leu Pro Ala Glu Val Leu				
418	423	428	433	
gct gga ggc tgt gct gga ggc tct cag gtc att ttt acc aac cca ttg				1461
Ala Gly Gly Cys Ala Gly Gly Ser Gln Val Ile Phe Thr Asn Pro Leu				
434	439	444	449	
gag ata gtg aag att cgt ctg caa gta gct gga gag atc acc acg gga				1509
Glu Ile Val Lys Ile Arg Leu Gln Val Ala Gly Glu Ile Thr Thr Gly				
450	455	460	465	
ccc aga gtc agc gcc ctg aat gtg ctc cgg gac ttg gga att ttt ggt				1557
Pro Arg Val Ser Ala Leu Asn Val Leu Arg Asp Leu Gly Ile Phe Gly				
466	471	476	481	
ctg tat aag ggt gcc aaa gcg tgt ttc ctc cga gac att ccc ttc tct				1605
Leu Tyr Lys Gly Ala Lys Ala Cys Phe Leu Arg Asp Ile Pro Phe Ser				
482	487	492	497	
gca atc tat ttt cct gtt tat gct cat tgc aaa cta ctt ctg gct gat				1653
Ala Ile Tyr Phe Pro Val Tyr Ala His Cys Lys Leu Leu Leu Ala Asp				
498	503	508	513	
gaa aat gga cac gtg gga ggt tta aat ctt ctt gca gct gga gcc atg				1701
Glu Asn Gly His Val Gly Gly Leu Asn Leu Leu Ala Ala Gly Ala Met				
514	519	524	529	
gca ggt gtc cca gct gca tct ctg gtg acc cct gct gat gtc atc aag				1749
Ala Gly Val Pro Ala Ala Ser Leu Val Thr Pro Ala Asp Val Ile Lys				
530	535	540	545	

aca aga ctg cag gtg gct gcc cgc gct ggc cag acg aca tac agt ggt	1797
Thr Arg Leu Gln Val Ala Ala Arg Ala Gly Gln Thr Thr Tyr Ser Gly	
546 551 556 561	
gtc atc gac tgt ttc agg aag att ctc cgg gaa gaa ggg ccc tca gca	1845
Val Ile Asp Cys Phe Arg Lys Ile Leu Arg Glu Glu Gly Pro Ser Ala	
562 567 572 577	
ttt tgg aaa ggg act gca gct cga gtg ttt cga tcc tct ccc cag ttt	1893
Phe Trp Lys Gly Thr Ala Ala Arg Val Phe Arg Ser Ser Pro Gln Phe	
578 583 588 593	
ggg gtt acc ttg gtc act tat gaa gtt ctc cag cgg tgg ttt tac att	1941
Gly Val Thr Leu Val Thr Tyr Glu Val Leu Gln Arg Trp Phe Tyr Ile	
594 599 604 609	
gat ttt gga ggc ctc aaa ccc gct ggt tca gaa cca aca cct aag tca	1989
Asp Phe Gly Gly Leu Lys Pro Ala Gly Ser Glu Pro Thr Pro Lys Ser	
610 615 620 625	
cgc att gca gac ctt cct cct gcc aac cct gat cac atc ggt gga tac	2037
Arg Ile Ala Asp Leu Pro Pro Ala Asn Pro Asp His Ile Gly Gly Tyr	
626 631 636 641	
aga ctc gcc aca gcc acg ttt gca ggc atc gaa aac aaa ttt ggc ctt	2085
Arg Leu Ala Thr Ala Thr Phe Ala Gly Ile Glu Asn Lys Phe Gly Leu	
642 647 652 657	
tat ctc ccg aaa ttt aag tct cct agt gtt gct gtg gtt cag cca aag	2133
Tyr Leu Pro Lys Phe Lys Ser Pro Ser Val Ala Val Val Gln Pro Lys	
658 663 668 673	
gca gca gtg gca gcc act cag tga tgagacaact gttgagtgtg gcaaaatggc	2187
Ala Ala Val Ala Ala Thr Gln *	
674 679	
gccttgaaga aagagcctag gagagcagcc ctgtaatgta tccagtcagc tgcattggtac	2247
tgactgagct gaggagtcaa actcttcttt ctgtatgaca tatacatata cttgtttata	2307
aaataatcat ttgccaggg aaaaaaccac aacgctgttt caagcttttag tcttatgtgt	2367
tgaaatgttt ttgtaagcct tggcatgaat tagtggttcta gactctgctt tgcacagctt	2427
gcacttacag tgattgtaca tattgtacat ctttgtacag agacatcttg gcacctcatc	2487
ccaacaaatc acatttgtag aaatgtaatg cggttctgag tggcttgaaa tgtacagaat	2547
gttttgaaag tgttttatta agaatacacac aaaaataaat gtattaaaat taaattcatt	2607
ctcttattgg tgacttatgg aaataaagca tcaatattgg atgtaaaaaa aaaaaa	2663

<211> 1725
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1488)

<400> 284

atg gta acg tgg ctt tac aga ttt tta ccc act tca aat atg gcc gcc 48
 Met Val Thr Trp Leu Tyr Arg Phe Leu Pro Thr Ser Asn Met Ala Ala
 1 5 10

aag ctc cgt tct ctt tta ccg cct gat cta cgg cta caa ttc tgg ctt 96
 Lys Leu Arg Ser Leu Leu Pro Pro Asp Leu Arg Leu Gln Phe Trp Leu
 17 22 27 32

cat gcc cgc ctc caa aag tgc ttc ctc tcg agg ggt tgt ggt tct tac 144
 His Ala Arg Leu Gln Lys Cys Phe Leu Ser Arg Gly Cys Gly Ser Tyr
 33 38 43 48

tgc gca ggc gca aaa gca agt cct ctt ccg ggc aaa atg gcg atg gga 192
 Cys Ala Gly Ala Lys Ala Ser Pro Leu Pro Gly Lys Met Ala Met Gly
 49 54 59 64

cta atg tgc gga cgc cgg gag ctt ctg cgc ttg cta cag tcc ggg cgt 240
 Leu Met Cys Gly Arg Arg Glu Leu Leu Arg Leu Leu Gln Ser Gly Arg
 65 70 75 80

cgg gtc cac agc gtc gca ggg ccc tcg caa tgg ctt ggg aaa ccg ctg 288
 Arg Val His Ser Val Ala Gly Pro Ser Gln Trp Leu Gly Lys Pro Leu
 81 86 91 96

acc aca cgg ctc cta ttc cca gta gcc ccg tgc tgc tgt cgc cca cac 336
 Thr Thr Arg Leu Leu Phe Pro Val Ala Pro Cys Cys Cys Arg Pro His
 97 102 107 112

tac ctc ttc ctt gcg gct tcc ggc ccc cgc agc ctc agt acc tct gct 384
 Tyr Leu Phe Leu Ala Ala Ser Gly Pro Arg Ser Leu Ser Thr Ser Ala
 113 118 123 128

atc tct ttt gca gaa gtc cag gtt cag gcc cct cct gtt gtt gct gca 432
 Ile Ser Phe Ala Glu Val Gln Val Gln Ala Pro Pro Val Val Ala Ala
 129 134 139 144

act ccc tca ccc aca gca gta cct gag gtg gct tct gga gag act gca 480
 Thr Pro Ser Pro Thr Ala Val Pro Glu Val Ala Ser Gly Glu Thr Ala
 145 150 155 160

gat gta gtc caa act gct gca gag cag agc ttc gct gaa ctg ggg ctg 528
 Asp Val Val Gln Thr Ala Ala Glu Gln Ser Phe Ala Glu Leu Gly Leu
 161 166 171 176

ggg tca tac acc cca gtg gga ctg atc cag aat tta ctg gaa ttt atg 576
 Gly Ser Tyr Thr Pro Val Gly Leu Ile Gln Asn Leu Leu Glu Phe Met
 177 182 187 192

cat gtt gat ctg ggc cta cct tgg tgg ggg gcc att gct gca tgt aca	624
His Val Asp Leu Gly Leu Pro Trp Trp Gly Ala Ile Ala Ala Cys Thr	
193 198 203 208	
gtc ttt gcc cgc tgc ctg att ttt cct ctc atc gtg acg ggc cag cga	672
Val Phe Ala Arg Cys Leu Ile Phe Pro Leu Ile Val Thr Gly Gln Arg	
209 214 219 224	
gag gca gcc agg atc cac aat cac ttg cca gag atc cag aag ttt tcc	720
Glu Ala Ala Arg Ile His Asn His Leu Pro Glu Ile Gln Lys Phe Ser	
225 230 235 240	
agt cga atc aga gag gcc aag tta gca gga gac cat att gag tat tac	768
Ser Arg Ile Arg Glu Ala Lys Leu Ala Gly Asp His Ile Glu Tyr Tyr	
241 246 251 256	
aag gct tcc tgc gag atg gca ctt tac cag aaa aaa cat ggt att aaa	816
Lys Ala Ser Ser Glu Met Ala Leu Tyr Gln Lys Lys His Gly Ile Lys	
257 262 267 272	
ctc tat aaa cct ctc att ctc cct gtg act cag gcc cca atc ttc atc	864
Leu Tyr Lys Pro Leu Ile Leu Pro Val Thr Gln Ala Pro Ile Phe Ile	
273 278 283 288	
tcc ttc ttc att gct ttg aga gag atg gcc aac ctt cct gtg ccc agc	912
Ser Phe Phe Ile Ala Leu Arg Glu Met Ala Asn Leu Pro Val Pro Ser	
289 294 299 304	
ctg cag aca ggt ggc ctc tgg tgg ttc cag gat ctc acg gta tcc gat	960
Leu Gln Thr Gly Gly Leu Trp Trp Phe Gln Asp Leu Thr Val Ser Asp	
305 310 315 320	
ccc atc tac ata tta cca ctg gca gtc act gct aca atg tgg gct gtt	1008
Pro Ile Tyr Ile Leu Pro Leu Ala Val Thr Ala Thr Met Trp Ala Val	
321 326 331 336	
ctt gag cta ggt gct gag aca ggt gtg caa agt tct gac ctt cag tgg	1056
Leu Glu Leu Gly Ala Glu Thr Gly Val Gln Ser Ser Asp Leu Gln Trp	
337 342 347 352	
atg aga aat gtc atc aga atg atg ccc ctg ata acc ttg ccc ata acc	1104
Met Arg Asn Val Ile Arg Met Met Pro Leu Ile Thr Leu Pro Ile Thr	
353 358 363 368	
atg cat ttc ccc acg gca gtg ttt atg tac tgg ctc tcc tcc aat ttg	1152
Met His Phe Pro Thr Ala Val Phe Met Tyr Trp Leu Ser Ser Asn Leu	
369 374 379 384	
ttt tcc ctg gtc caa gta tcc tgt ctc cgg att cca gca gta cgc act	1200
Phe Ser Leu Val Gln Val Ser Cys Leu Arg Ile Pro Ala Val Arg Thr	
385 390 395 400	
gta ctt aaa atc ccc cag cgt gtt gta cat gac ctg gac aaa tta cct	1248
Val Leu Lys Ile Pro Gln Arg Val Val His Asp Leu Asp Lys Leu Pro	
401 406 411 416	
cca cgg gaa ggc ttc cta gag agc ttc aaa aaa ggc tgg aaa aat gct	1296

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

1344

1392

1440

1488

1548

1608

1668

1725

<211> 3197

<213> Homo sapiens

<221> CDS

<400> 285

60

120

178

22 €

274

322

Glu Thr Thr Arg Gln Leu Ser Leu Ala Val Lys Asp Gly Leu Ile Val	
34 39 44 49	
gaa act cta aca gtg ggc tgc aaa ggt tca aaa gct ggt att gaa caa	370
Glu Thr Leu Thr Val Gly Cys Lys Gly Ser Lys Ala Gly Ile Glu Gln	
50 55 60 65	
gaa gga tat tgg ttg cca gga gat gag att gac tgg gaa aca gaa aat	418
Glu Gly Tyr Trp Leu Pro Gly Asp Glu Ile Asp Trp Glu Thr Glu Asn	
66 71 76 81	
cat gac tgg tat tgt ttt gaa tgc cat ttg cct gga gag gtg ttg ata	466
His Asp Trp Tyr Cys Phe Glu Cys His Leu Pro Gly Glu Val Leu Ile	
82 87 92 97	
tgt gac ctg tgt ttt cgt gtg tat cat tcc aag tgt ttg tct gat gag	514
Cys Asp Leu Cys Phe Arg Val Tyr His Ser Lys Cys Leu Ser Asp Glu	
98 103 108 113	
ttc agg ctt aga gac agc agt agt ccc tgg cag tgc cca gtt tgc agg	562
Phe Arg Leu Arg Asp Ser Ser Ser Pro Trp Gln Cys Pro Val Cys Arg	
114 119 124 129	
agc att aag aag aag aat aca aac aaa cag gag atg ggc aca tac ctc	610
Ser Ile Lys Lys Lys Asn Thr Asn Lys Gln Glu Met Gly Thr Tyr Leu	
130 135 140 145	
aga ttc att gtc tcc cgc atg aag gag agg gct ata gat ctt aat aaa	658
Arg Phe Ile Val Ser Arg Met Lys Glu Arg Ala Ile Asp Leu Asn Lys	
146 151 156 161	
aag ggg aag gac aat aaa cac ccg atg tac agg agg ctg gtg cac tca	706
Lys Gly Lys Asp Asn Lys His Pro Met Tyr Arg Arg Leu Val His Ser	
162 167 172 177	
gct gtg gac gtt ccc acc att caa gag aaa gtg aat gaa ggg aaa tac	754
Ala Val Asp Val Pro Thr Ile Gln Glu Lys Val Asn Glu Gly Lys Tyr	
178 183 188 193	
cga agt tat gaa gag ttc aaa gct gat gcc caa ttg ctt ctc cac aat	802
Arg Ser Tyr Glu Glu Phe Lys Ala Asp Ala Gln Leu Leu Leu His Asn	
194 199 204 209	
acc gtg att ttc tat gga gca gac agt gag caa gct gac att gcg agg	850
Thr Val Ile Phe Tyr Gly Ala Asp Ser Glu Gln Ala Asp Ile Ala Arg	
210 215 220 225	
atg cta tat aaa gac aca tgt cat gag ctg gat gaa ctg cag ctt tgc	898
Met Leu Tyr Lys Asp Thr Cys His Glu Leu Asp Glu Leu Gln Leu Cys	
226 231 236 241	
aag aat tgc ttt tac ttg tca aat gct cgt cct gac aac tgg ttc tgt	946
Lys Asn Cys Phe Tyr Leu Ser Asn Ala Arg Pro Asp Asn Trp Phe Cys	
242 247 252 257	
tat cct tgt ata cct aat cat gag ctg gtt tgg gct aaa atg aaa ggt	994
Tyr Pro Cys Ile Pro Asn His Glu Leu Val Trp Ala Lys Met Lys Gly	

258	263	268	273	
ttt ggg ttt tgg cca gcc aaa gtc atg cag	aaa gaa gac aat caa gtc	1042		
Phe Gly Phe Trp Pro Ala Lys Val Met Gln	Lys Glu Asp Asn Gln Val			
274	279	284 289		
gac gtt cgc ttc ttt ggc cac cac cac cag	agg gcc tgg att cct tct	1090		
Asp Val Arg Phe Phe Gly His His His Gln	Arg Ala Trp Ile Pro Ser			
290	295	300 305		
gaa aac att caa gat atc aca gtc aac att	cat cgg ctg cac gtg aag	1138		
Glu Asn Ile Gln Asp Ile Thr Val Asn Ile	His Arg Leu His Val Lys			
306	311	316 321		
cgc agt atg ggt tgg aaa aag gcc tgt gat	gag ctg gag ctg cat cag	1186		
Arg Ser Met Gly Trp Lys Lys Ala Cys Asp	Glu Leu Glu Leu His Gln			
322	327	332 337		
cgt ttc cta cga gaa ggg aga ttt tgg aaa	tct aag aat gag gac cga	1234		
Arg Phe Leu Arg Glu Gly Arg Phe Trp Lys	Ser Lys Asn Glu Asp Arg			
338	343	348 353		
ggt gag gaa gag gca gaa tcc agt atc tcc	tcc acc agt aat gag cag	1282		
Gly Glu Glu Glu Ala Glu Ser Ser Ile Ser	Ser Thr Ser Asn Glu Gln			
354	359	364 369		
cta aag gtc act caa gaa cca aga gca aag	aaa gga cga cgt aat caa	1330		
Leu Lys Val Thr Gln Glu Pro Arg Ala Lys	Lys Gly Arg Arg Asn Gln			
370	375	380 385		
agt gtg gag ccc aaa aag gaa gaa cca gag	cct gaa aca gaa gca gta	1378		
Ser Val Glu Pro Lys Lys Glu Glu Pro Glu	Pro Glu Thr Glu Ala Val			
386	391	396 401		
agt tct agc cag gaa ata ccc acg atg cct	cag ccc atc gaa aaa gtc	1426		
Ser Ser Ser Gln Glu Ile Pro Thr Met Pro	Gln Pro Ile Glu Lys Val			
402	407	412 417		
tcc gtg tca act cag aca aag aag tta agt	gcc tct tca cca aga atg	1474		
Ser Val Ser Thr Gln Thr Lys Lys Leu Ser	Ala Ser Ser Pro Arg Met			
418	423	428 433		
ctg cat cgg agc acc cag acc aca aac gac	ggc gtg tgt cag agc atg	1522		
Leu His Arg Ser Thr Gln Thr Thr Asn Asp	Gly Val Cys Gln Ser Met			
434	439	444 449		
tgc cat gac aaa tac acc aag atc ttc aat	gac ttc aaa gac cgg atg	1570		
Cys His Asp Lys Tyr Thr Lys Ile Phe Asn	Asp Phe Lys Asp Arg Met			
450	455	460 465		
aag tcg gac cac aag cgg gag aca gag cgt	gtt gtc cga gaa gct ctg	1618		
Lys Ser Asp His Lys Arg Glu Thr Glu Arg	Val Val Arg Glu Ala Leu			
466	471	476 481		
gag aag ctg cgt tct gaa atg gaa gaa gaa	aag aga caa gct gta aat	1666		
Glu Lys Leu Arg Ser Glu Met Glu Glu Glu	Lys Arg Gln Ala Val Asn			
482	487	492 497		

aaa gct gta gcc aac atg cag ggt gag atg gac aga aaa tgt aag caa	1714
Lys Ala Val Ala Asn Met Gln Gly Glu Met Asp Arg Lys Cys Lys Gln	
498 503 508 513	
gta aag gaa aag tgt aag gag gaa ttt gta gaa gaa atc aag aag ctg	1762
Val Lys Glu Lys Cys Lys Glu Glu Phe Val Glu Glu Ile Lys Lys Leu	
514 519 524 529	
gca aca cag cac aag caa ctg att tct cag acc aag aag aag cag tgg	1810
Ala Thr Gln His Lys Gln Leu Ile Ser Gln Thr Lys Lys Lys Gln Trp	
530 535 540 545	
tgc tac aac tgt gag gag gag gcc atg tac cac tgc tgc tgg aac aca	1858
Cys Tyr Asn Cys Glu Glu Glu Ala Met Tyr His Cys Cys Trp Asn Thr	
546 551 556 561	
tcc tac tgc tcc atc aag tgc cag cag gag cac tgg cac gcg gag cac	1906
Ser Tyr Cys Ser Ile Lys Cys Gln Gln Glu His Trp His Ala Glu His	
562 567 572 577	
aag cgc acc tgc cgc cgg aaa aga tga agctg gcccttcccg gagtcacccc	1958
Lys Arg Thr Cys Arg Arg Lys Arg *	
578 583	
gatgattact cttttcagac acagcggttt ttgtttccaa gaagccaaaa ttgttttagaa	2018
tttgcttccc attttgcacc agcctttaa cacttttctg gaagaaattt tgcacagtag	2078
tttaaattct ttgttaatgc tcttccgaag tttttcaggg ggtaaaagta acatcagtgg	2138
agggattat tttaaataaa ttttaattga gaatttggtg cattttcagc aaattttaaa	2198
acatttttag gttttacaga gattttaacc tttaaacaac agatcttttaaaaacacaggtg	2258
aatacaagtg agtttaacaa agaaacattt agaatatagtc tgaatgtaag aactacagaa	2318
ctgtttcaga aataaaacat actacctga tgtgacattt ttttcttaac cttgttgagc	2378
tggttttggt cagcttaatt tactgttcaa aggcatatc tgttggtcac accagtgggt	2438
atatgattga atttaggga caggggtgac acagcagggc tagtctgca tttttttct	2498
taaatatttc ccaatttgtt ttttcattat ttcttttcaa tatataactt ttataacaaa	2558
ttattagctt tgatcttgta gtttaaaatt gcaggggaact ggggtaattt tttactgagc	2618
tggatcttag agaaaatgaa tatttaaatt ttaaagtttg cacatttcat ctttgccta	2678
acatgagtgc ttgtaacaaa ataaacaaca aaaacaaagc caaaaactac ctttatccat	2738
atgtgaaatt atagatgagg catacgaatt tgtttaatgc ttcccttccc ttcccacata	2798
tcatctcact gctattatc tgggtgtcac tcatgtatcg taagttaata ctaaaagaag	2858
agaaagcact taagtttcac agaagccgtt atgtttgtag taatgggtca ttgctacta	2918

atgaactcca tcaactgtaca cagaatgaag aataatgcat gttaattttc ttgtattaaa 2978
gatgccgtga tttgtaaaaa gtctgtatct tgcggaatgt ctggattaag aagcattacc 3038
aataggaatg gatcgatagt tgaataatga ttttttatac atagatatat aaaatacagc 3098
caggaaaact taaattactt ttctttttaa atatctcaca atttatgtgg tattttttaa 3158
gactgatctt agaccaagtc aaattcccat ttatcatctt 3197

<210> 286
<211> 3035
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (176) .. (1771)

<400> 286
ggagcataat gctaaagaag taaacaggtc atggcacggt taacaaaaag acgacaggcg 60
atacaaaagc tatccagcat ctttgggcag ccattgagat tatacggaac cagaagcaga 120
ttgccaacat tgaccgtatt acaaaatgtg aaacaactac attattottg aacct atg 178
Met
1
gtg att ttt aca tca tta cac aga tat gtc att ttc att agt tgt atc 226
Val Ile Phe Thr Ser Leu His Arg Tyr Val Ile Phe Ile Ser Cys Ile
2 7 12 17
att gtt ata aac tgg tat atg tct cga gtc cac ggt atg cac cct aaa 274
Ile Val Ile Asn Trp Tyr Met Ser Arg Val His Gly Met His Pro Lys
18 23 28 33
gag acc acc cgt cag ctg agc tta gct gtg aaa gat ggt ctt att gtc 322
Glu Thr Thr Arg Gln Leu Ser Leu Ala Val Lys Asp Gly Leu Ile Val
34 39 44 49
gaa act cta aca gtg ggc tgc aaa ggt tca aaa gct ggt att gaa caa 370
Glu Thr Leu Thr Val Gly Cys Lys Gly Ser Lys Ala Gly Ile Glu Gln
50 55 60 65
gaa gga tat tgg ttg cca gga gat gag att agc att aag aag aag aat 418
Glu Gly Tyr Trp Leu Pro Gly Asp Glu Ile Ser Ile Lys Lys Lys Asn
66 71 76 81
aca aac aaa cag gag atg ggc aca tac ctc aga ttc att gtc tcc cgc 466
Thr Asn Lys Gln Glu Met Gly Thr Tyr Leu Arg Phe Ile Val Ser Arg
82 87 92 97
atg aag gag agg gct ata gat ctt aat aaa aag ggg aag gac aat aaa 514
Met Lys Glu Arg Ala Ile Asp Leu Asn Lys Lys Gly Lys Asp Asn Lys

gaa gaa cca gag cct gaa aca gaa gca gta agt tct agc cag gaa ata	1234
Glu Glu Pro Glu Pro Glu Thr Glu Ala Val Ser Ser Ser Gln Glu Ile	
338 343 348 353	
ccc acg atg cct cag ccc atc gaa aaa gtc tcc gtg tca act cag aca	1282
Pro Thr Met Pro Gln Pro Ile Glu Lys Val Ser Val Ser Thr Gln Thr	
354 359 364 369	
aag aag tta agt gcc tct tca cca aga atg ctg cat cgg agc acc cag	1330
Lys Lys Leu Ser Ala Ser Ser Pro Arg Met Leu His Arg Ser Thr Gln	
370 375 380 385	
acc aca aac gac ggc gtg tgt cag agc atg tgc cat gac aaa tac acc	1378
Thr Thr Asn Asp Gly Val Cys Gln Ser Met Cys His Asp Lys Tyr Thr	
386 391 396 401	
aag atc ttc aat gac ttc aaa gac cgg atg aag tcg gac cac aag cgg	1426
Lys Ile Phe Asn Asp Phe Lys Asp Arg Met Lys Ser Asp His Lys Arg	
402 407 412 417	
gag aca gag cgt gtt gtc cga gaa gct ctg gag aag ctg cgt tct gaa	1474
Glu Thr Glu Arg Val Val Arg Glu Ala Leu Glu Lys Leu Arg Ser Glu	
418 423 428 433	
atg gaa gaa gaa aag aga caa gct gta aat aaa gct gta gcc aac atg	1522
Met Glu Glu Glu Lys Arg Gln Ala Val Asn Lys Ala Val Ala Asn Met	
434 439 444 449	
cag ggt gag atg gac aga aaa tgt aag caa gta aag gaa aag tgt aag	1570
Gln Gly Glu Met Asp Arg Lys Cys Lys Gln Val Lys Glu Lys Cys Lys	
450 455 460 465	
gag gaa ttt gta gaa gaa atc aag aag ctg gca aca cag cac aag caa	1618
Glu Glu Phe Val Glu Glu Ile Lys Lys Leu Ala Thr Gln His Lys Gln	
466 471 476 481	
ctg att tct cag acc aag aag aag cag tgg tgc tac aac tgt gag gag	1666
Leu Ile Ser Gln Thr Lys Lys Lys Gln Trp Cys Tyr Asn Cys Glu Glu	
482 487 492 497	
gag gcc atg tac cac tgc tgc tgg aac aca tcc tac tgc tcc atc aag	1714
Glu Ala Met Tyr His Cys Cys Trp Asn Thr Ser Tyr Cys Ser Ile Lys	
498 503 508 513	
tgc cag cag gag cac tgg cac gcg gag cac aag cgc acc tgc cgc cgg	1762
Cys Gln Gln Glu His Trp His Ala Glu His Lys Arg Thr Cys Arg Arg	
514 519 524 529	
aaa aga tga agctggc ccttcccgga gtcaccccgga tgattactct tttcagacac	1818
Lys Arg *	
530	
agcgggttttt gtttccaaga agccaaaatt gtttagaatt tgcttcccat tttgcaccag	1878
cctttaaaca cttttcgtga agaaattttg cacagtagtt taaatctttt gttaatgctc	1938

ccggcagcaa ggagtgttcc tgggacctca gagaccaggc tcagagcctg acatccctgc 240

gaggggacag cctcatccgc ccaggccagt gggggtctct acaagtgcc aggctcaggt 300

gcagccccca gca atg cat cgc cgg aga ctg gcc ctg ggt ctg ggg ttc 349
Met His Arg Arg Arg Leu Ala Leu Gly Leu Gly Phe
1 5 10

tgc ctg ttg gcg ggc aca agc ctc agt gtc ctg tgg gtg tat ctt gag 397
Cys Leu Leu Ala Gly Thr Ser Leu Ser Val Leu Trp Val Tyr Leu Glu
13 18 23 28

aac tgg ctg cca gtc tcc tat gtc ccc tat tat ctg ccc tgc cca gag 445
Asn Trp Leu Pro Val Ser Tyr Val Pro Tyr Tyr Leu Pro Cys Pro Glu
29 34 39 44

atc ttc aac atg aag ctg cac tac aag agg gag aag cca ctc cag ccc 493
Ile Phe Asn Met Lys Leu His Tyr Lys Arg Glu Lys Pro Leu Gln Pro
45 50 55 60

gtg gta tgg tca cag tac cct cag ccc aag ctg ctg gag cac agg ccc 541
Val Val Trp Ser Gln Tyr Pro Gln Pro Lys Leu Leu Glu His Arg Pro
61 66 71 76

aca cag ctg ctg aca ctc aca ccc tgg ttg gcg ccc atc gtc tcc gag 589
Thr Gln Leu Leu Thr Leu Thr Pro Trp Leu Ala Pro Ile Val Ser Glu
77 82 87 92

gga acc ttc aac cca gag ctt ctg cag cac atc tac cag cca ctg aac 637
Gly Thr Phe Asn Pro Glu Leu Leu Gln His Ile Tyr Gln Pro Leu Asn
93 98 103 108

ctg acc att ggg gtc acg gtg ttt gcc gtg ggg aag tac act cat ttc 685
Leu Thr Ile Gly Val Thr Val Phe Ala Val Gly Lys Tyr Thr His Phe
109 114 119 124

atc cag tcc ttc ctg gag tca gcc gag gag ttc ttc atg cgt ggg tac 733
Ile Gln Ser Phe Leu Glu Ser Ala Glu Glu Phe Phe Met Arg Gly Tyr
125 130 135 140

cgg gtg cac tac tac atc ttc act gac aac cct gca gcc gtt ccc ggg 781
Arg Val His Tyr Tyr Ile Phe Thr Asp Asn Pro Ala Ala Val Pro Gly
141 146 151 156

gtc ccg ctg ggt ccc cac cgg ctt ctc agc tcc atc ccc atc cag ggt 829
Val Pro Leu Gly Pro His Arg Leu Leu Ser Ser Ile Pro Ile Gln Gly
157 162 167 172

cac tcc cac tgg gag gag aca tcc atg cgc cgg atg gag acc atc agc 877
His Ser His Trp Glu Glu Thr Ser Met Arg Arg Met Glu Thr Ile Ser
173 178 183 188

cag cac att gct aag agg gct cac cgg gag gtg gac tac ctc ttc tgc 925
Gln His Ile Ala Lys Arg Ala His Arg Glu Val Asp Tyr Leu Phe Cys
189 194 199 204

ctt gat gtg gac atg gtg ttt cgg aac ccg tgg ggc cct gag acc ttg 973

Leu Asp Val Asp Met Val Phe Arg Asn Pro Trp Gly Pro Glu Thr Leu	
205 210 215 220	
gga gac ctg gtg gct gcc att cac cca agc tac tac gcc gtt ccc cgc	1021
Gly Asp Leu Val Ala Ala Ile His Pro Ser Tyr Tyr Ala Val Pro Arg	
221 226 231 236	
cag cag ttc ccc tat gag cgc agg cgt gtt tcc act gcc ttt gtg gca	1069
Gln Gln Phe Pro Tyr Glu Arg Arg Arg Val Ser Thr Ala Phe Val Ala	
237 242 247 252	
gac agc gaa ggg gac ttc tat tat ggt ggg gca gtc ttc ggg ggg cag	1117
Asp Ser Glu Gly Asp Phe Tyr Tyr Gly Gly Ala Val Phe Gly Gly Gln	
253 258 263 268	
gtg gcc agg gta tat gag ttt act agg ggc tgc cac atg gcc atc ctg	1165
Val Ala Arg Val Tyr Glu Phe Thr Arg Gly Cys His Met Ala Ile Leu	
269 274 279 284	
gcg gac aag gcc aat ggc atc atg gct gcc tgg cgg gag gaa agc cac	1213
Ala Asp Lys Ala Asn Gly Ile Met Ala Ala Trp Arg Glu Glu Ser His	
285 290 295 300	
ctg aac cgt cac ttc atc tca aac aag ccg tcc aag gtg ctg tcc ccc	1261
Leu Asn Arg His Phe Ile Ser Asn Lys Pro Ser Lys Val Leu Ser Pro	
301 306 311 316	
gag tac ctc tgg gac gac agg aag ccc cag cca ccc agc ctg aag ctg	1309
Glu Tyr Leu Trp Asp Asp Arg Lys Pro Gln Pro Pro Ser Leu Lys Leu	
317 322 327 332	
atc cgc ttt tct aca ctg gac aag gat atc agc tgc ctg agg agc tga	1357
Ile Arg Phe Ser Thr Leu Asp Lys Asp Ile Ser Cys Leu Arg Ser *	
333 338 343 348	
ccacggagct gggggttgcc atggatgggg acccaaagac ctgcagccac cagtgtttca	1417
ctagcgtgca gaccagccct gtcccgctc cctgtcagtc aggcgaattc aaccggaaaa	1477
gggacgtgga aaggccactg tgaactgcag agggctgtgc acacagtagc acacaggatc	1537
tcacagtaac gcggcatggg aacagtgaga cagggggagg ggaggcgcag ttacaaaggc	1597
agggcccggc aggettcca cgttctgcag ccgtgccttt gcggggcagg ctctgaagcc	1657
tcagcccgcac tcagagtgcc tgaaccg	1684

<210> 288
 <211> 1535
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (290)..(1036)

<400> 288

```
cccaggtgac tttgcgaagg catggcgggg acactgtgaa tgtcagccca gaaggtgatc      60
agagcctgtt aattaaaatg gaaagaagac agaaggggaag gtagacatca ggttctccct      120
ggagactttt cgttttcatt tacgctgcgg aaactgaagt ttttgcctaa caccatgt      180
aatgtaaacy tataggcttg agtacgtgtc aggccgcagt tgtagtgaac cctaaagctt      240
tcctaattgt agttagcatc gtcctaagc ggaacgattt tccgtgaac      atg att      295
                               Met Ile
                               1

tgt act ttt cta cga gcc gta cag tat acg gag aag ctg cac agg tcc      343
Cys Thr Phe Leu Arg Ala Val Gln Tyr Thr Glu Lys Leu His Arg Ser
   3                               8                               13                               18

tcg gca aag cga ttg ctt ttg cca tac atc gtg ctt aac aaa gcg tgc      391
Ser Ala Lys Arg Leu Leu Leu Pro Tyr Ile Val Leu Asn Lys Ala Cys
  19                               24                               29                               34

ttg aag act gag ccc agt ttg aga tgt ggg ctt caa tat caa aag aaa      439
Leu Lys Thr Glu Pro Ser Leu Arg Cys Gly Leu Gln Tyr Gln Lys Lys
  35                               40                               45                               50

acg ctg cga cct aga tgt att ctt gga gtc acc cag aaa acc atc tgg      487
Thr Leu Arg Pro Arg Cys Ile Leu Gly Val Thr Gln Lys Thr Ile Trp
  51                               56                               61                               66

acg cag gga ccg agc ccc cga aaa gca aag gag gat agc agc acc caa      535
Thr Gln Gly Pro Ser Pro Arg Lys Ala Lys Glu Asp Ser Ser Thr Gln
  67                               72                               77                               82

gtg tct gtg cac agg agt cag aga ggg gga acc gcc gtt cca aca tca      583
Val Ser Val His Arg Ser Gln Arg Gly Gly Thr Ala Val Pro Thr Ser
  83                               88                               93                               98

caa tta gtg aat gaa gcc gga aga gat ttt acc tat tta ata gtg gtg      631
Gln Leu Val Asn Glu Ala Gly Arg Asp Phe Thr Tyr Leu Ile Val Val
  99                               104                               109                               114

ctt ttt gga atc agc att aca ggt ggc ttg ttt tac acg att ttc aaa      679
Leu Phe Gly Ile Ser Ile Thr Gly Gly Leu Phe Tyr Thr Ile Phe Lys
 115                               120                               125                               130

gaa ctt ttt tct tca tcc agt cct agc aag ata tat ggg aga gcc tta      727
Glu Leu Phe Ser Ser Ser Ser Pro Ser Lys Ile Tyr Gly Arg Ala Leu
 131                               136                               141                               146

gaa aaa tgc aga tca cat cct gag gtg atc ggt gtc ttt ggt gag tct      775
Glu Lys Cys Arg Ser His Pro Glu Val Ile Gly Val Phe Gly Glu Ser
 147                               152                               157                               162

gtt aaa ggc tat ggg gag gtg aca agg cgg ggt cgc cgg cag cat gtc      823
Val Lys Gly Tyr Gly Glu Val Thr Arg Arg Gly Arg Arg Gln His Val
```

163	168	173	178	
agg ttc act gaa tat	gta aaa gat ggg ctg	aaa cac acg tgt gtg aaa		871
Arg Phe Thr Glu Tyr	Val Lys Asp Gly Leu	Lys His Thr Cys Val Lys		
179	184	189	194	
ttc tac att gag ggc	tct gag cca ggg aag	caa gga acg gtg tat gcg		919
Phe Tyr Ile Glu Gly	Ser Glu Pro Gly Lys	Gln Gly Thr Val Tyr Ala		
195	200	205	210	
caa gtg aaa gag aac	cca gga agt ggt gaa	tat gat ttt cga tat ata		967
Gln Val Lys Glu Asn	Pro Gly Ser Gly Glu	Tyr Asp Phe Arg Tyr Ile		
211	216	221	226	
ttt gta gaa att gaa	tct tat cct aga aga	act att atc att gaa gat		1015
Phe Val Glu Ile Glu	Ser Tyr Pro Arg Arg	Thr Ile Ile Ile Glu Asp		
227	232	237	242	
aat cga tcc caa gat	gat taa aa taatcaagca	agcagggtttc tgatggatgt		1068
Asn Arg Ser Gln Asp	Asp *			
243	248			
tgaatggcgt ggactcgcta	ctccgttctt cacagctgcc	ttccagaatg tgttcaaaag		1128
aaagacaaga aggagtgtat	ggcttataaa gtgaatctaa	tacagtatgt gttgcattta		1188
aacaaactag acattttctt	acggaaaaat tatgaaatac	agcatatgtt atgttctccc		1248
attgactcaa tcatgacaat	atttctgctt taacaccatc	tttcgtgatt agaaatgttt		1308
gttattggaa atgttacacc	atgtaaataa aggaaataga	ttttagtatt gtattcattt		1368
tatattatag aactgcataa	tgtctgcaga ataaaaattaa	aactaacaaa tatgtcatta		1428
gcagctgccc tccgcatact	ttggaatctg acttgagata	agcatgtgaa aatgggtgag		1488
ggccataggg aaccagatgg	taaatacatt cttcaaaatt	gaaaaaa		1535

<210> 289
 <211> 6775
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (197) .. (4471)

<400> 289	
ccgaattccc gggttcgacga	tttcgtggcg gcaaaatggc
ggaccgcttc tcccgttca	
60	
acgaagaccg agactttcat	gttaatcact ttgatcacta
tgaggaagga cacttgga	aaa
120	
ttgaacaagc gtcacttgac	aagcctatat aatcgggaga
acagatccca ttccaatcgt	
180	

tgccaagtat gatgtc	atg ggc atg ggt cgc atg gaa atg gag ctt gat	229
	Met Gly Met Gly Arg Met Glu Met Glu Leu Asp	
	1 5	
tat gct gaa gat gct acc gaa cgg cgc cgt gtc cta gaa gta gaa aaa		277
Tyr Ala Glu Asp Ala Thr Glu Arg Arg Arg Val Leu Glu Val Glu Lys		
12 17 22 27		
gaa gac aca gaa gag ctg aga caa aag tac aag gat tat gtt gac aaa		325
Glu Asp Thr Glu Glu Leu Arg Gln Lys Tyr Lys Asp Tyr Val Asp Lys		
28 33 38 43		
gag aag gca att gcc aaa gcc ttg gaa gac ctc aga gcc aac ttt tat		373
Glu Lys Ala Ile Ala Lys Ala Leu Glu Asp Leu Arg Ala Asn Phe Tyr		
44 49 54 59		
tgt gaa ctg tgt gat aag caa tat cag aaa cat cag gaa ttt gat aac		421
Cys Glu Leu Cys Asp Lys Gln Tyr Gln Lys His Gln Glu Phe Asp Asn		
60 65 70 75		
cat atc aac tcc tat gat cat gca cac aag cag aga tta aaa gat ctg		469
His Ile Asn Ser Tyr Asp His Ala His Lys Gln Arg Leu Lys Asp Leu		
76 81 86 91		
aag cag aga gag ttt gct cga aat gtc tct tca aga tcc cgc aag gat		517
Lys Gln Arg Glu Phe Ala Arg Asn Val Ser Ser Arg Ser Arg Lys Asp		
92 97 102 107		
gag aaa aaa cag gaa aaa gcc ctt cgg cgg ctc cat gag ttg gca gag		565
Glu Lys Lys Gln Glu Lys Ala Leu Arg Arg Leu His Glu Leu Ala Glu		
108 113 118 123		
caa aga aaa caa gct gaa tgt gca cct gga agt ggt ccc atg ttc aaa		613
Gln Arg Lys Gln Ala Glu Cys Ala Pro Gly Ser Gly Pro Met Phe Lys		
124 129 134 139		
cca acc aca gtg gct gta gat gaa gaa ggt gga gaa gat gat aaa gat		661
Pro Thr Thr Val Ala Val Asp Glu Glu Gly Gly Glu Asp Asp Lys Asp		
140 145 150 155		
gaa tca gct aca aat agt ggc aca ggt gcc act gct tct tgt ggc ctg		709
Glu Ser Ala Thr Asn Ser Gly Thr Gly Ala Thr Ala Ser Cys Gly Leu		
156 161 166 171		
gga tct gaa ttc tcc aca gat aaa gga ggc cct ttc act gca gta caa		757
Gly Ser Glu Phe Ser Thr Asp Lys Gly Gly Pro Phe Thr Ala Val Gln		
172 177 182 187		
atc act aat acc act gga ctg gcc cag gct cct ggg tta gcc tcc caa		805
Ile Thr Asn Thr Thr Gly Leu Ala Gln Ala Pro Gly Leu Ala Ser Gln		
188 193 198 203		
ggc atc agc ttt ggc att aag aat aat ctg ggg acc cca ttg caa aaa		853
Gly Ile Ser Phe Gly Ile Lys Asn Asn Leu Gly Thr Pro Leu Gln Lys		
204 209 214 219		
ttg gga gtg tca ttt tct ttt gcc aaa aag gct cct gtc aaa ctc gaa		901

Leu Gly Val Ser Phe Ser Phe Ala Lys Lys Ala Pro Val Lys Leu Glu	
220 225 230 235	
tca ata gca tca gtt ttc aag gac cat gcg gag gaa ggg acc tct gaa	949
Ser Ile Ala Ser Val Phe Lys Asp His Ala Glu Glu Gly Thr Ser Glu	
236 241 246 251	
gat gga aca aaa ccc gat gag aag agt tct gac caa gga ctg cag aag	997
Asp Gly Thr Lys Pro Asp Glu Lys Ser Ser Asp Gln Gly Leu Gln Lys	
252 257 262 267	
gta gga gac tct gat ggg agc agt aat ctt gat ggt aaa aaa gag gat	1045
Val Gly Asp Ser Asp Gly Ser Ser Asn Leu Asp Gly Lys Lys Glu Asp	
268 273 278 283	
gaa gac cct cag gat gga ggg tcc ctt gcc tca aca tta tcc aaa tta	1093
Glu Asp Pro Gln Asp Gly Gly Ser Leu Ala Ser Thr Leu Ser Lys Leu	
284 289 294 299	
aaa agg atg aaa cga gaa gaa gga gct ggg gct aca gag cct gag tat	1141
Lys Arg Met Lys Arg Glu Glu Gly Ala Gly Ala Thr Glu Pro Glu Tyr	
300 305 310 315	
tac cac tac atc ccc cca gca cac tgc aaa gta aaa cct aat ttt ccc	1189
Tyr His Tyr Ile Pro Pro Ala His Cys Lys Val Lys Pro Asn Phe Pro	
316 321 326 331	
ttt cta ctt ttt atg aga gcc agt gaa caa atg gat ggt gat aat act	1237
Phe Leu Leu Phe Met Arg Ala Ser Glu Gln Met Asp Gly Asp Asn Thr	
332 337 342 347	
aca cac cca aag aat gcc cca gag agt aaa aaa ggc agt tct ccc aag	1285
Thr His Pro Lys Asn Ala Pro Glu Ser Lys Lys Gly Ser Ser Pro Lys	
348 353 358 363	
cct aaa agc tgc atc aag gcg gca gca agc caa gga gca gaa aag aca	1333
Pro Lys Ser Cys Ile Lys Ala Ala Ala Ser Gln Gly Ala Glu Lys Thr	
364 369 374 379	
gtt agt gaa gtc tct gag cag ccg aag gaa acc agc atg acc gag ccc	1381
Val Ser Glu Val Ser Glu Gln Pro Lys Glu Thr Ser Met Thr Glu Pro	
380 385 390 395	
tca gaa cca gga agc aaa gct gag gca aag aag gcc tta gga ggg gat	1429
Ser Glu Pro Gly Ser Lys Ala Glu Ala Lys Lys Ala Leu Gly Gly Asp	
396 401 406 411	
gta agt gat cag agt tta gaa agt cat agt cag aag gtt tca gag acc	1477
Val Ser Asp Gln Ser Leu Glu Ser His Ser Gln Lys Val Ser Glu Thr	
412 417 422 427	
caa atg tgt gag tcc aac tct tct aaa gaa acc tct ctg gcc acc cca	1525
Gln Met Cys Glu Ser Asn Ser Ser Lys Glu Thr Ser Leu Ala Thr Pro	
428 433 438 443	
gca ggg aaa gaa agc caa gaa gga ccc aaa cat cct act ggt ccc ttc	1573
Ala Gly Lys Glu Ser Gln Glu Gly Pro Lys His Pro Thr Gly Pro Phe	

444	449	454	459	
ttc cca gtt ttg agc	aaa gat gaa agc act	gcc ctc cag tgg cca tca	1621	
Phe Pro Val Leu Ser	Lys Asp Glu Ser Thr	Ala Leu Gln Trp Pro Ser		
460	465	470	475	
gaa cta tta att ttc	acc aag gca gaa ccc	tcc att tca tac agt tgt	1669	
Glu Leu Leu Ile Phe	Thr Lys Ala Glu Pro	Ser Ile Ser Tyr Ser Cys		
476	481	486	491	
aac cct tta tat ttt	gac ttt aaa ctt tca	agg aac aaa gat gcc aga	1717	
Asn Pro Leu Tyr Phe	Asp Phe Lys Leu Ser	Arg Asn Lys Asp Ala Arg		
492	497	502	507	
act aaa gga aca gaa	aaa cca aag gat ata	gga agc tcc tca aag gac	1765	
Thr Lys Gly Thr Glu	Lys Pro Lys Asp Ile	Gly Ser Ser Ser Lys Asp		
508	513	518	523	
cat ctc caa ggc cta	gat cct ggt gag cca	aat aaa agc aag gaa gtg	1813	
His Leu Gln Gly Leu	Asp Pro Gly Glu Pro	Asn Lys Ser Lys Glu Val		
524	529	534	539	
ggc gga gag aaa ata	gta cgt tcc tca gga	ggc aga atg gac gca cct	1861	
Gly Gly Glu Lys Ile	Val Arg Ser Ser Gly	Gly Arg Met Asp Ala Pro		
540	545	550	555	
gct tca ggg tct gcc	tgt agc ggc ctg aac	aag cag gag cct ggg ggt	1909	
Ala Ser Gly Ser Ala	Cys Ser Gly Leu Asn	Lys Gln Glu Pro Gly Gly		
556	561	566	571	
agc cat ggg tct gag	aca gaa gac aca ggg	aga agc ctt ccc agc aag	1957	
Ser His Gly Ser Glu	Thr Glu Asp Thr Gly	Arg Ser Leu Pro Ser Lys		
572	577	582	587	
aaa gaa cga tct ggg	aag tcc cac cgg cac	aaa aag aaa aag aag cac	2005	
Lys Glu Arg Ser Gly	Lys Ser His Arg His	Lys Lys Lys Lys Lys His		
588	593	598	603	
aaa aaa tcc agc aaa	cac aaa cgt aaa cac	aag gct gac aca gaa gag	2053	
Lys Lys Ser Ser Lys	His Lys Arg Lys His	Lys Ala Asp Thr Glu Glu		
604	609	614	619	
aaa agc tct aag gca	gag tca ggg gag aaa	tct aag aag cgc aag aaa	2101	
Lys Ser Ser Lys Ala	Glu Ser Gly Glu Lys	Ser Lys Lys Arg Lys Lys		
620	625	630	635	
cga aaa cga aag aag	aat aag tca tca gcc	cca gca gat tct gaa cga	2149	
Arg Lys Arg Lys Lys	Asn Lys Ser Ser Ala	Pro Ala Asp Ser Glu Arg		
636	641	646	651	
gga ccc aaa cca gaa	ccc cct ggg agt ggc	agt ccc gca cca cca aga	2197	
Gly Pro Lys Pro Glu	Pro Pro Gly Ser Gly	Ser Pro Ala Pro Pro Arg		
652	657	662	667	
aga agg cgg aga gct	caa gat gac tcc cag	cgg aga tcc ctc cca gct	2245	
Arg Arg Arg Arg Ala	Gln Asp Asp Ser Gln	Arg Arg Ser Leu Pro Ala		
668	673	678	683	

gaa gag ggg agc agt ggc aaa aag gat gaa ggt ggg ggt ggt agc agc	2293
Glu Glu Gly Ser Ser Gly Lys Lys Asp Glu Gly Gly Gly Gly Ser Ser	
684 689 694 699	
tcc caa gac cat ggt ggg agg aaa cac aaa ggt gaa ctt cca cct tca	2341
Ser Gln Asp His Gly Gly Arg Lys His Lys Gly Glu Leu Pro Pro Ser	
700 705 710 715	
tcc tgc cag cga aga gca ggc acc aaa cgg agc agc cgg tct agc cat	2389
Ser Cys Gln Arg Arg Ala Gly Thr Lys Arg Ser Ser Arg Ser Ser His	
716 721 726 731	
cgg agc caa ccc agt agt gga gat gag gat agt gat gat gct tcc tca	2437
Arg Ser Gln Pro Ser Ser Gly Asp Glu Asp Ser Asp Asp Ala Ser Ser	
732 737 742 747	
cac cgg ctg cac cag aag tct cca tcc cag tac agt gag gaa gaa gaa	2485
His Arg Leu His Gln Lys Ser Pro Ser Gln Tyr Ser Glu Glu Glu Glu	
748 753 758 763	
gag gaa gat tca ggc agt gag cat tcc cgc agc cgc tca agg tct ggc	2533
Glu Glu Asp Ser Gly Ser Glu His Ser Arg Ser Arg Ser Arg Ser Gly	
764 769 774 779	
cgg cgc cat tcc tcg cat cgt tcc tcc cgg cgt tct tac tca agt agc	2581
Arg Arg His Ser Ser His Arg Ser Ser Arg Arg Ser Tyr Ser Ser Ser	
780 785 790 795	
tca gat gcc tct tca gac cag agc tgc tat agt aga cag cgc agt tac	2629
Ser Asp Ala Ser Ser Asp Gln Ser Cys Tyr Ser Arg Gln Arg Ser Tyr	
796 801 806 811	
tct gat gac agc tac agt gac tac agt gac aga tca cga agg cac tcc	2677
Ser Asp Asp Ser Tyr Ser Asp Tyr Ser Asp Arg Ser Arg Arg His Ser	
812 817 822 827	
aag cgc tcc cat gac tca gat gac tca gac tat gcc agc tcc aaa cac	2725
Lys Arg Ser His Asp Ser Asp Asp Ser Asp Tyr Ala Ser Ser Lys His	
828 833 838 843	
cga tca aaa cgg cac aaa tat tca tct tct gat gat gac tat agc ctc	2773
Arg Ser Lys Arg His Lys Tyr Ser Ser Ser Asp Asp Asp Tyr Ser Leu	
844 849 854 859	
agt tgc agc cag tcc cga agc cga tct cgg agt cat acc aga gag cgc	2821
Ser Cys Ser Gln Ser Arg Ser Arg Ser Arg Ser His Thr Arg Glu Arg	
860 865 870 875	
tca aga tcc cgg ggc cgc agc cgc agc agc agt tgt agt cgt agt cga	2869
Ser Arg Ser Arg Gly Arg Ser Arg Ser Ser Ser Cys Ser Arg Ser Arg	
876 881 886 891	
agc aag cgg aga agc cgt agc acc aca gcc cac agc tgg caa cgg agc	2917
Ser Lys Arg Arg Ser Arg Ser Thr Thr Ala His Ser Trp Gln Arg Ser	
892 897 902 907	

cgg agc tat agc cgg gac cgc agc cgc agc acc agg agc cct tcc cag	2965
Arg Ser Tyr Ser Arg Asp Arg Ser Arg Ser Thr Arg Ser Pro Ser Gln	
908 913 918 923	
aga tca ggc tcc agg aag aga tca tgg ggt cac gag agc cct gag gag	3013
Arg Ser Gly Ser Arg Lys Arg Ser Trp Gly His Glu Ser Pro Glu Glu	
924 929 934 939	
agg cat tct ggg cgt cgg gac ttc att cgt tct aag atc tac cgc tcc	3061
Arg His Ser Gly Arg Arg Asp Phe Ile Arg Ser Lys Ile Tyr Arg Ser	
940 945 950 955	
cag tcc ccc cac tat ttc cga tca ggc cgg gga gaa ggt cct ggg aag	3109
Gln Ser Pro His Tyr Phe Arg Ser Gly Arg Gly Glu Gly Pro Gly Lys	
956 961 966 971	
aaa gat gat ggc aga gga gat gac agt aaa gca aca ggt cca cct tcc	3157
Lys Asp Asp Gly Arg Gly Asp Asp Ser Lys Ala Thr Gly Pro Pro Ser	
972 977 982 987	
cag aac agc aac att ggc aca gga aga ggg tca gaa ggt gac tgc agt	3205
Gln Asn Ser Asn Ile Gly Thr Gly Arg Gly Ser Glu Gly Asp Cys Ser	
988 993 998 1003	
cct gaa gac aag aac tct gtc act gcc aaa ctg cta ctg gag aag atc	3253
Pro Glu Asp Lys Asn Ser Val Thr Ala Lys Leu Leu Leu Glu Lys Ile	
1004 1009 1014 1019	
cag tca agg aaa gtg gag agg aaa cct agt gtg agt gag gag gtg cag	3301
Gln Ser Arg Lys Val Glu Arg Lys Pro Ser Val Ser Glu Glu Val Gln	
1020 1025 1030 1035	
gcc acc cct aat aaa gct ggg ccc aag ctc aag gac ccc cca caa ggt	3349
Ala Thr Pro Asn Lys Ala Gly Pro Lys Leu Lys Asp Pro Pro Gln Gly	
1036 1041 1046 1051	
tac ttt ggg ccc aag ctc ccc cca tct ctt ggc aat aag cct gtc ctt	3397
Tyr Phe Gly Pro Lys Leu Pro Pro Ser Leu Gly Asn Lys Pro Val Leu	
1052 1057 1062 1067	
cca ctg ata ggg aag ctc cca gct acg cga aag ccc aat aag aag tgt	3445
Pro Leu Ile Gly Lys Leu Pro Ala Thr Arg Lys Pro Asn Lys Lys Cys	
1068 1073 1078 1083	
gaa gag tct ggc ttg gaa agg ggg gaa gag caa gaa cag tca gag aca	3493
Glu Glu Ser Gly Leu Glu Arg Gly Glu Glu Gln Glu Gln Ser Glu Thr	
1084 1089 1094 1099	
gaa gag ggg ccc cca ggg agt agt gat gcc cta ttt ggg cat cag ttc	3541
Glu Glu Gly Pro Pro Gly Ser Ser Asp Ala Leu Phe Gly His Gln Phe	
1100 1105 1110 1115	
cct tca gag gaa aca act ggc ccc tta tta gac cca ccc cca gaa gag	3589
Pro Ser Glu Glu Thr Thr Gly Pro Leu Leu Asp Pro Pro Pro Glu Glu	
1116 1121 1126 1131	
tca aag tct gga gaa gct act gct gat cac cct gtg gct cca cta ggc	3637

1356	1361	1366	1371	
ggg ccc ttc acc ttt cac cct gtc cca cat gct gcc ctc tac ccc acc				4357
Gly Pro Phe Thr Phe His Pro Val Pro His Ala Ala Leu Tyr Pro Thr				
1372	1377	1382	1387	
cta ctt gct cca cgg cct gct gca gca gct gcc act gca ott cac ctt				4405
Leu Leu Ala Pro Arg Pro Ala Ala Ala Ala Thr Ala Leu His Leu				
1388	1393	1398	1403	
cac cca cta ctt cac ccc atc ttc tca ggt cag gac ctg caa cat ccc				4453
His Pro Leu Leu His Pro Ile Phe Ser Gly Gln Asp Leu Gln His Pro				
1404	1409	1414	1419	
ccc agc cat ggc acg tga gttggg ggatgggac ctaggtaggg ccaggggagg				4507
Pro Ser His Gly Thr *				
1420	1425			
agaccataa atgttccctt ggggggtgttg agccattaat accagcaagt agaagctggg				4567
atgggcagtg tctgacagcc aaagaattga gttttggctt gcaggggtgg gtttagattt				4627
gaagtttgct ttcagtttac tatcagggat ttctttttcc tgtcctctctc tcaatttgct				4687
cctccctctt ctgtgtttct aagctaggga acaccagtaa gtgctaccca cccctctgca				4747
gcaacatctc caaactgtca agtttagata atccctctct cctctgtctt ttttctctg				4807
ctcttccctt ctgtaaattt taaaacattt tcctccctc tggccagtgg gttgtcacca				4867
gagcacttgc tgtgggcca tctggtcttg ccttctcagc gccacaggga aggccaagct				4927
gttctagtgg tggaagtgcc accatttttg ggtagtatct ttgaccatct ttggtgacgt				4987
tacgttatcc caggtgaggt ggaaagcgtc tcacctggaa cctgatataa ctcaggctgc				5047
aattocatcc agttcccaca tcaacggagc cacacatttg gcactgttat cttggtatcc				5107
ctcatcccag aagaggcatc tccatatccc agaaaagaag atcctatcat gaataaaagc				5167
tgtatggccc agagaggagc tcatgtgtct aaagtgaagg gtatattttc ttctgttggtg				5227
ttgatgtttc cttcttaatt tataggattt ttttaatgta aaaaattgca ctgaactcta				5287
taaacgtaaa tgctgctttt tgtagctcat ataaaaaagg ttccatattt gtagtatact				5347
gcaataatat tttttacatc cagctcttta agtgatcctc gttctggtgg ctttgtgtaa				5407
atatgtttgc cctagttgaa ttaagaaact cttaaaggta taaatgaaa acaaaaaata				5467
aaatatttgt tttctgctag atgcaaaact gactaagcat gtatatttta ccaaacttat				5527
gtattttttg aagttatgaa ctataaaatg ttaaaacatt ttttgctggg acaaaatggt				5587
aagtaatttg cagtatgtag tgccccagc attgggattt ttgagctaat gggcagcagt				5647
cagctggggg cttctgaggg atgctcatct ttaacagtct ccctcatgta cttttgctgt				5707

ttacacaga gaaacaggta gacccacag aggagaagga ggggattcaa cagctttatt 5767
 gtctggaagc agtgagattt ggtgattgtc tggggggatt cctgggtttc cctgggtacc 5827
 ttgttccagg cagtcagtc atttgccttc ctagtactta gccccctctg acaatttttt 5887
 ttttaatgtg ctttttgggt tggtagaaac ggaagtagaa gtaggctgga ggatgagttg 5947
 ggacagtctt ctttttgttg ggaggtgagc acatttacag atattttgct tcatagtttc 6007
 catgcccctc gccagctca gtttagacag taaacgttcc ttgtttcttt tctcccatga 6067
 cactgacaag aggaattacc acctcagcct cttttgcccc tcttcttgcc tttcaccag 6127
 gctctcagcc ctaattaaca cactgacca aaggtgcttg tgttgaggt cccatctcct 6187
 ttgatgaggt taacaattcc cactttggca ttttcctaac tattcgtgtg gctagaattg 6247
 gttggttggc cacttgacaa gaaaaaccat acttacctgg gccaggctc tgttctgccc 6307
 ttgcgaaatt ctcaaaagag taaagtttat gaaaagaaag tggcaggcaa acacaactct 6367
 tgactgcctt cccaccctcc tacctgttca gtactcatct gattcagaag catcacttct 6427
 tggataacta gcactggaaa aatgaaatca tctgtgtaag tgaagggact catttttctt 6487
 tgctttcagc ccatgtaaat aaataatata gtattaacat tttcgtgctg cttcccatga 6547
 gcttgtagat tgagccatac tctggctgcc tctttgcctt cctaggggca ttttctttaa 6607
 cttccagaat agtgatttta aaagtaaaaa taaaaataaa ccttacttac aagcataaca 6667
 gattgtattt aactttatca catatgatag agatatatat gctgtaaaaat gagggaaagg 6727
 aactttctaa taaaccaatg atttgtggaa acttaaaaaa aaaaaaaaa 6775

<210> 290
 <211> 2523
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (81)..(2138)

<400> 290
 gtcttttttc ccgggtcgca cccacgcgtc cgccacgcg ttcgggaaaa taaagctttt 60
 tatattttgt tgggtgtggac atg gat aac cct att ggc aac tgg gat gga 110
 Met Asp Asn Pro Ile Gly Asn Trp Asp Gly
 / 1 5
 aga ttt gat gga gtg cag ctt tgt agt ttt gcg tgt gtt gaa agt aca 158

Arg	Phe	Asp	Gly	Val	Gln	Leu	Cys	Ser	Phe	Ala	Cys	Val	Glu	Ser	Thr	
11					16					21					26	
att	cta	ttg	cac	atc	aat	gat	atc	atc	cca	gag	agt	gtg	acg	cag	gaa	206
Ile	Leu	Leu	His	Ile	Asn	Asp	Ile	Ile	Pro	Glu	Ser	Val	Thr	Gln	Glu	
27					32					37					42	
agg	agg	cct	ccc	aaa	ctt	gcc	ttt	atg	tca	aga	ggg	gtt	ggg	gac	aaa	254
Arg	Arg	Pro	Pro	Lys	Leu	Ala	Phe	Met	Ser	Arg	Gly	Val	Gly	Asp	Lys	
43					48					53					58	
ggg	tca	tcc	agt	cat	aat	aaa	cca	aag	gct	aca	gga	tct	acc	tca	gac	302
Gly	Ser	Ser	Ser	His	Asn	Lys	Pro	Lys	Ala	Thr	Gly	Ser	Thr	Ser	Asp	
59					64					69					74	
cct	gga	aat	aga	aac	aga	tct	gaa	tta	ttt	tat	acc	tta	aat	ggg	tct	350
Pro	Gly	Asn	Arg	Asn	Arg	Ser	Glu	Leu	Phe	Tyr	Thr	Leu	Asn	Gly	Ser	
75					80					85					90	
tct	gtt	gac	tca	caa	cca	caa	tcc	aaa	tca	aaa	aat	aca	tgg	tac	att	398
Ser	Val	Asp	Ser	Gln	Pro	Gln	Ser	Lys	Ser	Lys	Asn	Thr	Trp	Tyr	Ile	
91					96					101					106	
gat	gaa	gtt	gca	gaa	gac	cct	gca	aaa	tct	ctt	aca	gag	ata	tct	aca	446
Asp	Glu	Val	Ala	Glu	Asp	Pro	Ala	Lys	Ser	Leu	Thr	Glu	Ile	Ser	Thr	
107					112					117					122	
gac	ttt	gac	cgt	tct	tca	cca	cca	ctc	cag	cct	cct	cct	gtg	aac	tca	494
Asp	Phe	Asp	Arg	Ser	Ser	Pro	Pro	Leu	Gln	Pro	Pro	Pro	Val	Asn	Ser	
123					128					133					138	
ctg	acc	acc	gag	aac	aga	ttc	cac	tct	tta	cca	ttc	agt	ctc	acc	aag	542
Leu	Thr	Thr	Glu	Asn	Arg	Phe	His	Ser	Leu	Pro	Phe	Ser	Leu	Thr	Lys	
139					144					149					154	
atg	ccc	aat	acc	aat	gga	agt	att	ggc	cac	agt	cca	ctt	tct	ctg	tca	590
Met	Pro	Asn	Thr	Asn	Gly	Ser	Ile	Gly	His	Ser	Pro	Leu	Ser	Leu	Ser	
155					160					165					170	
gcc	cag	tct	gta	atg	gaa	gag	cta	aac	act	gca	ccc	gtc	caa	gag	agt	638
Ala	Gln	Ser	Val	Met	Glu	Glu	Leu	Asn	Thr	Ala	Pro	Val	Gln	Glu	Ser	
171					176					181					186	
cca	ccc	ttg	gcc	atg	cct	cct	ggg	aac	tca	cat	ggg	cta	gaa	gtg	ggc	686
Pro	Pro	Leu	Ala	Met	Pro	Pro	Gly	Asn	Ser	His	Gly	Leu	Glu	Val	Gly	
187					192					197					202	
tca	ttg	gct	gaa	gtt	aag	gag	aac	cct	cct	ttc	tat	ggg	gta	atc	cgt	734
Ser	Leu	Ala	Glu	Val	Lys	Glu	Asn	Pro	Pro	Phe	Tyr	Gly	Val	Ile	Arg	
203					208					213					218	
tgg	atc	ggg	cag	cca	cca	gga	ctg	aat	gaa	gtg	ctc	gct	gga	ctg	gaa	782
Trp	Ile	Gly	Gln	Pro	Pro	Gly	Leu	Asn	Glu	Val	Leu	Ala	Gly	Leu	Glu	
219					224					229					234	
ctg	gaa	gat	gag	tgt	gca	ggc	tgt	acg	gat	gga	acc	ttc	aga	ggc	act	830
Leu	Glu	Asp	Glu	Cys	Ala	Gly	Cys	Thr	Asp	Gly	Thr	Phe	Arg	Gly	Thr	

235	240	245	250	
cgg tat ttc acc tgt gcc ctg aag aag gcg ctg ttt gtg aaa ctg aag				878
Arg Tyr Phe Thr Cys Ala Leu Lys Lys Ala Leu Phe Val Lys Leu Lys				
251	256	261	266	
agc tgc agg cct gac tct agg ttt gca tca ttg cag ccg gtt tcc aat				926
Ser Cys Arg Pro Asp Ser Arg Phe Ala Ser Leu Gln Pro Val Ser Asn				
267	272	277	282	
cag att gag cgc tgt aac tct tta gca ttt gga ggc tac tta agt gaa				974
Gln Ile Glu Arg Cys Asn Ser Leu Ala Phe Gly Gly Tyr Leu Ser Glu				
283	288	293	298	
gta gta gaa gaa aat act cca cca aaa atg gaa aaa gaa ggc ttg gag				1022
Val Val Glu Glu Asn Thr Pro Pro Lys Met Glu Lys Glu Gly Leu Glu				
299	304	309	314	
ata atg att ggg aag aag aaa ggc atc cag ggt cat tac aat tct tgt				1070
Ile Met Ile Gly Lys Lys Lys Gly Ile Gln Gly His Tyr Asn Ser Cys				
315	320	325	330	
tac tta gac tca acc tta ttc tgc tta ttt gct ttt agt tct gtt ctg				1118
Tyr Leu Asp Ser Thr Leu Phe Cys Leu Phe Ala Phe Ser Ser Val Leu				
331	336	341	346	
gac act gtg tta ctt aga ccc aaa gaa aag aac gat gta gaa tat tat				1166
Asp Thr Val Leu Leu Arg Pro Lys Glu Lys Asn Asp Val Glu Tyr Tyr				
347	352	357	362	
agt gaa acc caa gag cta ctg agg aca gaa att gtt aat cct ctg aga				1214
Ser Glu Thr Gln Glu Leu Leu Arg Thr Glu Ile Val Asn Pro Leu Arg				
363	368	373	378	
ata tat gga tat gtg tgt gcc aca aaa att atg aaa ctg agg aaa ata				1262
Ile Tyr Gly Tyr Val Cys Ala Thr Lys Ile Met Lys Leu Arg Lys Ile				
379	384	389	394	
ctt gaa aag gtg gag gct gca tca gga ttt acc tct gaa gaa aaa gat				1310
Leu Glu Lys Val Glu Ala Ala Ser Gly Phe Thr Ser Glu Glu Lys Asp				
395	400	405	410	
cct gag gaa ttc ttg aat att ctg ttt cat cat att tta agg gta gaa				1358
Pro Glu Glu Phe Leu Asn Ile Leu Phe His His Ile Leu Arg Val Glu				
411	416	421	426	
cct ttg cta aaa ata aga tca gca ggt caa aag gta caa gat tgt tac				1406
Pro Leu Leu Lys Ile Arg Ser Ala Gly Gln Lys Val Gln Asp Cys Tyr				
427	432	437	442	
ttc tat caa att ttt atg gaa aaa aat gag aaa gtt ggc gtt ccc aca				1454
Phe Tyr Gln Ile Phe Met Glu Lys Asn Glu Lys Val Gly Val Pro Thr				
443	448	453	458	
att cag cag ttg tta gaa tgg tct ttt atc aac agt aac ctg aaa ttt				1502
Ile Gln Gln Leu Leu Glu Trp Ser Phe Ile Asn Ser Asn Leu Lys Phe				
459	464	469	474	

aacgttgcat cttattcgag ctggcagttc tgttcacgtc cattgccggc aatggatgtc 2241
 tttgtggtga tgatccttca gaaaaggatg cctctgttta aaaacaaatt gcttttgtgt 2301
 ccctgaagta ttttaataaga agcattttgc actctagaaa gtatgtttgt gttggttttt 2361
 taagaagtct aaatgaagtt attaatacct gaagctttta gttaagtgca ttgatcatat 2421
 gatatttttg gaagcatata attttaattg tggaagttaa aagcctcttt tagtccattg 2481
 agaatgtaaa taaatgtgtc ttctttatgg aaaaaaaaaa aa 2523

<210> 291
 <211> 467
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (223)..(465)

<400> 291
 ctacgatcca cccgattcct cccctcattg atattcagga agcagctctc cttcccctgc 60
 cttcagctca agtttgctga gcttttgttt catttgtgaa tacttcttgc tggaagtccc 120
 tcacccagag accagtgtc ccaacggcag agcagcgggg gagataaaga actggtgaca 180
 cgtggctgta cattcagcac agctgtggtg tccccagtgc cc atg acc cag gag 234
 Met Thr Gln Glu
 1
 cca ttc aga gag gag ctg gcc tat gac cgg atg ccc acg ctg gag cgg 282
 Pro Phe Arg Glu Glu Leu Ala Tyr Asp Arg Met Pro Thr Leu Glu Arg
 5 10 15 20
 ggc cgg caa gac ccc gcc agc tat gcc cca gac gcg aag ccg agc gac 330
 Gly Arg Gln Asp Pro Ala Ser Tyr Ala Pro Asp Ala Lys Pro Ser Asp
 21 26 31 36
 ctg cag ctg tcg aag aga ctg ccc ccc tgc ttc agc cac aag acg tgg 378
 Leu Gln Leu Ser Lys Arg Leu Pro Pro Cys Phe Ser His Lys Thr Trp
 37 42 47 52
 gtc ttc tct gcg ctg atg gga acc tgc ctc ctg gag acc tcg ggg ttt 426
 Val Phe Ser Ala Leu Met Gly Thr Cys Leu Leu Glu Thr Ser Gly Phe
 53 58 63 68
 tct ctg aac ttg gaa acg tgt ccc ggt gtg aaa ggg taa tt 467
 Ser Leu Asn Leu Glu Thr Cys Pro Gly Val Lys Gly *
 69 74 79

<210> 292
 <211> 3570
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (162)..(2012)

<400> 292

```

gtcgactaca aggtggctac gagttttcca gatttaggag acttcagaaa ggtggggcag      60
atagaatgga gatggcaaag atctctttgg gcatatatgg gcctggcgaa gtaatggaat      120
aatttctaat ttctcgagaa ggcaagtgcc ctcatgccgg g      atg gca gaa gat      173
                                     Met Ala Glu Asp
                                     1

gag cct gat gct aag agc ccc aag act ggg gga agg gcc ccc cca ggt      221
Glu Pro Asp Ala Lys Ser Pro Lys Thr Gly Gly Arg Ala Pro Pro Gly
   5                      10                      15                      20

ggg gct gag gct ggg gaa cct acc acc ctt ctt cag agg ctc cga ggt      269
Gly Ala Glu Ala Gly Glu Pro Thr Thr Leu Leu Gln Arg Leu Arg Gly
  21                      26                      31                      36

acc att tcc aag gcc gtg cag aac aaa gta gag ggg atc ctg caa gat      317
Thr Ile Ser Lys Ala Val Gln Asn Lys Val Glu Gly Ile Leu Gln Asp
  37                      42                      47                      52

gta cag aaa ttt tct gac aat gac aag ctg tat ctc tac ctt cag ctc      365
Val Gln Lys Phe Ser Asp Asn Asp Lys Leu Tyr Leu Tyr Leu Gln Leu
  53                      58                      63                      68

ccc tca gga ccc acc act gga gac aaa agc tca gag cca agt aca ctg      413
Pro Ser Gly Pro Thr Thr Gly Asp Lys Ser Ser Glu Pro Ser Thr Leu
  69                      74                      79                      84

agc aat gag gag tac atg tat gcc tat agg tgg atc cgc aac cac ctg      461
Ser Asn Glu Glu Tyr Met Tyr Ala Tyr Arg Trp Ile Arg Asn His Leu
  85                      90                      95                      100

gaa gag cac act gac acc tgt ctg cca aag caa agt gtt tat gat gcc      509
Glu Glu His Thr Asp Thr Cys Leu Pro Lys Gln Ser Val Tyr Asp Ala
 101                      106                      111                      116

tat cgg aag tac tgt gag agt ctt gcc tgt tgc cgc cca ctc agc aca      557
Tyr Arg Lys Tyr Cys Glu Ser Leu Ala Cys Cys Arg Pro Leu Ser Thr
 117                      122                      127                      132

gcc aac ttt ggc aag atc atc aga gag atc ttc cct gac atc aaa gct      605
Ala Asn Phe Gly Lys Ile Ile Arg Glu Ile Phe Pro Asp Ile Lys Ala
 133                      138                      143                      148

cga agg ctt ggt ggc cgg ggc cag tcc aaa tat tgc tac agt ggc ata      653

```

Arg	Arg	Leu	Gly	Gly	Arg	Gly	Gln	Ser	Lys	Tyr	Cys	Tyr	Ser	Gly	Ile		
149					154					159					164		
agg	agg	aag	acc	ttg	gtg	tct	atg	cca	ccc	ctg	cct	gga	ctt	gac	cta	701	
Arg	Arg	Lys	Thr	Leu	Val	Ser	Met	Pro	Pro	Leu	Pro	Gly	Leu	Asp	Leu		
165					170					175					180		
aag	ggt	tct	gag	agt	cca	gaa	atg	ggc	cca	gaa	gta	acc	cca	gca	cct	749	
Lys	Gly	Ser	Glu	Ser	Pro	Glu	Met	Gly	Pro	Glu	Val	Thr	Pro	Ala	Pro		
181					186					191					196		
cga	gat	gaa	ctg	gtg	gag	gca	gcg	tgt	gcc	ctg	acc	tgt	gac	tggt	gca	797	
Arg	Asp	Glu	Leu	Val	Glu	Ala	Ala	Cys	Ala	Leu	Thr	Cys	Asp	Trp	Ala		
197					202					207					212		
gag	cgg	atc	ctg	aaa	cgg	tcc	ttc	agt	tcc	atc	gtt	gag	gtc	gcc	cgc	845	
Glu	Arg	Ile	Leu	Lys	Arg	Ser	Phe	Ser	Ser	Ile	Val	Glu	Val	Ala	Arg		
213					218					223					228		
ttc	ctg	cta	cag	cag	cat	ctc	atc	tct	gcc	cga	tct	gca	cat	gcc	cat	893	
Phe	Leu	Leu	Gln	Gln	His	Leu	Ile	Ser	Ala	Arg	Ser	Ala	His	Ala	His		
229					234					239					244		
gtg	ctt	aag	gcc	atg	ggg	ctt	gct	gaa	gag	gac	gaa	cat	gca	cct	cgg	941	
Val	Leu	Lys	Ala	Met	Gly	Leu	Ala	Glu	Glu	Asp	Glu	His	Ala	Pro	Arg		
245					250					255					260		
gaa	cgg	tca	tct	aaa	cca	aag	aat	ggt	tta	gag	aac	cca	gag	ggt	gga	989	
Glu	Arg	Ser	Ser	Lys	Pro	Lys	Asn	Gly	Leu	Glu	Asn	Pro	Glu	Gly	Gly		
261					266					271					276		
gcc	cac	aag	aag	cca	gag	aga	ctg	gcc	cag	cct	cct	aag	gat	ctg	gaa	1037	
Ala	His	Lys	Lys	Pro	Glu	Arg	Leu	Ala	Gln	Pro	Pro	Lys	Asp	Leu	Glu		
277					282					287					292		
gcc	cga	act	ggg	gcc	ggt	cct	ctc	gca	cgt	gga	gag	cgg	aag	aag	agt	1085	
Ala	Arg	Thr	Gly	Ala	Gly	Pro	Leu	Ala	Arg	Gly	Glu	Arg	Lys	Lys	Ser		
293					298					303					308		
gta	gtt	gag	agc	tcg	gcc	cca	gga	gcc	aat	aac	ctg	cag	gtt	aat	gcc	1133	
Val	Val	Glu	Ser	Ser	Ala	Pro	Gly	Ala	Asn	Asn	Leu	Gln	Val	Asn	Ala		
309					314					319					324		
cta	gtg	gct	cgg	ctg	cct	ctg	ctc	ctt	ccc	cgg	gcc	cct	cgc	tca	cta	1181	
Leu	Val	Ala	Arg	Leu	Pro	Leu	Leu	Leu	Pro	Arg	Ala	Pro	Arg	Ser	Leu		
325					330					335					340		
att	cgg	cca	atc	cca	gtc	tct	cca	cct	att	ctg	gcc	ccc	agg	ctt	tct	1229	
Ile	Pro	Pro	Ile	Pro	Val	Ser	Pro	Pro	Ile	Leu	Ala	Pro	Arg	Leu	Ser		
341					346					351					356		
tca	ggt	gcc	ctg	aaa	gtg	gct	aca	ctg	cct	ctg	tct	agt	agg	gcc	ggg	1277	
Ser	Gly	Ala	Leu	Lys	Val	Ala	Thr	Leu	Pro	Leu	Ser	Ser	Arg	Ala	Gly		
357					362					367					372		
gca	ccc	cca	gca	gct	gtg	ccc	atc	att	aac	atg	atc	tta	cca	act	gtt	1325	
Ala	Pro	Pro	Ala	Ala	Val	Pro	Ile	Ile	Asn	Met	Ile	Leu	Pro	Thr	Val		

373	378	383	388	
cct gct ttg cct gga cct gga cct ggg cct ggg cga gct cca cct ggg				1373
Pro Ala Leu Pro Gly Pro Gly Pro Gly Pro Gly Arg Ala Pro Pro Gly				
389	394	399	404	
gga ctc act cag ccc cgg ggc aca gag aac aga gag gta ggc ata ggt				1421
Gly Leu Thr Gln Pro Arg Gly Thr Glu Asn Arg Glu Val Gly Ile Gly				
405	410	415	420	
ggg gac caa gga cca cat gac aag ggt gtc aag agg aca gct gaa gta				1469
Gly Asp Gln Gly Pro His Asp Lys Gly Val Lys Arg Thr Ala Glu Val				
421	426	431	436	
cct gtg agt gag gcc agt ggg cag gct cca cca gct aaa gca gca aag				1517
Pro Val Ser Glu Ala Ser Gly Gln Ala Pro Pro Ala Lys Ala Ala Lys				
437	442	447	452	
cag gat ata gag gat aca gca agt gat gcc aaa agg aaa cgg ggg cgc				1565
Gln Asp Ile Glu Asp Thr Ala Ser Asp Ala Lys Arg Lys Arg Gly Arg				
453	458	463	468	
cct cga aaa aag tca ggt gga agt ggg gaa agg aat tct acc cct ctc				1613
Pro Arg Lys Lys Ser Gly Gly Ser Gly Glu Arg Asn Ser Thr Pro Leu				
469	474	479	484	
aag tca gca gct gcc atg gaa tct gcc cag tcc tca agg tta cca tgg				1661
Lys Ser Ala Ala Ala Met Glu Ser Ala Gln Ser Ser Arg Leu Pro Trp				
485	490	495	500	
gag aca tgg ggc tca gga ggg gaa ggc aac tca gct gga ggg gca gag				1709
Glu Thr Trp Gly Ser Gly Gly Glu Gly Asn Ser Ala Gly Gly Ala Glu				
501	506	511	516	
agg cca ggg cca atg gga gag gct gaa aag ggg gca gta ctt gcc cag				1757
Arg Pro Gly Pro Met Gly Glu Ala Glu Lys Gly Ala Val Leu Ala Gln				
517	522	527	532	
ggg cag gga gat ggt act gtt tcc aaa gga gga agg ggc ccc ggt tcc				1805
Gly Gln Gly Asp Gly Thr Val Ser Lys Gly Gly Arg Gly Pro Gly Ser				
533	538	543	548	
cag cat acc aaa gaa gca gaa gat aaa att ccc ttg gtc ccc tca aaa				1853
Gln His Thr Lys Glu Ala Glu Asp Lys Ile Pro Leu Val Pro Ser Lys				
549	554	559	564	
gtg agt gtc atc aag ggc agc aga agc caa aag gag gct ttt cct ttg				1901
Val Ser Val Ile Lys Gly Ser Arg Ser Gln Lys Glu Ala Phe Pro Leu				
565	570	575	580	
gca aag gga gag gta gac act gca cca cag ggt aat aaa gac tta aag				1949
Ala Lys Gly Glu Val Asp Thr Ala Pro Gln Gly Asn Lys Asp Leu Lys				
581	586	591	596	
gag cat gtg ctt caa agt tcc tta tcc cag gag cat aaa gac cca aaa				1997
Glu His Val Leu Gln Ser Ser Leu Ser Gln Glu His Lys Asp Pro Lys				
597	602	607	612	

gca aca ccc cca tga tacaggtctg tggggaagag tgtttatatc cctacgttaa 2052
 Ala Thr Pro Pro *
 613

ctttgcctag tagaggccct tctttgcact tgcttctcat ttggctattc ttttcctaag 2112
 gaagtccatt ctctctgtga cagacagctg agtcacccag tctacttagt acctgggtgc 2172
 tgcctctgac cttttcagct tgataccctg ggcttttagt taaccaataa atctgtagtg 2232
 accttacctg tattccctgt gctatcctgt gggaaggtag gaatgggcta agtatgatga 2292
 atgtataggt tagggatctt ttggttttta atcacagaaa acctaatcca aactggctta 2352
 aaataaaaag gattttattg ttcagtgaac tagaaagtcc ataggtagtg ctggctccag 2412
 gtgaagactt gaccagtag ttcagtatgt ctctaaatac cggactgact tttttctcac 2472
 tgttgcatct tctgtaggac catttaagtc tgggccactt aatggctgcc agcattccta 2532
 agattacact tttcccccatt tatgtccaat cagaaaaaga aggcatcttt gtaccagaaa 2592
 tctcagcaaa agccctaata ttcacactga ttaggcctgg gtcacatgtc caccctgacc 2652
 aatcactgtg gccaggagga tgatacatgc taatttgctt attctatatc atggacaaca 2712
 cctttgggga aaaggggtgg ggtcagcctc cccaaaatca catggattcc ccaagtggaa 2772
 actaggagca gggagttgct tgggtggccg ctaacaccag gctactctta ttttagcttg 2832
 ctaagttgag atcagctaga cctgctttct tttctcctca gtcttgcatc tccctcaata 2892
 caagctgtag cctctttcct cgtttctagt ctcagaagga aggagaggga agccattctc 2952
 ctctagggac tcttcagtct catttagatg atagtcctt tttttctacc tccatattag 3012
 agatggagct ccttcctttt cctgtttctt aatttttgtc ttctcattcc tgcttccctc 3072
 tcacctatt gccagttcca ccaactagag tgaaagactt cctagccatt tcattaaatc 3132
 tattctgtat ccaccaggtg gcagcatctt gtcatacgtg tcaggactta ggactgcggg 3192
 gtttaggtta gatgtcacgg aaaaagctag ttctgtggtc aggcggcacc aatgagaaag 3252
 gaatgcagac cctccagatg tatccttggg aaaagcagta aaccaactaa tatttattga 3312
 agacctactt tgtcctctac atagggtagc ttctgtcagg gaatcttggt tcttcccaag 3372
 aaacactgat tttctttcag ggagacttca tgtgttcatt tatttccacc acagcagatt 3432
 ttaagaaatt ataatatgta atatttgata tctataaaga gtatatctaa cgtgaataaa 3492
 ttatgaagca tactaatgag tacctatgac ccataacaca tatacatcaa aacattttta 3552
 ataccaaaaa aaaaaaaaaa 3570

<210> 293
 <211> 4503
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (233)..(2305)

<220>
 <221> misc_feature
 <222> (1)...(4503)
 <223> n = a,t,c or g

<400> 293

tccgggtcccc	ctccctcaga	cgcgctgctc	ctgctccaga	tgaggatgatg	gcaacgccaa	60
cttcggcaag	atccagatcg	ggatttacgt	ggagatcaag	cgcagtcggg	atagagtctt	120
attctgtctc	ccagactgga	gtgcaatggg	gtgatgtcgg	ttcactgcaa	cctctgcctc	180
ctggggtcaa	ctgatcctcc	ccgctcagcc	tcccaagtag	ctgggactac	ag atg	235
					Met	
					1	
cac acc aca	tcc ggc cga	ata cat caa	gca atg gta	aca tct tta	aat	283
His Thr Thr	Ser Gly Arg	Ile His Gln	Ala Met Val	Thr Ser Leu	Asn	
2	7		12		17	
gaa gat aat	gaa agt gta	act gtt gaa	tgg ata gaa	aat gga gat	aca	331
Glu Asp Asn	Glu Ser Val	Thr Val Glu	Trp Ile Glu	Asn Gly Asp	Thr	
18	23		28		33	
aaa ggc aaa	gag att gac	ctg gag agc	atc ttt tca	ctt aac cct	gac	379
Lys Gly Lys	Glu Ile Asp	Leu Glu Ser	Ile Phe Ser	Leu Asn Pro	Asp	
34	39		44		49	
ctt gtt cct	gat gaa gaa	att gaa ccc	agt cca gaa	aca cct cca	cct	427
Leu Val Pro	Asp Glu Glu	Ile Glu Pro	Ser Pro Glu	Thr Pro Pro	Pro	
50	55		60		65	
cca gca tcc	tca gcc aaa	gta aac aaa	att gta aag	aat cga cgg	act	475
Pro Ala Ser	Ser Ala Lys	Val Asn Lys	Ile Val Lys	Asn Arg Arg	Thr	
66	71		76		81	
gta gct tct	att aag aat	gac cct cct	tca aga gat	aat aga gtg	gtt	523
Val Ala Ser	Ile Lys Asn	Asp Pro Pro	Ser Arg Asp	Asn Arg Val	Val	
82	87		92		97	
ggg tca gca	cgt gca cgg	ccc agt caa	ttt cct gaa	cag tct tcc	tct	571
Gly Ser Ala	Arg Ala Arg	Pro Ser Gln	Phe Pro Glu	Gln Ser Ser	Ser	
98	103		108		113	
gca caa cag	aat ggt agt	gtt tca gat	ata tct cca	gtt caa gct	gca	619

Ala Gln Gln Asn Gly Ser Val Ser Asp Ile Ser Pro Val Gln Ala Ala	
114 119 124 129	
aaa aag gaa ttt gga ccc cct tca cgt aga aaa tct aat tgt gtg aaa	667
Lys Lys Glu Phe Gly Pro Pro Ser Arg Arg Lys Ser Asn Cys Val Lys	
130 135 140 145	
gaa gta gaa aaa ctg caa gaa aaa cga gag aaa agg aga ttg caa cag	715
Glu Val Glu Lys Leu Gln Glu Lys Arg Glu Lys Arg Arg Leu Gln Gln	
146 151 156 161	
caa gaa ctt aga gaa aaa aga gcc cag gac gtt gat gct aca aac cca	763
Gln Glu Leu Arg Glu Lys Arg Ala Gln Asp Val Asp Ala Thr Asn Pro	
162 167 172 177	
aat tat gaa att atg tgt atg atc aga gac ttt aga gga agt ttg gat	811
Asn Tyr Glu Ile Met Cys Met Ile Arg Asp Phe Arg Gly Ser Leu Asp	
178 183 188 193	
tat aga cca tta aca aca gca gat cct att gat gaa cat agg ata tgt	859
Tyr Arg Pro Leu Thr Thr Ala Asp Pro Ile Asp Glu His Arg Ile Cys	
194 199 204 209	
gtg tgt gta aga aaa cga cca ctc aat aaa aaa gaa act caa atg aaa	907
Val Cys Val Arg Lys Arg Pro Leu Asn Lys Lys Glu Thr Gln Met Lys	
210 215 220 225	
gat ctt gat gta atc aca att cct agt aaa gat gtt gtg atg gta cat	955
Asp Leu Asp Val Ile Thr Ile Pro Ser Lys Asp Val Val Met Val His	
226 231 236 241	
gaa cca aaa caa aaa gta gat tta aca agg tac cta gaa aac caa aca	1003
Glu Pro Lys Gln Lys Val Asp Leu Thr Arg Tyr Leu Glu Asn Gln Thr	
242 247 252 257	
ttt cgt ttt gat tat gcc ttt gat gac tca gct cct aat gaa atg gtt	1051
Phe Arg Phe Asp Tyr Ala Phe Asp Asp Ser Ala Pro Asn Glu Met Val	
258 263 268 273	
tac agg ttt act gct aga cca cta gtg gaa act ata ttt gaa agg gga	1099
Tyr Arg Phe Thr Ala Arg Pro Leu Val Glu Thr Ile Phe Glu Arg Gly	
274 279 284 289	
atg gct aca tgc ttt gct tat ggg cag act gga agt gga aaa act cat	1147
Met Ala Thr Cys Phe Ala Tyr Gly Gln Thr Gly Ser Gly Lys Thr His	
290 295 300 305	
act atg ggt ggt gac ttt tca gga aag aac caa gat tgt tct aaa gga	1195
Thr Met Gly Gly Asp Phe Ser Gly Lys Asn Gln Asp Cys Ser Lys Gly	
306 311 316 321	
att tat gca tta gca gct cga gat gtc ttt tta atg cta aag aag cca	1243
Ile Tyr Ala Leu Ala Ala Arg Asp Val Phe Leu Met Leu Lys Lys Pro	
322 327 332 337	
aac tat aag aag cta gaa ctt caa gta tat gca acc ttc ttt gaa att	1291
Asn Tyr Lys Lys Leu Glu Leu Gln Val Tyr Ala Thr Phe Phe Glu Ile	

338	343	348	353	
tat agt gga aag gtg	ttt gac ttg cta aac	agg aaa aca aaa tta	aga	1339
Tyr Ser Gly Lys Val	Phe Asp Leu Leu Asn	Arg Lys Thr Lys Leu	Arg	
354	359	364	369	
ggt cta gaa gat gga	aaa cag cag gtt caa	gtg gtg gga tta cag	gaa	1387
Val Leu Glu Asp Gly	Lys Gln Gln Val Gln	Val Val Gly Leu Gln	Glu	
370	375	380	385	
cgg gag gtc aaa tgt	gtt gaa gat gta ctg	aaa ctc att gac ata	ggc	1435
Arg Glu Val Lys Cys	Val Glu Asp Val Leu	Lys Leu Ile Asp Ile	Gly	
386	391	396	401	
aac agt tgc aga aca	tcc ggt caa aca tct	gca aat gca cat tca	tct	1483
Asn Ser Cys Arg Thr	Ser Gly Gln Thr Ser	Ala Asn Ala His Ser	Ser	
402	407	412	417	
cgg agc cat gca gtg	ttt cag att att ctt	aga agg aaa gga aaa	cta	1531
Arg Ser His Ala Val	Phe Gln Ile Ile Leu	Arg Arg Lys Gly Lys	Leu	
418	423	428	433	
cat ggc aaa ttt tct	ctc att gat ttg gct	gga aat gaa aga gga	gct	1579
His Gly Lys Phe Ser	Leu Ile Asp Leu Ala	Gly Asn Glu Arg Gly	Ala	
434	439	444	449	
gat act tcc agt gcg	gac agg caa act agg	ctt gaa ggt gct gaa	att	1627
Asp Thr Ser Ser Ala	Asp Arg Gln Thr Arg	Leu Glu Gly Ala Glu	Ile	
450	455	460	465	
aat aaa agc ctt tta	gca ctc aag gag tgc	atc aga gcc tta ggt	aga	1675
Asn Lys Ser Leu Leu	Ala Leu Lys Glu Cys	Ile Arg Ala Leu Gly	Arg	
466	471	476	481	
aat aaa cct cat act	cct ttc cgt gca agt	aaa ctc act cag gtg	tta	1723
Asn Lys Pro His Thr	Pro Phe Arg Ala Ser	Lys Leu Thr Gln Val	Leu	
482	487	492	497	
aga gat tct ttc ata	ggt gaa aac tct cgt	acc tgc atg att gcc	aca	1771
Arg Asp Ser Phe Ile	Gly Glu Asn Ser Arg	Thr Cys Met Ile Ala	Thr	
498	503	508	513	
atc tct cca gga atg	gca tcc tgt gaa aat	act ctt aat aca tta	aga	1819
Ile Ser Pro Gly Met	Ala Ser Cys Glu Asn	Thr Leu Asn Thr Leu	Arg	
514	519	524	529	
tat gca aat agg gtc	aaa gaa ttg act gta	gat cca act gct gct	ggt	1867
Tyr Ala Asn Arg Val	Lys Glu Leu Thr Val	Asp Pro Thr Ala Ala	Gly	
530	535	540	545	
gat gtt cgt cca ata	atg cac cat cca cca	aac cag att gat gac	tta	1915
Asp Val Arg Pro Ile	Met His His Pro Pro	Asn Gln Ile Asp Asp	Leu	
546	551	556	561	
gag aca cag tgg ggt	gtg ggg agt tcc cct	cag aga gat gat cta	aaa	1963
Glu Thr Gln Trp Gly	Val Gly Ser Ser Pro	Gln Arg Asp Asp Leu	Lys	
562	567	572	577	

ctt ctt tgt gaa caa aat gaa gaa gaa gtc tct cca cag ttg ttt act	2011
Leu Leu Cys Glu Gln Asn Glu Glu Glu Val Ser Pro Gln Leu Phe Thr	
578 583 588 593	
ttc cac gaa gct gtt tca caa atg gta gaa atg gaa gaa caa gtt gta	2059
Phe His Glu Ala Val Ser Gln Met Val Glu Met Glu Glu Gln Val Val	
594 599 604 609	
gaa gat cac agg gca gtg ttc cag gaa tct att cgg tgg tta gaa gat	2107
Glu Asp His Arg Ala Val Phe Gln Glu Ser Ile Arg Trp Leu Glu Asp	
610 615 620 625	
gaa aag gcc ctc tta gag atg act gaa gaa gta gat ¹ tat gat gtc gat	2155
Glu Lys Ala Leu Leu Glu Met Thr Glu Glu Val Asp Tyr Asp Val Asp	
626 631 636 641	
tca tat gct aca caa ctt gaa gct att ctt gag caa aaa ata gac att	2203
Ser Tyr Ala Thr Gln Leu Glu Ala Ile Leu Glu Gln Lys Ile Asp Ile	
642 647 652 657	
tta act gaa ctg cgg gat aaa gtg aaa tct ttc cgt gca gct cta caa	2251
Leu Thr Glu Leu Arg Asp Lys Val Lys Ser Phe Arg Ala Ala Leu Gln	
658 663 668 673	
gag gag gaa caa gcc agc aag caa atc aac ccg aag aga ccc cgt gcc	2299
Glu Glu Glu Gln Ala Ser Lys Gln Ile Asn Pro Lys Arg Pro Arg Ala	
674 679 684 689	
ctt taa accggcattt gctgctaaag gataccaga accctcacta ctgtaacata	2355
Leu *	
690	
caacggttca gctgtaaggg ccatttgaaa gtttgggaatt ttaagtgtct gtggaaaatg	2415
ttttgtcctt cacctgaatt acatttcaat tttgtgaaac actcttttgt ctacaaaatg	2475
cttctagtcc aggaggcaca accaagaact gggattaatg aagcattttg tttcatttac	2535
acaaatagtg atttactttt ggagatcctt gtcagtttta ttttctatth gatgaagtaa	2595
gactgtggac tcaatccaga gccagatagt agggggaagc cacagcattt ccttttaact	2655
cagttcaatt tttgtagtga gactgagcag ttttaaattcc tttgcgtgca tgcatacctc	2715
atcagtgatt gtacatacct tgcccactcc tagagacagc tgtgctcacc ttttctgtct	2775
ttgtgccttg attaaggcta ctgaccctaa atttctgaag cacagccaag aaaaattaca	2835
ttccttgtca ttgtaaatta cctttgtgtg tacattttta ctgtatttga gacatttttt	2895
gtgtgtgact agttaatttt gcaggatgtg ccatatcatt gaacggaact aaagtctgtg	2955
acagtggata tagctgctgg accattccat cttatatgta aagaaatctg gaattattat	3015
tttaaaacca tataacatgt gattataatt tttcttagca ttttctttgt aaagaactac	3075

aatataaaact agttggtgta taataaaaaag taatgaaatt ctgagaagag ttttatotta	3135
ggaaaataca tatatatgca gtgtgtgtgc cagtgtggta ttaacaagac taatagtgc	3195
gtttgatcct taccaatatc attacttaat ttgaagtgtt cattagcacc ccaaaatata	3255
ccttttctat gtactgttaa aagaaattgg cttctgatgc atgaacattt acatgtacat	3315
tgaaagtagt ccataataga agttagttta agccaagtgt agacagtaca ttactccott	3375
gaaaaagaat taagttgaaa gagttgactt tgccttaaaa ggcagatcta acccaagctc	3435
catccagtac caaatgtgaa acttcattgt tgtttggtga gaatcgcaa attctcacta	3495
atacattggt atggtgtagg gcatgctact ttttaaacag cagcacttat ttttacagat	3555
tgctactoca aggaagaaaa ctggccactt ttcatgtaaa tattttgttc aaagatttgt	3615
atatctctct aggagttttc cctcagttcc caggatgggg tccaggagta gattaacagc	3675
taaaaatctc ccaaggatat cttgttttga tttatttact ccagggaaact atcagctcct	3735
tcacaggagc caaaggggag ctatgaatag agggtcacat gagccagatt ctttactgtt	3795
cataaaaccc agagagtagt tgtgaaagat cctaatacaa ttgtgaaaag ctctgtaaac	3855
atgaaatcta aaacaaatgt agattttcac aatatgctta ttaataaatg aagtctatgg	3915
aataagtttt agagataatt tacttcagtc acctttgttt tggaaaggac tcaggttttc	3975
ttgcagctgt aagatatatt ctatttgtgt ttatttcaaa gggaagagga aggatggaca	4035
actgttaciaa ttgaccttgc aaaggatat taaaaaaaag gtagtttttg agattaacca	4095
actttcaaag ggcaataaag acatgtgaat ttgctcattt taaagcaca cagatgatta	4155
gcttcaaatt tattatttgc attggatggg tactgtcttt ggaaagtctc cttatagaca	4215
aatatgctgc cttacactat gatggcttca ttctgatcag gtattttaaa aattagtacc	4275
agaaaagata ctggaggtaa tataatacag tccttcagct ttacagatag tgaaaactga	4335
aggccagaaa aggaactaaa actcagcagt tcataggggt agaggggaaat aacctgagaa	4395
agccgagtta aatcttaaaa tttttactat aaggntagag atgatacaag tgaactctgc	4455
aaaatagttt tgtgaaatta aacaaaaaaa tctactctta atgtatat	4503

<210> 294
 <211> 4617
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> (233)..(2419)

<220>
 <221> misc_feature
 <222> (1)...(4617)
 <223> n = a,t,c or g

<400> 294

tccgggtcccc	ctccctcaga	cgcgctgctc	ctgctccaga	tgaggtgatg	gcaacgccaa	60
cttcgggaag	atccagatcg	ggatttacgt	ggagatcaag	cgcagtcggg	atagagtctt	120
attctgtctc	ccagactgga	gtgcaatggg	gtgatgtcgg	ttcactgcaa	cctctgcctc	180
ctgggctcaa	ctgatcctcc	ccgctcagcc	tccaagtag	ctgggactac	ag	235
					atg	
					Met	
					1	
cac acc aca tcc ggc cga ata cat caa gca atg gta aca tct tta aat	283					
His Thr Thr Ser Gly Arg Ile His Gln Ala Met Val Thr Ser Leu Asn						
2 7 12 17						
gaa gat aat gaa agt gta act gtt gaa tgg ata gaa aat gga gat aca	331					
Glu Asp Asn Glu Ser Val Thr Val Glu Trp Ile Glu Asn Gly Asp Thr						
18 23 28 33						
aaa ggc aaa gag att gac ctg gag agc atc ttt tca ctt aac cct gac	379					
Lys Gly Lys Glu Ile Asp Leu Glu Ser Ile Phe Ser Leu Asn Pro Asp						
34 39 44 49						
ctt gtt cct gat gaa gaa att gaa ccc agt cca gaa aca cct cca cct	427					
Leu Val Pro Asp Glu Glu Ile Glu Pro Ser Pro Glu Thr Pro Pro Pro						
50 55 60 65						
cca gca tcc tca gcc aaa gta aac aaa att gta aag aat cga cgg act	475					
Pro Ala Ser Ser Ala Lys Val Asn Lys Ile Val Lys Asn Arg Arg Thr						
66 71 76 81						
gta gct tct att aag aat gac cct cct tca aga gat aat aga gtg gtt	523					
Val Ala Ser Ile Lys Asn Asp Pro Pro Ser Arg Asp Asn Arg Val Val						
82 87 92 97						
ggg tca gca cgt gca cgg ccc agt caa ttt cct gaa cag tct tcc tct	571					
Gly Ser Ala Arg Ala Arg Pro Ser Gln Phe Pro Glu Gln Ser Ser Ser						
98 103 108 113						
gca caa cag aat ggt agt gtt tca gat ata tct cca gtt caa gct gca	619					
Ala Gln Gln Asn Gly Ser Val Ser Asp Ile Ser Pro Val Gln Ala Ala						
114 119 124 129						
aaa aag gaa ttt gga ccc cct tca cgt aga aaa tct aat tgt gtg aaa	667					
Lys Lys Glu Phe Gly Pro Pro Ser Arg Arg Lys Ser Asn Cys Val Lys						
130 135 140 145						
gaa gta gaa aaa ctg caa gaa aaa cga gag aaa agg aga ttg caa cag	715					
Glu Val Glu Lys Leu Gln Glu Lys Arg Glu Lys Arg Arg Leu Gln Gln						

146	151	156	161	
caa gaa ctt aga gaa	aaa aga gcc cag gac gtt gat gct aca aac cca			763
Gln Glu Leu Arg Glu	Lys Arg Ala Gln Asp Val Asp Ala Thr Asn Pro			
162	167	172	177	
aat tat gaa att atg	tgt atg atc aga gac ttt aga gga agt ttg gat			811
Asn Tyr Glu Ile Met	Cys Met Ile Arg Asp Phe Arg Gly Ser Leu Asp			
178	183	188	193	
tat aga cca tta aca	aca gca gat cct att gat gaa cat agg ata tgt			859
Tyr Arg Pro Leu Thr	Thr Ala Asp Pro Ile Asp Glu His Arg Ile Cys			
194	199	204	209	
gtg tgt gta aga aaa	cga cca ctc aat aaa gaa act caa atg aaa			907
Val Cys Val Arg Lys	Arg Pro Leu Asn Lys Lys Glu Thr Gln Met Lys			
210	215	220	225	
gat ctt gat gta atc	aca att cct agt aaa gat gtt gtg atg gta cat			955
Asp Leu Asp Val Ile	Thr Ile Pro Ser Lys Asp Val Val Met Val His			
226	231	236	241	
gaa cca aaa caa aaa	gta gat tta aca agg tac cta gaa aac caa aca			1003
Glu Pro Lys Gln Lys	Val Asp Leu Thr Arg Tyr Leu Glu Asn Gln Thr			
242	247	252	257	
ttt cgt ttt gat tat	gcc ttt gat gac tca gct cct aat gaa atg gtt			1051
Phe Arg Phe Asp Tyr	Ala Phe Asp Asp Ser Ala Pro Asn Glu Met Val			
258	263	268	273	
tac agg ttt act gct	aga cca cta gtg gaa act ata ttt gaa agg gga			1099
Tyr Arg Phe Thr Ala	Arg Pro Leu Val Glu Thr Ile Phe Glu Arg Gly			
274	279	284	289	
atg gct aca tgc ttt	gct tat ggg cag act gga agt gga aaa act cat			1147
Met Ala Thr Cys Phe	Ala Tyr Gly Gln Thr Gly Ser Gly Lys Thr His			
290	295	300	305	
act atg ggt ggt gac	ttt tca gga aag aac caa gat tgt tct aaa gga			1195
Thr Met Gly Gly Asp	Phe Ser Gly Lys Asn Gln Asp Cys Ser Lys Gly			
306	311	316	321	
att tat gca tta gca	gct cga gat gtc ttt tta atg cta aag aag cca			1243
Ile Tyr Ala Leu Ala	Ala Arg Asp Val Phe Leu Met Leu Lys Lys Pro			
322	327	332	337	
aac tat aag aag cta	gaa ctt caa gta tat gca acc ttc ttt gaa att			1291
Asn Tyr Lys Lys Leu	Glu Leu Gln Val Tyr Ala Thr Phe Phe Glu Ile			
338	343	348	353	
tat agt gga aag gtg	ttt gac ttg cta aac agg aaa aca aaa tta aga			1339
Tyr Ser Gly Lys Val	Phe Asp Leu Leu Asn Arg Lys Thr Lys Leu Arg			
354	359	364	369	
gtt cta gaa gat gga	aaa cag cag gtt caa gtg gtg gga tta cag gaa			1387
Val Leu Glu Asp Gly	Lys Gln Gln Val Gln Val Val Gly Leu Gln Glu			
370	375	380	385	

cgg gag gtc aaa tgt gtt gaa gat gta ctg aaa ctc att gac ata ggc	1435
Arg Glu Val Lys Cys Val Glu Asp Val Leu Lys Leu Ile Asp Ile Gly	
386 391 396 401	
aac agt tgc aga aca tcc ggt caa aca tct gca aat gca cat tca tct	1483
Asn Ser Cys Arg Thr Ser Gly Gln Thr Ser Ala Asn Ala His Ser Ser	
402 407 412 417	
cgg agc cat gca gtg ttt cag att att ctt aga agg aaa gga aaa cta	1531
Arg Ser His Ala Val Phe Gln Ile Ile Leu Arg Arg Lys Gly Lys Leu	
418 423 428 433	
cat ggc aaa ttt tct ctc att gat ttg gct gga aat gaa aga gga gct	1579
His Gly Lys Phe Ser Leu Ile Asp Leu Ala Gly Asn Glu Arg Gly Ala	
434 439 444 449	
gat act tcc agt gcg gac agg caa act agg ctt gaa ggt gct gaa att	1627
Asp Thr Ser Ser Ala Asp Arg Gln Thr Arg Leu Glu Gly Ala Glu Ile	
450 455 460 465	
aat aaa agc ctt tta gca ctc aag gag tgc atc aga gcc tta ggt aga	1675
Asn Lys Ser Leu Leu Ala Leu Lys Glu Cys Ile Arg Ala Leu Gly Arg	
466 471 476 481	
aat aaa cct cat act cct ttc cgt gca agt aaa ctc act cag gtg tta	1723
Asn Lys Pro His Thr Pro Phe Arg Ala Ser Lys Leu Thr Gln Val Leu	
482 487 492 497	
aga gat tct ttc ata ggt gaa aac tct cgt acc tgc atg att gcc aca	1771
Arg Asp Ser Phe Ile Gly Glu Asn Ser Arg Thr Cys Met Ile Ala Thr	
498 503 508 513	
atc tct cca gga atg gca tcc tgt gaa aat act ctt aat aca tta aga	1819
Ile Ser Pro Gly Met Ala Ser Cys Glu Asn Thr Leu Asn Thr Leu Arg	
514 519 524 529	
tat gca aat aga gta aag gag ttt gga att agt cca tca gac att ccc	1867
Tyr Ala Asn Arg Val Lys Glu Phe Gly Ile Ser Pro Ser Asp Ile Pro	
530 535 540 545	
ttc tca cag ggt agt ggc agt cgc cct gat ctc tct cct tct tat gaa	1915
Phe Ser Gln Gly Ser Gly Ser Arg Pro Asp Leu Ser Pro Ser Tyr Glu	
546 551 556 561	
tat gac gac ttt tct cct tca gtt acc agg gtc aaa gaa ttg act gta	1963
Tyr Asp Asp Phe Ser Pro Ser Val Thr Arg Val Lys Glu Leu Thr Val	
562 567 572 577	
gat cca act gct gct ggt gat gtt cgt cca ata atg cac cat cca cca	2011
Asp Pro Thr Ala Ala Gly Asp Val Arg Pro Ile Met His His Pro Pro	
578 583 588 593	
aac cag att gat gac tta gag aca cag tgg ggt gtc ggg agt tcc cct	2059
Asn Gln Ile Asp Asp Leu Glu Thr Gln Trp Gly Val Gly Ser Ser Pro	
594 599 604 609	

cag aga gat gat cta aaa ctt ctt tgt gaa caa aat gaa gaa gaa gtc	2107
Gln Arg Asp Asp Leu Lys Leu Leu Cys Glu Gln Asn Glu Glu Glu Val	
610 615 620 625	
tct cca cag ttg ttt act ttc cac gaa gct gtt tca caa atg gta gaa	2155
Ser Pro Gln Leu Phe Thr Phe His Glu Ala Val Ser Gln Met Val Glu	
626 631 636 641	
atg gaa gaa caa gtt gta gaa gat cac agg gca gtg ttc cag gaa tct	2203
Met Glu Glu Gln Val Val Glu Asp His Arg Ala Val Phe Gln Glu Ser	
642 647 652 657	
att cgg tgg tta gaa gat gaa aag gcc ctc tta gag atg act gaa gaa	2251
Ile Arg Trp Leu Glu Asp Glu Lys Ala Leu Leu Glu Met Thr Glu Glu	
658 663 668 673	
gta gat tat gat gtc gat tca tat gct aca caa ctt gaa gct att ctt	2299
Val Asp Tyr Asp Val Asp Ser Tyr Ala Thr Gln Leu Glu Ala Ile Leu	
674 679 684 689	
gag caa aaa ata gac att tta act gaa ctg cgg gat aaa gtg aaa tct	2347
Glu Gln Lys Ile Asp Ile Leu Thr Glu Leu Arg Asp Lys Val Lys Ser	
690 695 700 705	
ttc cgt gca gct cta caa gag gag gaa caa gcc agc aag caa atc aac	2395
Phe Arg Ala Ala Leu Gln Glu Glu Glu Gln Ala Ser Lys Gln Ile Asn	
706 711 716 721	
ccg aag aga ccc cgt gcc ctt taa accggcattt gctgctaaag gatacccaga	2449
Pro Lys Arg Pro Arg Ala Leu *	
722 727	
accctcacta ctgtaacata caacggttca gctgtaaggg ccatttgaaa gtttggaatt	2509
ttaagtgtct gtggaaaatg ttttgtcctt cacctgaatt acatttcaat tttgtgaaac	2569
actcttttgt ctacaaaatg cttctagtcc aggaggcaca accaagaact gggattaatg	2629
aagcattttg tttcatttac acaaatagtg atttactttt ggagatcctt gtcagtttta	2689
ttttctatct gatgaagtaa gactgtggac tcaatccaga gccagatagt agggggaagc	2749
cacagcattt ctttttaact cagttcaatt tttgtagtga gactgagcag ttttaaatec	2809
tttgcggtgca tgcatacctc atcagtgatt gtacatacct tgcccactcc tagagacagc	2869
tgtgctcacc ttttcctgct ttgtgccttg attaaggcta ctgaccctaa atttctgaag	2929
cacagccaag aaaaattaca ttcttgttca ttgtaaatta cttttgtgtg tacattttta	2989
ctgtatttga gacatttttt gtgtgtgact agttaatttt gcaggatgtg ccatatcatt	3049
gaacggaact aaagtctgtg acagtggata tagctgctgg accattccat cttatatgta	3109
aagaaatctg gaattattat tttaaaacca tataacatgt gattataatt tttcttagca	3169
ttttctttgt aaagaactac aatataaact agttggtgta taataaaaag taatgaaatt	3229

ctgagaagag ttttatctta ggaaaataca tatatatgca gtgtgtgtgc cagtgtggta 3289
 ttaacaagac taatagtgc gtttgatcct taccaatc attacttaatt ttgaagtgtt 3349
 cattagcacc ccaaaatata ccttttctat gtactgttaa aagaaattgg cttctgatgc 3409
 atgaacattt acatgtacat tgaaagtagt ccataataga agttagttta agccaagtgt 3469
 agacagtaca ttactccctt gaaaaagaat taagttgaaa gagttgactt tgccttaaaa 3529
 ggcagatcta acccaagctc catccagtac caaatgtgaa acttcattgt tgtttggtga 3589
 gaatcgccaa attctcacta atacattggg atgggtgtagg gcctgctact ttttaaacag 3649
 cagcacttat ttttacagat tgctactcca aggaagaaaa ctggccactt ttcattgtaa 3709
 tattttgttc aaagatttgt atatctctct aggagttttc cctcagttcc caggatgggg 3769
 tccaggagta gattaacagc taaaaatctc ccaaggatat cttgttttga tttatttact 3829
 ccagggaact atcagctcct tcacaggagc caaaggggag ctatgaatag agggtcacat 3889
 gagccagatt ctttactggt cataaaaacc agagagtagt tgtgaaagat cctaatacaa 3949
 ttgtgaaaag ctctgtaaac atgaaatcta aaacaaatgt agattttcac aatatgctta 4009
 ttaataaatg aagtctatgg aataagtttt agagataatt tacttcagtc acctttgttt 4069
 tggaaaggac tcaggttttc ttgcagctgt aagatatatt ctatttgtgt ttatttcaaa 4129
 ggaagagga aggatggaca actgttacia ttgacctgc aaaggatatt taaaaaaaaag 4189
 gtagtttttg agattaacca actttcaaag ggcaataaag acatgtgaat ttgctcattt 4249
 taaagcacia cagatgatta gcttcaaatt tattatttgc attggatggg tactgtcttt 4309
 ggaaagtctc cttatagaca aatatgctgc cttacactat gatggcttca ttctgatcag 4369
 gtattttaaa aattagtacc agaaaagata ctggaggtaa tataatacag tccttcagct 4429
 ttacagatag tgaaaactga aggccagaaa aggaactaaa actcagcagt tcataggggt 4489
 agaggggaaat aacctgagaa agccgagtta aatcttaaaa tttttactat aaggntagag 4549
 atgatacaag tgaactctgc aaaatagttt tgtgaaatta aacaaaaaaaa tctactctta 4609
 atgtatat 4617

<210> 295
 <211> 4215
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (92)..(3928)

<220>
 <221> misc_feature
 <222> (1)...(4215)
 <223> n = a,t,c or g

<400> 295

ggcagcagga aacctctagg tccaccacct ccattcttaca cgtgtttccg ttgtggtaaa 60

cctggacatt atattaagaa ttgcccaca a atg ggg ata aaa act ttg aat 112
 Met Gly Ile Lys Thr Leu Asn
 1 5

ctg gtc cta gga tta aaa aga gca ctg gaa ttc cca gaa gtt ttc atg 160
 Leu Val Leu Gly Leu Lys Arg Ala Leu Glu Phe Pro Glu Val Phe Met
 8 13 18 23

atg gaa gtg aaa gat cct aat atg aaa ggt gca atg ctt acc aac act 208
 Met Glu Val Lys Asp Pro Asn Met Lys Gly Ala Met Leu Thr Asn Thr
 24 29 34 39

gga aaa tat gca ata cca act ata gat gca gaa gca tat gca att ggg 256
 Gly Lys Tyr Ala Ile Pro Thr Ile Asp Ala Glu Ala Tyr Ala Ile Gly
 40 45 50 55

aag aaa gag aaa cct ccc ttc tta cca gag gag cca tct tct tcc tca 304
 Lys Lys Glu Lys Pro Pro Phe Leu Pro Glu Glu Pro Ser Ser Ser Ser
 56 61 66 71

gaa gaa gat gat cct atc cca gat gaa ttg ttg tgt ctc atc tgc aag 352
 Glu Glu Asp Asp Pro Ile Pro Asp Glu Leu Leu Cys Leu Ile Cys Lys
 72 77 82 87

gat att atg act gat gct gtt gtg att ccc tgc tgt gga aac agt tac 400
 Asp Ile Met Thr Asp Ala Val Val Ile Pro Cys Cys Gly Asn Ser Tyr
 88 93 98 103

tgt gat gaa tgt ata aga aca gca ctc ctg gaa tca gat gag cac aca 448
 Cys Asp Glu Cys Ile Arg Thr Ala Leu Leu Glu Ser Asp Glu His Thr
 104 109 114 119

tgt ccg acg tgt cat caa aat gat gtt tct cct gat gct tta att gcc 496
 Cys Pro Thr Cys His Gln Asn Asp Val Ser Pro Asp Ala Leu Ile Ala
 120 125 130 135

aat aaa ttt tta cga cag gct gta aat aac ttc aaa aat gaa act ggc 544
 Asn Lys Phe Leu Arg Gln Ala Val Asn Asn Phe Lys Asn Glu Thr Gly
 136 141 146 151

tat aca aaa aga cta cga aaa cag tta cct cct cca cca ccc cca ata 592
 Tyr Thr Lys Arg Leu Arg Lys Gln Leu Pro Pro Pro Pro Pro Ile
 152 157 162 167

cca cct ccg aga cca ctg att cag agg aac cta caa cct ctg atg aga 640

Pro	Pro	Pro	Arg	Pro	Leu	Ile	Gln	Arg	Asn	Leu	Gln	Pro	Leu	Met	Arg	
168					173					178					183	
tct	ccg	ata	tca	aga	caa	caa	gat	cct	ctt	atg	att	cca	gtg	aca	tct	688
Ser	Pro	Ile	Ser	Arg	Gln	Gln	Asp	Pro	Leu	Met	Ile	Pro	Val	Thr	Ser	
184					189					194					199	
tca	tca	act	cac	cca	gct	ccg	tct	ata	tct	tca	tta	act	tct	aat	cag	736
Ser	Ser	Thr	His	Pro	Ala	Pro	Ser	Ile	Ser	Ser	Leu	Thr	Ser	Asn	Gln	
200					205					210					215	
tct	tcc	ttg	gcc	cct	cct	gtg	tct	gga	aat	ccg	tct	tct	gct	cca	gct	784
Ser	Ser	Leu	Ala	Pro	Pro	Val	Ser	Gly	Asn	Pro	Ser	Ser	Ala	Pro	Ala	
216					221					226					231	
cct	gta	cct	gat	ata	act	gca	aca	gta	tcc	ata	tca	gtt	cat	tca	gaa	832
Pro	Val	Pro	Asp	Ile	Thr	Ala	Thr	Val	Ser	Ile	Ser	Val	His	Ser	Glu	
232					237					242					247	
aaa	tca	gat	gga	cct	ttt	cgg	gat	tct	gat	aat	aaa	ata	ttg	cca	gct	880
Lys	Ser	Asp	Gly	Pro	Phe	Arg	Asp	Ser	Asp	Asn	Lys	Ile	Leu	Pro	Ala	
248					253					258					263	
gca	gct	ctt	gca	tca	gag	cac	tca	aag	gga	acc	tcc	tca	att	gca	att	928
Ala	Ala	Leu	Ala	Ser	Glu	His	Ser	Lys	Gly	Thr	Ser	Ser	Ile	Ala	Ile	
264					269					274					279	
acc	gct	ctt	atg	gaa	gag	aag	ggg	tac	cag	gtg	cct	gtt	ctt	gga	acc	976
Thr	Ala	Leu	Met	Glu	Glu	Lys	Gly	Tyr	Gln	Val	Pro	Val	Leu	Gly	Thr	
280					285					290					295	
cca	tct	ttg	ctt	gga	cag	tca	tta	ttg	cat	gga	cag	ttg	atc	ccc	aca	1024
Pro	Ser	Leu	Leu	Gly	Gln	Ser	Leu	Leu	His	Gly	Gln	Leu	Ile	Pro	Thr	
296					301					306					311	
act	ggg	cca	gta	aga	ata	aat	act	gct	cgt	cca	ggg	ggg	ggg	cga	cca	1072
Thr	Gly	Pro	Val	Arg	Ile	Asn	Thr	Ala	Arg	Pro	Gly	Gly	Gly	Arg	Pro	
312					317					322					327	
ggc	tgg	gaa	cat	tcc	aac	aaa	ctt	ggc	tat	ctg	gtt	tct	cca	cca	caa	1120
Gly	Trp	Glu	His	Ser	Asn	Lys	Leu	Gly	Tyr	Leu	Val	Ser	Pro	Pro	Gln	
328					333					338					343	
caa	att	aga	aga	ggg	gag	agg	agc	tgc	tac	aga	agt	ata	aac	cgt	ggg	1168
Gln	Ile	Arg	Arg	Gly	Glu	Arg	Ser	Cys	Tyr	Arg	Ser	Ile	Asn	Arg	Gly	
344					349					354					359	
cga	cac	cac	agc	gaa	aga	tca	cag	agg	act	caa	ggc	ccg	tca	cta	cca	1216
Arg	His	His	Ser	Glu	Arg	Ser	Gln	Arg	Thr	Gln	Gly	Pro	Ser	Leu	Pro	
360					365					370					375	
gca	act	cca	gtc	ttt	gta	cct	gtt	cca	cca	cct	cct	ttg	tat	ccg	cct	1264
Ala	Thr	Pro	Val	Phe	Val	Pro	Val	Pro	Pro	Pro	Pro	Leu	Tyr	Pro	Pro	
376					381					386					391	
cct	ccc	cat	aca	ctt	cct	ctc	cct	ccg	ggg	gtt	cct	cct	cca	cag	ttt	1312
Pro	Pro	His	Thr	Leu	Pro	Leu	Pro	Pro	Gly	Val	Pro	Pro	Pro	Gln	Phe	

392	397	402	407	
tct cct cag ttt cct cct ggc cag cca gcc acc gct ggg tat agt gtc				1360
Ser Pro Gln Phe Pro Pro Gly Gln Pro Ala Thr Ala Gly Tyr Ser Val				
408	413	418	423	
cct cct cca ggg ttt cct cca gct cct gcc aat tta tca aca cct tgg				1408
Pro Pro Pro Gly Phe Pro Pro Ala Pro Ala Asn Leu Ser Thr Pro Trp				
424	429	434	439	
gta tca tca gga gtg cag aca gct cat tca aat acc atc cca aca aca				1456
Val Ser Ser Gly Val Gln Thr Ala His Ser Asn Thr Ile Pro Thr Thr				
440	445	450	455	
caa gca cca cct ttg tcc agg gaa gaa ttc tat aga gag cag cga cga				1504
Gln Ala Pro Pro Leu Ser Arg Glu Glu Phe Tyr Arg Glu Gln Arg Arg				
456	461	466	471	
cta aaa gaa gag gaa aag aaa aag tcc aag cta gat gag ttt aca aat				1552
Leu Lys Glu Glu Glu Lys Lys Lys Ser Lys Leu Asp Glu Phe Thr Asn				
472	477	482	487	
gat ttt gct aag gaa ttg atg gaa tac aaa aag att caa aag gag cgt				1600
Asp Phe Ala Lys Glu Leu Met Glu Tyr Lys Lys Ile Gln Lys Glu Arg				
488	493	498	503	
agg cgc tca ttt tcc agg tct aaa tct ccc tat agt ggt tct tcg tat				1648
Arg Arg Ser Phe Ser Arg Ser Lys Ser Pro Tyr Ser Gly Ser Ser Tyr				
504	509	514	519	
tca aga agt tca tat act tat tct aaa tca aga tct ggg tca aca cgt				1696
Ser Arg Ser Ser Tyr Thr Tyr Ser Lys Ser Arg Ser Gly Ser Thr Arg				
520	525	530	535	
tca cgc tct tat tct cga tca ttc agc cgc tca cat tct cgt tcc tat				1744
Ser Arg Ser Tyr Ser Arg Ser Phe Ser Arg Ser His Ser Arg Ser Tyr				
536	541	546	551	
tca cgg tca cct cca tac ccc aga aga ggc aga ggc aag agc cgc aat				1792
Ser Arg Ser Pro Pro Tyr Pro Arg Arg Gly Arg Gly Lys Ser Arg Asn				
552	557	562	567	
tac cgt tca cgg tct aga tct cat gga tat cat cga tct agg tca agg				1840
Tyr Arg Ser Arg Ser Arg Ser His Gly Tyr His Arg Ser Arg Ser Arg				
568	573	578	583	
tca ccc cct tac aga cgc tat cat tca cga tca aga tct cct caa gcg				1888
Ser Pro Pro Tyr Arg Arg Tyr His Ser Arg Ser Arg Ser Pro Gln Ala				
584	589	594	599	
ttt agg gga cag tct cct aat aaa cgt aat gta cct caa ggg gaa aca				1936
Phe Arg Gly Gln Ser Pro Asn Lys Arg Asn Val Pro Gln Gly Glu Thr				
600	605	610	615	
gaa cgt gaa tat ttt aat aga tac aga gaa gtt cca cca cca tat gac				1984
Glu Arg Glu Tyr Phe Asn Arg Tyr Arg Glu Val Pro Pro Pro Tyr Asp				
616	621	626	631	

atg aaa gca tat tat ggg aga agt gtt gac ttt aga gac cca ttt gaa	2032
Met Lys Ala Tyr Tyr Gly Arg Ser Val Asp Phe Arg Asp Pro Phe Glu	
632 637 642 647	
aaa gaa cgc tac cga gaa tgg gag aga aaa tat aga gag tgg tat gaa	2080
Lys Glu Arg Tyr Arg Glu Trp Glu Arg Lys Tyr Arg Glu Trp Tyr Glu	
648 653 658 663	
aaa tat tat aaa ggt tat gct gct gga gca cag cct aga ccc tca gca	2128
Lys Tyr Tyr Lys Gly Tyr Ala Ala Gly Ala Gln Pro Arg Pro Ser Ala	
664 669 674 679	
aat aga gag aac ttt tct cca gag aga ttt ttg cca ctt aac atc agg	2176
Asn Arg Glu Asn Phe Ser Pro Glu Arg Phe Leu Pro Leu Asn Ile Arg	
680 685 690 695	
aat tct ccc ttc aca aga ggc cgc aga gaa gac tat gtt ggt ggg caa	2224
Asn Ser Pro Phe Thr Arg Gly Arg Arg Glu Asp Tyr Val Gly Gly Gln	
696 701 706 711	
agt cat aga agt cga aac ata ggt agc aac tat cca gaa aag ctt tca	2272
Ser His Arg Ser Arg Asn Ile Gly Ser Asn Tyr Pro Glu Lys Leu Ser	
712 717 722 727	
gca aga gat ggt cac aat cag aag gat aat aca aag tca aaa gag aag	2320
Ala Arg Asp Gly His Asn Gln Lys Asp Asn Thr Lys Ser Lys Glu Lys	
728 733 738 743	
gag agt gaa aac gct cca gga gat ggt aaa gga aat aag cat aag aaa	2368
Glu Ser Glu Asn Ala Pro Gly Asp Gly Lys Gly Asn Lys His Lys Lys	
744 749 754 759	
cac aga tta aga aga aaa ggg gag gaa agt gag ggt ttt ctg aac cca	2416
His Arg Leu Arg Arg Lys Gly Glu Glu Ser Glu Gly Phe Leu Asn Pro	
760 765 770 775	
gag tta tta gag act tct agg aaa tca aga gaa cct aca ggt gtt gaa	2464
Glu Leu Leu Glu Thr Ser Arg Lys Ser Arg Glu Pro Thr Gly Val Glu	
776 781 786 791	
gaa aat aaa aca gac tca ttg ttt gtt ctc cca agt aga gat gat gcc	2512
Glu Asn Lys Thr Asp Ser Leu Phe Val Leu Pro Ser Arg Asp Asp Ala	
792 797 802 807	
aca cct gtt aga gat gaa cca atg gat gca gaa tca atc act ttt aaa	2560
Thr Pro Val Arg Asp Glu Pro Met Asp Ala Glu Ser Ile Thr Phe Lys	
808 813 818 823	
tca gtg tct gaa aaa gac aag aga gaa agg gat aaa cca aaa gca aag	2608
Ser Val Ser Glu Lys Asp Lys Arg Glu Arg Asp Lys Pro Lys Ala Lys	
824 829 834 839	
ggt gat aaa acc aaa cgg aag aat gat gga tct gct gtg tcc aaa aaa	2656
Gly Asp Lys Thr Lys Arg Lys Asn Asp Gly Ser Ala Val Ser Lys Lys	
840 845 850 855	

gaa aat att gta aaa cct gct aaa gga ccc caa gaa aaa gta gat gga Glu Asn Ile Val Lys Pro Ala Lys Gly Pro Gln Glu Lys Val Asp Gly 856 861 866 871	2704
gaa cgt gag aga tct cct cga tct gaa cct cca att aaa aaa gcc aaa Glu Arg Glu Arg Ser Pro Arg Ser Glu Pro Pro Ile Lys Lys Ala Lys 872 877 882 887	2752
gag gag act ccg aag act gac aat act aaa tca tca tct tcc tct cag Glu Glu Thr Pro Lys Thr Asp Asn Thr Lys Ser Ser Ser Ser Ser Gln 888 893 898 903	2800
aag gat gaa aaa atc act gga acc ccc aga aaa gct cac tct aaa tca Lys Asp Glu Lys Ile Thr Gly Thr Pro Arg Lys Ala His Ser Lys Ser 904 909 914 919	2848
gca aaa gaa cac caa gaa aca aaa cca gtc aaa gag gaa aaa gtg aag Ala Lys Glu His Gln Glu Thr Lys Pro Val Lys Glu Glu Lys Val Lys 920 925 930 935	2896
aag gac tat tcc aaa gat gtc aaa tca gaa aag cta aca act aag gaa Lys Asp Tyr Ser Lys Asp Val Lys Ser Glu Lys Leu Thr Thr Lys Glu 936 941 946 951	2944
gaa aag gcc aag aag cct aat gag aaa aac aaa cca ctt gat aat aag Glu Lys Ala Lys Lys Pro Asn Glu Lys Asn Lys Pro Leu Asp Asn Lys 952 957 962 967	2992
gga gaa aaa aga aaa aga aaa act gaa gaa aaa ggc gta gat aaa gat Gly Glu Lys Arg Lys Arg Lys Thr Glu Glu Lys Gly Val Asp Lys Asp 968 973 978 983	3040
ttt gag tct tct tca atg aaa atc tcg aaa cta gaa gtg act gaa ata Phe Glu Ser Ser Ser Met Lys Ile Ser Lys Leu Glu Val Thr Glu Ile 984 989 994 999	3088
gtg aaa cca tca cca aag cgc aaa atg gaa cct gat act gaa aaa atg Val Lys Pro Ser Pro Lys Arg Lys Met Glu Pro Asp Thr Glu Lys Met 1000 1005 1010 1015	3136
gat agg acc cct gaa aag gac aaa att tct tta agt gcg cca gcc aaa Asp Arg Thr Pro Glu Lys Asp Lys Ile Ser Leu Ser Ala Pro Ala Lys 1016 1021 1026 1031	3184
aaa atc aaa ctc aac aga gaa act ggg aag aaa att gga agt aca gaa Lys Ile Lys Leu Asn Arg Glu Thr Gly Lys Lys Ile Gly Ser Thr Glu 1032 1037 1042 1047	3232
aat ata tca aac aca aaa gaa ccc tct gaa aaa ttg gag tca aca tct Asn Ile Ser Asn Thr Lys Glu Pro Ser Glu Lys Leu Glu Ser Thr Ser 1048 1053 1058 1063	3280
agc aaa gtt aaa caa gaa aaa gtc aaa gga aag gtc aga cga aaa gtg Ser Lys Val Lys Gln Glu Lys Val Lys Gly Lys Val Arg Arg Lys Val 1064 1069 1074 1079	3328
act gga act gaa gga tcc agc tca act ctg gtg gat tac acc agt acg	3376

Thr Gly Thr Glu Gly Ser Ser Ser Thr Leu Val Asp Tyr Thr Ser Thr	
1080 1085 1090 1095	
agc tca act gga ggc agt cct gtg cgg aaa tct gaa gaa aaa aca gat	3424
Ser Ser Thr Gly Gly Ser Pro Val Arg Lys Ser Glu Glu Lys Thr Asp	
1096 1101 1106 1111	
aca aag cga act gtg att aaa acg atg gaa gaa tat aat aat gac aat	3472
Thr Lys Arg Thr Val Ile Lys Thr Met Glu Glu Tyr Asn Asn Asp Asn	
1112 1117 1122 1127	
acc gcg cca gct gaa gat gtt atc att atg att cag gtt cct caa tcc	3520
Thr Ala Pro Ala Glu Asp Val Ile Ile Met Ile Gln Val Pro Gln Ser	
1128 1133 1138 1143	
aaa tgg gat aaa gat gac ttt gaa tct gaa gaa gaa gat gtt aaa tcc	3568
Lys Trp Asp Lys Asp Asp Phe Glu Ser Glu Glu Glu Asp Val Lys Ser	
1144 1149 1154 1159	
aca cag cct ata tca agt gta gga aaa cct gct agt gtt ata aaa aat	3616
Thr Gln Pro Ile Ser Ser Val Gly Lys Pro Ala Ser Val Ile Lys Asn	
1160 1165 1170 1175	
gtt agt aca aag cca tca aat ata gtc aag tat cct gag aaa gaa agt	3664
Val Ser Thr Lys Pro Ser Asn Ile Val Lys Tyr Pro Glu Lys Glu Ser	
1176 1181 1186 1191	
gag cca tcc gag aaa att cag aaa ttc acc aag gac gtg agc cat gaa	3712
Glu Pro Ser Glu Lys Ile Gln Lys Phe Thr Lys Asp Val Ser His Glu	
1192 1197 1202 1207	
atc ata caa cat gag gtt aaa agt tca aaa aac tct gca tct agt gaa	3760
Ile Ile Gln His Glu Val Lys Ser Ser Lys Asn Ser Ala Ser Ser Glu	
1208 1213 1218 1223	
aaa ggg aaa acc aaa gat cga gat tat tca gtg ttg gaa aag gag aac	3808
Lys Gly Lys Thr Lys Asp Arg Asp Tyr Ser Val Leu Glu Lys Glu Asn	
1224 1229 1234 1239	
cct gaa aag agg aag aac agc act cag cca gag aaa gag agt aat ttg	3856
Pro Glu Lys Arg Lys Asn Ser Thr Gln Pro Glu Lys Glu Ser Asn Leu	
1240 1245 1250 1255	
gac cgt ctg aat gaa caa gga aat ttt aaa agt ctg tct caa tct tcc	3904
Asp Arg Leu Asn Glu Gln Gly Asn Phe Lys Ser Leu Ser Gln Ser Ser	
1256 1261 1266 1271	
aaa gag gct aga acc gtc aga taa acatgattcc actcgtgctt cctcaaataa	3958
Lys Glu Ala Arg Thr Val Arg *	
1272 1277	
agacttcact cccaatagag acaaaaaaac tgactatgac accagagagt attcaagttc	4018
caaacgtaga gatgaaaaga atgaattaac aagacgaaaa gactctccct tctcggaat	4078
aaagattctg gcattctggga ccaggaaaaa taaaccaag gggaagaaga gagatttgnc	4138

ctaaaaaagg gaccgggggn ttcccaaaaa aggtaattcc taggtcccc agggggccgg 4198
 aaacctcctt ggttccc 4215

<210> 296
 <211> 1522
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (374)..(1318)

<400> 296
 gcacgagggg cgcgagtga gcaaagcgag gacagacagc tcccagaggg cgaggggtgc 60
 gtgtgcgctc gcttctcacc tcaggtctcc ctccggcccc gctgccctcc ctccgaggctg 120
 ggtgacagct gggtcgggtc cgtcgcgggc tgcctggggg gcgaggatcg cgcaccccgct 180
 ctccgcgctc tgtgctgccc gccccgcccc ctccgccccg ccgtcccgctc gcgtcgcgtc 240
 ccgtcccgctc ggggtgctgcc agccgggtgc tgatgcgagt cgggtggcagc gaggacattt 300
 tctgactccc tggccctga cacggctgca cttccatcc cgtcgcgggg ccggccgcta 360
 ctccggcccc agg atg cag aat gtg att aat act gtg aag gga aag gca 409
 Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala
 1 5 10
 ctg gaa gtg gct gag tac ctg acc ccg gtc ctc aag gaa tca aag ttt 457
 Leu Glu Val Ala Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe
 13 18 23 28
 aag gaa aca ggt gta att acc cca gaa gag ttt gtg gca gct gga gat 505
 Lys Glu Thr Gly Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp
 29 34 39 44
 cac cta gtc cac cac tgt cca aca tgg caa tgg gct aca ggg gaa gaa 553
 His Leu Val His His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu
 45 50 55 60
 ttg aaa gtg aag gca tac cta cca aca ggc aaa caa ttt ttg gta acc 601
 Leu Lys Val Lys Ala Tyr Leu Pro Thr Gly Lys Gln Phe Leu Val Thr
 61 66 71 76
 aaa aat gtg ccg tgc tat aag cgg tgc aaa cag atg gaa tat tca gat 649
 Lys Asn Val Pro Cys Tyr Lys Arg Cys Lys Gln Met Glu Tyr Ser Asp
 77 82 87 92
 gaa ttg gaa gct atc att gaa gaa gat gat ggt gat ggc gga tgg gta 697
 Glu Leu Glu Ala Ile Ile Glu Glu Asp Asp Gly Asp Gly Gly Trp Val
 93 98 103 108

gat aca tat cac aac aca ggt att aca gga ata acg gaa gcc gtt aaa	745
Asp Thr Tyr His Asn Thr Gly Ile Thr Gly Ile Thr Glu Ala Val Lys	
109 114 119 124	
gag atc aca ctg gaa aat aag gac aat ata agg ctt caa gat tgc tca	793
Glu Ile Thr Leu Glu Asn Lys Asp Asn Ile Arg Leu Gln Asp Cys Ser	
125 130 135 140	
gca cta tgt gaa gag gaa gaa gat gaa gat gaa gga gaa gct gca gat	841
Ala Leu Cys Glu Glu Glu Glu Asp Glu Asp Glu Gly Glu Ala Ala Asp	
141 146 151 156	
atg gaa gaa tat gaa gag agt gga ttg ttg gaa aca gat gag gct acc	889
Met Glu Glu Tyr Glu Glu Ser Gly Leu Leu Glu Thr Asp Glu Ala Thr	
157 162 167 172	
cta gat aca agg aaa ata gta gaa gct tgt aaa gcc aaa act gat gct	937
Leu Asp Thr Arg Lys Ile Val Glu Ala Cys Lys Ala Lys Thr Asp Ala	
173 178 183 188	
ggc ggt gaa gat gct att ttg caa acc aga act tat gac ctt tac atc	985
Gly Gly Glu Asp Ala Ile Leu Gln Thr Arg Thr Tyr Asp Leu Tyr Ile	
189 194 199 204	
act tat gat aaa tat tac cag act cca cga tta tgg ttg ttt ggc tat	1033
Thr Tyr Asp Lys Tyr Tyr Gln Thr Pro Arg Leu Trp Leu Phe Gly Tyr	
205 210 215 220	
gat gag caa cgg cag cct tta aca gtt gag cac atg tat gaa gac atc	1081
Asp Glu Gln Arg Gln Pro Leu Thr Val Glu His Met Tyr Glu Asp Ile	
221 226 231 236	
agt cag gat cat gtg aag aaa aca gtg acc att gaa aat cac cct cat	1129
Ser Gln Asp His Val Lys Lys Thr Val Thr Ile Glu Asn His Pro His	
237 242 247 252	
ctg cca cca cct ccc atg tgt tca gtt cac cca tgc agg cat gct gag	1177
Leu Pro Pro Pro Pro Met Cys Ser Val His Pro Cys Arg His Ala Glu	
253 258 263 268	
gtg atg aag aaa atc att gag act gtt gca gaa gga ggg gga gaa ctt	1225
Val Met Lys Lys Ile Ile Glu Thr Val Ala Glu Gly Gly Gly Glu Leu	
269 274 279 284	
gga gtt cat atg tat ctt ctt att ttc ttg aaa ttt gta caa gct gtc	1273
Gly Val His Met Tyr Leu Leu Ile Phe Leu Lys Phe Val Gln Ala Val	
285 290 295 300	
att cca aca ata gaa tat gac tac aca aga cac ttc aca atg taa tga	1321
Ile Pro Thr Ile Glu Tyr Asp Tyr Thr Arg His Phe Thr Met *	
301 306 311	
agagagcata aaatctatcc taattattgg ttctgatttt taaagaatta acccatagat	1381
gtgaccattg accatattca tcaatatata cagtttctct aataaggac ttatatgttt	1441
atgcattaa taaaaatatg ttccactacc agccttactt gtttaataaa aatcagtgca	1501

aagagaaaaa aaaaaaaaaa a

1522

<210> 297
<211> 4394
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (316)..(3210)

<400> 297
cgctccgtaa tttccgggtc gacgatttcg tggcgcggtc gctggccggc ggctgagccg 60
ggagaaagga gctgcgggcca ccgttcgccc tactttctgcg cctcggggcg ggcgcgccgg 120
taaaaatggc gaaatggggg taggcggcgc tggacctgaa gagatggggc gcgaggtgg 180
ggcggttgct agagccccct gacgtgggcg ccgggctttt atcggcgatt tgatctggcg 240
acctcggggc ggcgctaag aggtcagact gcggagcctg cgggtcgcca gcggccccgc 300
cgagagccgg aggca atg gat gaa cag agc gtg gag agc att gct gag gtt 351
Met Asp Glu Gln Ser Val Glu Ser Ile Ala Glu Val
1 5 10
ttc cga tgt ttc att tgt atg gag aaa ttg cgg gat gca cgc ctg tgt 399
Phe Arg Cys Phe Ile Cys Met Glu Lys Leu Arg Asp Ala Arg Leu Cys
13 18 23 28
cct cat tgc tcc aaa ctg tgt tgt ttc agc tgt att agg cgc tgg ctg 447
Pro His Cys Ser Lys Leu Cys Cys Phe Ser Cys Ile Arg Arg Trp Leu
29 34 39 44
aca gag cag aga gct caa tgt cct cat tgc cgt gct cca ctc cag cta 495
Thr Glu Gln Arg Ala Gln Cys Pro His Cys Arg Ala Pro Leu Gln Leu
45 50 55 60
cga gaa cta gta aat tgt cgt tgg gca gaa gaa gta aca caa cag ctt 543
Arg Glu Leu Val Asn Cys Arg Trp Ala Glu Glu Val Thr Gln Gln Leu
61 66 71 76
gat act ctt caa ctc tgc agt ctc acc aaa cat gaa gaa aat gaa aag 591
Asp Thr Leu Gln Leu Cys Ser Leu Thr Lys His Glu Glu Asn Glu Lys
77 82 87 92
gac aaa tgt gaa aat cac cat gaa aaa ctt agt gta ttt tgc tgg act 639
Asp Lys Cys Glu Asn His His Glu Lys Leu Ser Val Phe Cys Trp Thr
93 98 103 108
tgt aag aag tgt atc tgc cat cag tgt gca ctt tgg gga gga atg cat 687
Cys Lys Lys Cys Ile Cys His Gln Cys Ala Leu Trp Gly Gly Met His
109 114 119 124

ggc gga cat acc ttt aaa cct ttg gca gaa att tat gag caa cac gtc	735
Gly Gly His Thr Phe Lys Pro Leu Ala Glu Ile Tyr Glu Gln His Val	
125 130 135 140	
act aaa gtg aat gaa gag gta gcc aaa ctt cgt cgg cgt ctc atg gaa	783
Thr Lys Val Asn Glu Glu Val Ala Lys Leu Arg Arg Arg Leu Met Glu	
141 146 151 156	
ctg atc agc tta gtt caa gaa gtg gaa agg aat gta gaa gct gta aga	831
Leu Ile Ser Leu Val Gln Glu Val Glu Arg Asn Val Glu Ala Val Arg	
157 162 167 172	
aat gca aaa gat gag cgt gtt cgg gaa att agg aat gca gtg gag atg	879
Asn Ala Lys Asp Glu Arg Val Arg Glu Ile Arg Asn Ala Val Glu Met	
173 178 183 188	
atg att gca cgg tta gac aca cag ctg aag aat aag ctt ata aca ctg	927
Met Ile Ala Arg Leu Asp Thr Gln Leu Lys Asn Lys Leu Ile Thr Leu	
189 194 199 204	
atg ggt cag aag aca tct cta acc caa gaa aca gag ctt ttg gaa tcc	975
Met Gly Gln Lys Thr Ser Leu Thr Gln Glu Thr Glu Leu Leu Glu Ser	
205 210 215 220	
tta ctt cag gag gtg gag cac cag ttg cgg tct tgt agt aag agt gag	1023
Leu Leu Gln Glu Val Glu His Gln Leu Arg Ser Cys Ser Lys Ser Glu	
221 226 231 236	
ttg ata tct aag agc tca gag atc ctt atg atg ttt cag caa gtt cat	1071
Leu Ile Ser Lys Ser Ser Glu Ile Leu Met Met Phe Gln Gln Val His	
237 242 247 252	
cgg aag ccc atg gca tct ttt gtt acc act cct gtt cca cca gac ttt	1119
Arg Lys Pro Met Ala Ser Phe Val Thr Thr Pro Val Pro Pro Asp Phe	
253 258 263 268	
acc agt gaa tta gtg cca tct tac gat tca gct act ttt gtt tta gag	1167
Thr Ser Glu Leu Val Pro Ser Tyr Asp Ser Ala Thr Phe Val Leu Glu	
269 274 279 284	
aat ttc agc act ttg cgt cag aga gca gat cct gtt tac agt cca cct	1215
Asn Phe Ser Thr Leu Arg Gln Arg Ala Asp Pro Val Tyr Ser Pro Pro	
285 290 295 300	
ctt caa gtt tca gga ctt tgc tgg agg tta aaa gtt tac cca gat gga	1263
Leu Gln Val Ser Gly Leu Cys Trp Arg Leu Lys Val Tyr Pro Asp Gly	
301 306 311 316	
aat gga gtt gtg cga ggt tac tac tta tct gtg ttt ctg gag ctc tca	1311
Asn Gly Val Val Arg Gly Tyr Tyr Leu Ser Val Phe Leu Glu Leu Ser	
317 322 327 332	
gct ggc ttg cct gaa act tct aaa tat gaa tat cgt gta gag atg gtt	1359
Ala Gly Leu Pro Glu Thr Ser Lys Tyr Glu Tyr Arg Val Glu Met Val	
333 338 343 348	

cac	cag	tcc	tgt	aat	gat	cct	aca	aaa	aat	atc	att	cga	gaa	ttt	gca	1407
His	Gln	Ser	Cys	Asn	Asp	Pro	Thr	Lys	Asn	Ile	Ile	Arg	Glu	Phe	Ala	
349					354					359					364	
tct	gac	ttt	gaa	gtt	gga	gaa	tgc	tgg	ggc	tat	aat	aga	ttt	ttc	cgt	1455
Ser	Asp	Phe	Glu	Val	Gly	Glu	Cys	Trp	Gly	Tyr	Asn	Arg	Phe	Phe	Arg	
365					370					375					380	
ttg	gac	tta	ctc	gca	aat	gaa	gga	tac	ttg	aat	cca	caa	aat	gat	aca	1503
Leu	Asp	Leu	Leu	Ala	Asn	Glu	Gly	Tyr	Leu	Asn	Pro	Gln	Asn	Asp	Thr	
381					386					391					396	
gtg	att	tta	agg	ttt	cag	gta	cgt	tca	cca	act	ttc	ttt	caa	aaa	tcc	1551
Val	Ile	Leu	Arg	Phe	Gln	Val	Arg	Ser	Pro	Thr	Phe	Phe	Gln	Lys	Ser	
397					402					407					412	
cgg	gac	cag	cat	tgg	tac	att	act	cag	ttg	gaa	gct	gca	cag	act	agt	1599
Arg	Asp	Gln	His	Trp	Tyr	Ile	Thr	Gln	Leu	Glu	Ala	Ala	Gln	Thr	Ser	
413					418					423					428	
tat	atc	caa	caa	ata	aac	aac	ctt	aaa	gag	aga	ctt	act	att	gag	ctg	1647
Tyr	Ile	Gln	Gln	Ile	Asn	Asn	Leu	Lys	Glu	Arg	Leu	Thr	Ile	Glu	Leu	
429					434					439					444	
tct	cga	act	cag	aag	tca	aga	gat	ttg	tca	cca	cca	gat	aac	cat	ctt	1695
Ser	Arg	Thr	Gln	Lys	Ser	Arg	Asp	Leu	Ser	Pro	Pro	Asp	Asn	His	Leu	
445					450					455					460	
agc	ccc	caa	aat	gat	gat	gct	ctg	gag	aca	cga	gct	aag	aag	tct	gca	1743
Ser	Pro	Gln	Asn	Asp	Asp	Ala	Leu	Glu	Thr	Arg	Ala	Lys	Lys	Ser	Ala	
461					466					471					476	
tgc	tct	gac	atg	ctt	ctc	gaa	ggg	ggg	cct	act	aca	gct	tct	gta	aga	1791
Cys	Ser	Asp	Met	Leu	Leu	Glu	Gly	Gly	Pro	Thr	Thr	Ala	Ser	Val	Arg	
477					482					487					492	
gag	gcc	aaa	gag	gat	gaa	gaa	gat	gag	gag	aag	att	cag	aat	gaa	gat	1839
Glu	Ala	Lys	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Lys	Ile	Gln	Asn	Glu	Asp	
493					498					503					508	
tat	cat	cac	gag	ctt	tca	gat	gga	gat	ctg	gat	ctg	gat	ctt	gtt	tat	1887
Tyr	His	His	Glu	Leu	Ser	Asp	Gly	Asp	Leu	Asp	Leu	Asp	Leu	Val	Tyr	
509					514					519					524	
gag	gat	gaa	gta	aat	cag	ctc	gat	ggc	agc	agt	tcc	tct	gct	agt	tcc	1935
Glu	Asp	Glu	Val	Asn	Gln	Leu	Asp	Gly	Ser	Ser	Ser	Ser	Ala	Ser	Ser	
525					530					535					540	
aca	gca	aca	agt	aat	aca	gaa	gaa	aat	gat	att	gat	gaa	gaa	act	atg	1983
Thr	Ala	Thr	Ser	Asn	Thr	Glu	Glu	Asn	Asp	Ile	Asp	Glu	Glu	Thr	Met	
541					546					551					556	
tct	gga	gaa	aat	gat	gtg	gaa	tat	aac	aac	atg	gaa	tta	gaa	gag	gga	2031
Ser	Gly	Glu	Asn	Asp	Val	Glu	Tyr	Asn	Asn	Met	Glu	Leu	Glu	Glu	Gly	
557					562					567					572	
gaa	ctc	atg	gaa	gat	gca	gct	gct	gca	gga	ccc	gca	ggg	agt	agc	cat	2079

Glu	Leu	Met	Glu	Asp	Ala	Ala	Ala	Ala	Gly	Pro	Ala	Gly	Ser	Ser	His	
573					578					583					588	
ggg	tat	gtg	ggg	tcc	agt	agt	aga	ata	tca	aga	aga	aca	cat	tta	tgc	2127
Gly	Tyr	Val	Gly	Ser	Ser	Ser	Arg	Ile	Ser	Arg	Arg	Thr	His	Leu	Cys	
589					594					599					604	
tcc	gct	gct	acc	agt	agt	tta	cta	gac	att	gat	cca	tta	att	tta	ata	2175
Ser	Ala	Ala	Thr	Ser	Ser	Leu	Leu	Asp	Ile	Asp	Pro	Leu	Ile	Leu	Ile	
605					610					615					620	
cat	ttg	ttg	gac	ctt	aag	gac	cgg	agc	agt	ata	gaa	aat	ttg	tgg	ggc	2223
His	Leu	Leu	Asp	Leu	Lys	Asp	Arg	Ser	Ser	Ile	Glu	Asn	Leu	Trp	Gly	
621					626					631					636	
tta	cag	cct	cgc	cca	cct	gct	tca	ctt	ctg	cag	ccc	aca	gca	tca	tat	2271
Leu	Gln	Pro	Arg	Pro	Pro	Ala	Ser	Leu	Leu	Gln	Pro	Thr	Ala	Ser	Tyr	
637					642					647					652	
tct	cga	aaa	gat	aaa	gac	caa	agg	aag	caa	cag	gca	atg	tgg	cga	gtg	2319
Ser	Arg	Lys	Asp	Lys	Asp	Gln	Arg	Lys	Gln	Gln	Ala	Met	Trp	Arg	Val	
653					658					663					668	
ccc	tct	gat	tta	aag	atg	cta	aaa	aga	ctc	aaa	act	caa	atg	gcc	gaa	2367
Pro	Ser	Asp	Leu	Lys	Met	Leu	Lys	Arg	Leu	Lys	Thr	Gln	Met	Ala	Glu	
669					674					679					684	
gtt	cga	tgt	atg	aaa	act	gat	gta	aag	aat	aca	ctt	tca	gaa	ata	aaa	2415
Val	Arg	Cys	Met	Lys	Thr	Asp	Val	Lys	Asn	Thr	Leu	Ser	Glu	Ile	Lys	
685					690					695					700	
agc	agc	agt	gct	gct	tct	gga	gac	atg	cag	aca	agc	ctt	ttt	tct	gct	2463
Ser	Ser	Ser	Ala	Ala	Ser	Gly	Asp	Met	Gln	Thr	Ser	Leu	Phe	Ser	Ala	
701					706					711					716	
gac	cag	gca	gct	ctg	gct	gca	tgt	gga	act	gaa	aac	tct	ggc	aga	ttg	2511
Asp	Gln	Ala	Ala	Leu	Ala	Ala	Cys	Gly	Thr	Glu	Asn	Ser	Gly	Arg	Leu	
717					722					727					732	
cag	gat	ttg	gga	atg	gaa	ctc	ctg	gca	aag	tca	tca	gtt	gcc	aat	tgt	2559
Gln	Asp	Leu	Gly	Met	Glu	Leu	Leu	Ala	Lys	Ser	Ser	Val	Ala	Asn	Cys	
733					738					743					748	
tac	ata	cga	aac	tcc	aca	aat	aag	aag	agt	aat	tcg	ccc	aag	cca	gct	2607
Tyr	Ile	Arg	Asn	Ser	Thr	Asn	Lys	Lys	Ser	Asn	Ser	Pro	Lys	Pro	Ala	
749					754					759					764	
cga	tcc	agt	gta	gca	ggg	agt	cta	tca	ctt	cga	aga	gca	gtg	gac	cct	2655
Arg	Ser	Ser	Val	Ala	Gly	Ser	Leu	Ser	Leu	Arg	Arg	Ala	Val	Asp	Pro	
765					770					775					780	
gga	gaa	aat	agt	cgt	tca	aag	gga	gac	tgt	cag	act	ctg	tct	gaa	ggc	2703
Gly	Glu	Asn	Ser	Arg	Ser	Lys	Gly	Asp	Cys	Gln	Thr	Leu	Ser	Glu	Gly	
781					786					791					796	
tcc	cca	gga	agc	tct	cag	tct	ggg	agc	agg	cac	agt	tct	ccc	cga	gcc	2751
Ser	Pro	Gly	Ser	Ser	Gln	Ser	Gly	Ser	Arg	His	Ser	Ser	Pro	Arg	Ala	

797	802	807	812	
ttg ata cat ggc agt atc ggt gat att ctg cca aaa act gaa gac cgg				2799
Leu Ile His Gly Ser Ile Gly Asp Ile Leu Pro Lys Thr Glu Asp Arg				
813	818	823	828	
cag tgt aaa gct ttg gat tca gat gct gtt gtg gtt gca gtt ttc agt				2847
Gln Cys Lys Ala Leu Asp Ser Asp Ala Val Val Val Ala Val Phe Ser				
829	834	839	844	
ggc ttg cct gcg gtt gag aaa agg agg aaa atg gtc acc ttg ggg gct				2895
Gly Leu Pro Ala Val Glu Lys Arg Arg Lys Met Val Thr Leu Gly Ala				
845	850	855	860	
aat gct aaa gga ggt cat ctg gaa gga ctg cag atg act gat ttg gaa				2943
Asn Ala Lys Gly Gly His Leu Glu Gly Leu Gln Met Thr Asp Leu Glu				
861	866	871	876	
aat aat tct gaa act gga gag tta cag cct gta cta cct gaa gga gct				2991
Asn Asn Ser Glu Thr Gly Glu Leu Gln Pro Val Leu Pro Glu Gly Ala				
877	882	887	892	
tca gct gcc cct gaa gaa gga atg agt agc gac agt gac att gaa tgt				3039
Ser Ala Ala Pro Glu Glu Gly Met Ser Ser Asp Ser Asp Ile Glu Cys				
893	898	903	908	
gac act gag aat gag gag cag gaa gag cat acc agt gtg ggc ggg ttt				3087
Asp Thr Glu Asn Glu Glu Gln Glu Glu His Thr Ser Val Gly Gly Phe				
909	914	919	924	
cac gac tcc ttc atg gtc atg aca cag ccc ccg gat gaa gat aca cat				3135
His Asp Ser Phe Met Val Met Thr Gln Pro Pro Asp Glu Asp Thr His				
925	930	935	940	
tcc agt ttt cct gat ggt gaa caa ata ggc cct gaa gat ctc agc ttc				3183
Ser Ser Phe Pro Asp Gly Glu Gln Ile Gly Pro Glu Asp Leu Ser Phe				
941	946	951	956	
aat aca gat gaa aat agt gga agg taa ttgcc aaatcaagag aactgacttg				3235
Asn Thr Asp Glu Asn Ser Gly Arg *				
957	962			
caagctacct tgacctgaa ttttgctgta gttggtgctc aaatttgtca tcagtcagat				3295
aatcagat ttt ggtcttattt cttcattatc togacctgaa atagtaattt ggaaactgtt				3355
ggaaggtggc acagtttagt ctaagacagc agtagtacat gggaaaaaca gtatgggaag				3415
agttctttgt aatgtaagga aataacaatg tagttctcta ttaatttagc aaatttgtac				3475
attcacaaaa ggcagtttgt ctactacagc agaaggctgg ttaactgcc aaaaatgtac				3535
ctccaggccc tgcattgccg cagtaacccg cccggcattg gtgctctact gtctttggct				3595
agagcttagt tgtgtttaaa taatcatctt tatatttggg gttttaatta cagttccatt				3655
agtgcctgta gattagttaa cagaaaattg ctttgaaga gattctgccc ttagacact				3715

atgtgaataa ctgaagtaac actagactga atctcctttt tggagtatgt atcttctctc 3775
 acttgttcaa gtacaggcac actgttcaac cgcattggtat ctttctgttg tgtgacttct 3835
 acaaagttaa ttttaaatga aattaagtta acatggattc attacgttcc tggccctgta 3895
 gacacgtgta agattattta aaattctttc atttttttct gcctcttact atacgactgt 3955
 agtgcaacaa atattttaaa gccccctttt cttcttttatt ttcattagtt gtacattgat 4015
 ttcagtgtca acacatttaa agattcattc atgttgacaca gtgggttaca tgaacgtgaa 4075
 actgtgatat aagggttttct ttcataactca taattagccc aaaacagttg ccaaactttg 4135
 ccattgtgct cctgcatttg tgtttgagct gctatatatt tgtggaaatt aactgaaag 4195
 ttgactaaga gactattgaa aaagcatgaa taattaaata tacatgtgag agacatctca 4255
 tctgctgtat tttacttagt gaatattggt cactcttcog tgtctgatgt cttgctgaat 4315
 gctgtgactc atagtttact tttgttcaaa atagtttgca ctttttgta ataaaatcaa 4375
 cttgagaaaa aaaaaaaaaa 4394

<210> 298
 <211> 4798
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (326) .. (2320)

<400> 298
 acactaggag gatcatgtat ataactatct attcgatgat gaagataccc caccaaacc 60
 aaaaaaagag atctctcgag gatccgaatt cgcggccgcg tcgacctgac ttagaacaac 120
 ttttttgact tctgcaggg aggaccctta cagtattttt ggagaagtta gtaaaaccga 180
 atctgacatc atcacctagc agttcatgca gctagcaagt ggtttgttct tagggtaaca 240
 gaggaggaaa ttgttcctcg tctgataaga caacagtgga gaaaggacgc atgctgtttc 300
 ttagggacac ggctgacttc cagat atg acc atg tat ttg tgg ctt aaa ctc 352
 Met Thr Met Tyr Leu Trp Leu Lys Leu
 1 5
 ttg gca ttt ggc ttt gcc ttt ctg gac aca gaa gta ttt gtg aca ggg 400
 Leu Ala Phe Gly Phe Ala Phe Leu Asp Thr Glu Val Phe Val Thr Gly
 10 15 / 20 25
 caa agc cca aca cct tcc ccc act gat gcc tac ctt aat gcc tct gaa 448

Gln	Ser	Pro	Thr	Pro	Ser	Pro	Thr	Asp	Ala	Tyr	Leu	Asn	Ala	Ser	Glu	
26					31					36					41	
aca	acc	act	ctg	agc	cct	tct	gga	agc	gct	gtc	att	tca	acc	aca	aca	496
Thr	Thr	Thr	Leu	Ser	Pro	Ser	Gly	Ser	Ala	Val	Ile	Ser	Thr	Thr	Thr	
42					47					52					57	
ata	gct	act	act	cca	tct	aag	cca	aca	tgt	gat	gaa	aaa	tat	gca	aac	544
Ile	Ala	Thr	Thr	Pro	Ser	Lys	Pro	Thr	Cys	Asp	Glu	Lys	Tyr	Ala	Asn	
58					63					68					73	
atc	act	gtg	gat	tac	tta	tat	aac	aag	gaa	act	aaa	tta	ttt	aca	gca	592
Ile	Thr	Val	Asp	Tyr	Leu	Tyr	Asn	Lys	Glu	Thr	Lys	Leu	Phe	Thr	Ala	
74					79					84					89	
aag	cta	aat	gtt	aat	gag	aat	gtg	gaa	tgt	gga	aac	aat	act	tgc	aca	640
Lys	Leu	Asn	Val	Asn	Glu	Asn	Val	Glu	Cys	Gly	Asn	Asn	Thr	Cys	Thr	
90					95					100					105	
aac	aat	gag	gtg	cat	aac	ctt	aca	gaa	tgt	aaa	aat	gcg	tct	gtt	tcc	688
Asn	Asn	Glu	Val	His	Asn	Leu	Thr	Glu	Cys	Lys	Asn	Ala	Ser	Val	Ser	
106					111					116					121	
ata	tct	cat	aat	tca	tgt	act	gct	cct	gat	aag	aca	tta	ata	tta	gat	736
Ile	Ser	His	Asn	Ser	Cys	Thr	Ala	Pro	Asp	Lys	Thr	Leu	Ile	Leu	Asp	
122					127					132					137	
gtg	cca	cca	ggg	gtt	gaa	aag	ttt	cag	tta	cat	gat	tgt	aca	caa	gtt	784
Val	Pro	Pro	Gly	Val	Glu	Lys	Phe	Gln	Leu	His	Asp	Cys	Thr	Gln	Val	
138					143					148					153	
gaa	aaa	gca	gat	act	act	att	tgt	tta	aaa	tgg	aaa	aat	att	gaa	acc	832
Glu	Lys	Ala	Asp	Thr	Thr	Ile	Cys	Leu	Lys	Trp	Lys	Asn	Ile	Glu	Thr	
154					159					164					169	
ttt	act	tgt	gat	aca	cag	aat	att	acc	tac	aga	ttt	cag	tgt	ggt	aat	880
Phe	Thr	Cys	Asp	Thr	Gln	Asn	Ile	Thr	Tyr	Arg	Phe	Gln	Cys	Gly	Asn	
170					175					180					185	
atg	ata	ttt	gat	aat	aaa	gaa	att	aaa	tta	gaa	aac	ctt	gaa	ccc	gaa	928
Met	Ile	Phe	Asp	Asn	Lys	Glu	Ile	Lys	Leu	Glu	Asn	Leu	Glu	Pro	Glu	
186					191					196					201	
cat	gag	tat	aag	tgt	gac	tca	gaa	ata	ctc	tat	aat	aac	cac	aag	ttt	976
His	Glu	Tyr	Lys	Cys	Asp	Ser	Glu	Ile	Leu	Tyr	Asn	Asn	His	Lys	Phe	
202					207					212					217	
act	aac	gca	agt	aaa	att	att	aaa	aca	gat	ttt	ggg	agt	cca	gga	gag	1024
Thr	Asn	Ala	Ser	Lys	Ile	Ile	Lys	Thr	Asp	Phe	Gly	Ser	Pro	Gly	Glu	
218					223					228					233	
cct	cag	att	att	ttt	tgt	aga	agt	gaa	gct	gca	cat	caa	gga	gta	att	1072
Pro	Gln	Ile	Ile	Phe	Cys	Arg	Ser	Glu	Ala	Ala	His	Gln	Gly	Val	Ile	
234					239					244					249	
acc	tgg	aat	ccc	cct	caa	aga	tca	ttt	cat	aat	ttt	acc	ctc	tgt	tat	1120
Thr	Trp	Asn	Pro	Pro	Gln	Arg	Ser	Phe	His	Asn	Phe	Thr	Leu	Cys	Tyr	

250	255	260	265
ata aaa gag aca gaa aaa gat tgc ctc aat ctg gat aaa aac ctg atc Ile Lys Glu Thr Glu Lys Asp Cys Leu Asn Leu Asp Lys Asn Leu Ile 266 271 276 281			1168
aaa tat gat ttg caa aat tta aaa cct tat acg aaa tat gtt tta tca Lys Tyr Asp Leu Gln Asn Leu Lys Pro Tyr Thr Lys Tyr Val Leu Ser 282 287 292 297			1216
tta cat gcc tac atc att gca aaa gtg caa cgt aat gga agt gct gca Leu His Ala Tyr Ile Ile Ala Lys Val Gln Arg Asn Gly Ser Ala Ala 298 303 308 313			1264
atg tgt cat ttc aca act aaa agt gct cct cca agc cag gtc tgg aac Met Cys His Phe Thr Thr Lys Ser Ala Pro Pro Ser Gln Val Trp Asn 314 319 324 329			1312
atg act gtc tcc atg aca tca gat aat agt atg cat gtc aag tgt agg Met Thr Val Ser Met Thr Ser Asp Asn Ser Met His Val Lys Cys Arg 330 335 340 345			1360
cct ccc agg gac cgt aat ggc ccc cat gaa cgt tac cat ttg gaa gtt Pro Pro Arg Asp Arg Asn Gly Pro His Glu Arg Tyr His Leu Glu Val 346 351 356 361			1408
gaa gct gga aat act ctg gtt aga aat gag tcg cat aag aat tgc gat Glu Ala Gly Asn Thr Leu Val Arg Asn Glu Ser His Lys Asn Cys Asp 362 367 372 377			1456
ttc cgt gta aaa gat ctt caa tat tca aca gac tac act ttt aag gcc Phe Arg Val Lys Asp Leu Gln Tyr Ser Thr Asp Tyr Thr Phe Lys Ala 378 383 388 393			1504
tat ttt cac aat gga gac tat cct gga gaa ccc ttt att tta cat cat Tyr Phe His Asn Gly Asp Tyr Pro Gly Glu Pro Phe Ile Leu His His 394 399 404 409			1552
tca aca tct tat aat tct aag gca ctg ata gca ttt ctg gca ttt ctg Ser Thr Ser Tyr Asn Ser Lys Ala Leu Ile Ala Phe Leu Ala Phe Leu 410 415 420 425			1600
att att gtg aca tca ata gcc ctg ctt gtt gtt ctc tac aaa atc tat Ile Ile Val Thr Ser Ile Ala Leu Leu Val Val Leu Tyr Lys Ile Tyr 426 431 436 441			1648
gat cta cat aag aaa aga tcc tgc aat tta gat gaa cag cag gag ctt Asp Leu His Lys Lys Arg Ser Cys Asn Leu Asp Glu Gln Gln Glu Leu 442 447 452 457			1696
gtt gaa agg gat gat gaa aaa caa ctg atg aat gtg gag cca atc cat Val Glu Arg Asp Asp Glu Lys Gln Leu Met Asn Val Glu Pro Ile His 458 463 468 473			1744
gca gat att ttg ttg gaa act tat aag agg aag att gct gat gaa gga Ala Asp Ile Leu Leu Glu Thr Tyr Lys Arg Lys Ile Ala Asp Glu Gly 474 479 484 489			1792

aga ctt ttt ctg gct gaa ttt cag agc atc ccg cgg gtg ttc agc aag	1840
Arg Leu Phe Leu Ala Glu Phe Gln Ser Ile Pro Arg Val Phe Ser Lys	
490 495 500 505	
ttt cct ata aag gaa gct cga aag ccc ttt aac cag aat aaa aac cgt	1888
Phe Pro Ile Lys Glu Ala Arg Lys Pro Phe Asn Gln Asn Lys Asn Arg	
506 511 516 521	
tat gtt gac att ctt cct tat gat tat aac cgt gtt gaa ctc tct gag	1936
Tyr Val Asp Ile Leu Pro Tyr Asp Tyr Asn Arg Val Glu Leu Ser Glu	
522 527 532 537	
ata aac gga gat gca ggg tca aac tac ata aat gcc agc tat att gat	1984
Ile Asn Gly Asp Ala Gly Ser Asn Tyr Ile Asn Ala Ser Tyr Ile Asp	
538 543 548 553	
ggg ttc aaa gaa ccc agg aaa tac att gct gca caa ggt ccc agg gat	2032
Gly Phe Lys Glu Pro Arg Lys Tyr Ile Ala Ala Gln Gly Pro Arg Asp	
554 559 564 569	
gaa act gtt gat gat ttc tgg agg atg att tgg gaa cag aaa gcc aca	2080
Glu Thr Val Asp Asp Phe Trp Arg Met Ile Trp Glu Gln Lys Ala Thr	
570 575 580 585	
gtt att gtc atg gtc act cga tgt gaa gaa gga aac agg aac aag tgt	2128
Val Ile Val Met Val Thr Arg Cys Glu Glu Gly Asn Arg Asn Lys Cys	
586 591 596 601	
gca gaa tac tgg ccg tca atg gaa gag ggc act cgg gct ttt gga gat	2176
Ala Glu Tyr Trp Pro Ser Met Glu Glu Gly Thr Arg Ala Phe Gly Asp	
602 607 612 617	
gtt gtt gta aag atc aac cag cac aaa aga tgt cca gat tac atc att	2224
Val Val Val Lys Ile Asn Gln His Lys Arg Cys Pro Asp Tyr Ile Ile	
618 623 628 633	
cag aaa ttg aac att gta aaa aaa aaa aaa aaa agc aac tgg aag aga	2272
Gln Lys Leu Asn Ile Val Lys Lys Lys Lys Lys Ser Asn Trp Lys Arg	
634 639 644 649	
ggg gac tca cat tca gtt cac cag ctg gcc aga cca cgg ggt gcc tga	2320
Gly Asp Ser His Ser Val His Gln Leu Ala Arg Pro Arg Gly Ala *	
650 655 660 665	
ggatcctcac ttgctcctca aactgagaag gagagtgaat gccttcagca atttcttcag	2380
tggtccatt gtggtgcact gcagtgtggt tggtgggcgc acaggaacct atctcggaat	2440
tgatgccatg ctagaaggcc tggaagccga gaacaaagtg gatgtttatg gttatgttgt	2500
caagctaagg cgacagagat gcctgatggt tcaagtagag gccaggtaca tcttgatcca	2560
tcaggctttg gtggaatata atcagtttgg agaaacagaa gtgaatttgt ctgaattaca	2620
tccatatcta cataacatga agaaaaggga tccaccaggt gagccgtctc cactagagggc	2680

tgaattccag agacttcctt catataggag ctggaggaca cagcacattg gaaatcaaga	2740
agaaaaataaa agtaaaaaaca ggaattctaa tgtcatccca tatgactata acagagtgcc	2800
acttaaacad gagctggaaa tgagtaaaga gagtgagcat gattcagatg aatcctctga	2860
tgatgacagt gattcagagg aaccaagcaa atacatcaat gcacctttta taatgagcta	2920
ctggaaacct gaagtgatga ttgctgctca gggaccactg aaggagacca ttggtgactt	2980
ttggcagatg atcttccaaa gaaaagtcaa agttattgtt atgctgacag aactgaaaca	3040
tggagaccag gaaatctgtg ctgagtactg gggagaagga aagcaaacad atggagatat	3100
tgaagttgac ctgaaagaca cagacaaatc ttcaacttat acccttcgtg tctttgaact	3160
gagacattcc aagaggaaag actctcgaa cgtgtaccag taccaatata caaactggag	3220
tgtggagcag cttcctgcag aaccaagga attaatctct atgattcagg tcgtcaaaca	3280
aaaacttccc cagaagaatt cctctgaagg gaacaagcat cacaagagta cacctctact	3340
cattcactgc agggatggat ctgagcaaac gggaaatatt tgtgctttgt taaatctctt	3400
agaaagtgcg gaaacagaag aggtagtgga tatttttcaa gtggtaaaag ctctacgcaa	3460
agctaggcca ggcattggtt ccacattcga gcaatatcaa ttcctatatg acgtcattgc	3520
cagcacctac cctgctcaga atggacaagt aaagaaaaac aaccatcaag aagataaaat	3580
tgaatttgat aatgaagtgg acaaagtaaa gcaggatgct aattgtgtta atccacttgg	3640
tgccccagaa aagctccctg aagcaaagga acaggctgaa ggctctgaac ccacgagtgg	3700
cactgagggg ccagaacatt ctgtcaatgg tctgcaagt ccagccttaa atcaagggtc	3760
ataggaaaag acataaatga ggaaactcca aacctcctgt tagctgttat ttctattttt	3820
gtagaagtag gaagtgaaaa taggtataca gtggattaat taaatgcagc gaaccaatat	3880
ttgtagaagg gttatatttt actactgtgg aaaaatattt aagatagttt tgccagaaca	3940
gtttgtacag acgtatgctt attttaaaat tttatctctt attcagtaaa aaacaacttc	4000
tttgtaatcg ttatgtgtgt atatgtatgt gtgtatgggt gtgtgtttgt gtgagagaca	4060
gagaaagaga gagaattctt tcaagtgaat ctaaaagctt ttgcttttcc tttgttttta	4120
tgaagaaaaa atacatttta tattagaagt gttaacttag cttgaaggat ctgtttttaa	4180
aaatcataaa ctgtgtgcag actcaataaa atcatgtaca tttctgaaat gacctcaaga	4240
tgctctcctt gttctactca tatatatcta tcttatatag ttactattt tacttctaga	4300
gatagtacat aaagggtggt tgtgtgtgta tgctactaca aaaaagttgt taactaaatt	4360
aacattggga aatcttatat tccatatatt agcatttagt ccaatgtctt ttttaagctta	4420

ttttaattaaa aaatttccag tgagcttatac atgctgtctt tacatgggggt tttcaatttt 4480
 gcatgctcga ttattccctg tacaatattt aaaatttatt gcttgatact tttgacaaca 4540
 aattagggtt tgtacaattg aacttaaata aatgtcatta aaataaataa atgcaatatg 4600
 tattaatatt cattgtataa aaatagaaga atacaaacat atttgttaaa tattttacata 4660
 tgaaatttaa tatagctatt tttatggaat ttttcattga tatgaaaaat atgatattgc 4720
 atatgcatag ttcccatgtt aaatcccatt cataactttc attaaagcat ttactttgaa 4780
 tttcaaaaaa aaaaaaaa 4798

<210> 299
 <211> 6799
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (249) .. (2405)

<400> 299
 tgcgggtaccg gtccggaatt cccgggtcga cccacgcgtc cgcggacgcg tggggctgta 60
 agcttcggcg cctccgcttc acctatggga ctcagactcg ggtcagcctg gcgctccctg 120
 gacagtatga actagtgcac acgctggttg ctcatcaggg caactgggag accatccctg 180
 aggaggatct ggagggtccaa gagaacaatg aggatgctgc tcatgtttta acggaactgg 240
 aggtaacg atg cac cat gct ctc tta cag gaa gtg gac gtt gtg gta gca 290
 Met His His Ala Leu Leu Gln Glu Val Asp Val Val Val Ala
 1 5 10
 cca tgc caa ggc ctc cgg ccc aca gtg gat gtt ctg ggt gac ttg gtg 338
 Pro Cys Gln Gly Leu Arg Pro Thr Val Asp Val Leu Gly Asp Leu Val
 15 20 25 30
 aat gat ttc ttg cct gtg ata acc tat gca ctc cac aaa gat gaa ctc 386
 Asn Asp Phe Leu Pro Val Ile Thr Tyr Ala Leu His Lys Asp Glu Leu
 31 36 41 46
 tct gag agg gat gag caa gag ctt cag gaa atc cga aag tat ttc tcc 434
 Ser Glu Arg Asp Glu Gln Glu Leu Gln Glu Ile Arg Lys Tyr Phe Ser
 47 52 57 62
 ttt cct gta ttc ttt ttc aaa gtg ccg aaa ctg ggc tcg gag ata ata 482
 Phe Pro Val Phe Phe Phe Lys Val Pro Lys Leu Gly Ser Glu Ile Ile
 63 68 73 78
 gac tcc tca acc agg aga atg gag agc gaa aga tca ccg ctt tat cgc 530

Asp	Ser	Ser	Thr	Arg	Arg	Met	Glu	Ser	Glu	Arg	Ser	Pro	Leu	Tyr	Arg		
79					84					89					94		
cag	cta	att	gac	ctg	ggc	tat	ctg	agc	agc	agt	cac	tgg	aac	tgt	ggg	578	
Gln	Leu	Ile	Asp	Leu	Gly	Tyr	Leu	Ser	Ser	Ser	His	Trp	Asn	Cys	Gly		
95					100					105					110		
gct	cct	ggc	cag	gat	act	aaa	gct	cag	agc	atg	ttg	gtg	gaa	cag	agt	626	
Ala	Pro	Gly	Gln	Asp	Thr	Lys	Ala	Gln	Ser	Met	Leu	Val	Glu	Gln	Ser		
111					116					121					126		
gaa	aag	ctg	aga	cac	ttg	agc	aca	ttt	tct	cac	cag	gtg	tta	cag	act	674	
Glu	Lys	Leu	Arg	His	Leu	Ser	Thr	Phe	Ser	His	Gln	Val	Leu	Gln	Thr		
127					132					137					142		
cgc	ctg	gtg	gat	gca	gcc	aag	gcc	ctg	aac	ctg	gtg	cac	tgc	cac	tgc	722	
Arg	Leu	Val	Asp	Ala	Ala	Lys	Ala	Leu	Asn	Leu	Val	His	Cys	His	Cys		
143					148					153					158		
ctt	gac	atc	ttt	att	aac	cag	gca	ttt	gac	atg	cag	cgg	gac	ctg	cag	770	
Leu	Asp	Ile	Phe	Ile	Asn	Gln	Ala	Phe	Asp	Met	Gln	Arg	Asp	Leu	Gln		
159					164					169					174		
atc	act	ccc	aaa	cgt	ctg	gaa	tat	act	cga	aaa	aag	gag	aat	gag	ttg	818	
Ile	Thr	Pro	Lys	Arg	Leu	Glu	Tyr	Thr	Arg	Lys	Lys	Glu	Asn	Glu	Leu		
175					180					185					190		
tat	gaa	tca	ttg	atg	aat	att	gcc	aac	cga	aag	cag	gag	gaa	atg	aag	866	
Tyr	Glu	Ser	Leu	Met	Asn	Ile	Ala	Asn	Arg	Lys	Gln	Glu	Glu	Met	Lys		
191					196					201					206		
gat	atg	att	gtt	gag	aca	ctt	aat	acc	atg	aag	gag	gaa	ctt	ctg	gat	914	
Asp	Met	Ile	Val	Glu	Thr	Leu	Asn	Thr	Met	Lys	Glu	Glu	Leu	Leu	Asp		
207					212					217					222		
gat	gct	act	aac	atg	gag	ttt	aaa	gac	gtc	att	gtc	cct	gag	agt	gga	962	
Asp	Ala	Thr	Asn	Met	Glu	Phe	Lys	Asp	Val	Ile	Val	Pro	Glu	Ser	Gly		
223					228					233					238		
gaa	cca	gta	ggc	acc	aga	gag	atc	aaa	tgc	tgc	atc	cga	cag	atc	cag	1010	
Glu	Pro	Val	Gly	Thr	Arg	Glu	Ile	Lys	Cys	Cys	Ile	Arg	Gln	Ile	Gln		
239					244					249					254		
gaa	ctc	atc	atc	tcc	cga	ctt	aat	cag	gca	gtg	gct	aat	aag	ctg	atc	1058	
Glu	Leu	Ile	Ile	Ser	Arg	Leu	Asn	Gln	Ala	Val	Ala	Asn	Lys	Leu	Ile		
255					260					265					270		
agc	tca	gtg	gat	tac	ctg	agg	gaa	agc	ttc	gtc	gga	acc	ctg	gaa	cga	1106	
Ser	Ser	Val	Asp	Tyr	Leu	Arg	Glu	Ser	Phe	Val	Gly	Thr	Leu	Glu	Arg		
271					276					281					286		
tgt	ctg	cag	agc	ctg	gag	aag	tct	cag	gat	gtc	tca	gtt	cac	atc	acc	1154	
Cys	Leu	Gln	Ser	Leu	Glu	Lys	Ser	Gln	Asp	Val	Ser	Val	His	Ile	Thr		
287					292					297					302		
agt	aat	tat	ctc	aaa	cag	atc	tta	aat	gct	gcc	tat	cat	gtt	gaa	gtc	1202	
Ser	Asn	Tyr	Leu	Lys	Gln	Ile	Leu	Asn	Ala	Ala	Tyr	His	Val	Glu	Val		

303	308	313	318	
acg ttt cac tca ggg tcg tca gtt aca agg atg cta tgg gag caa atc				1250
Thr Phe His Ser Gly Ser Ser Val Thr Arg Met Leu Trp Glu Gln Ile				
319	324	329	334	
aaa cag atc atc cag cgc atc aca tgg gtg agc cca cct gcc atc act				1298
Lys Gln Ile Ile Gln Arg Ile Thr Trp Val Ser Pro Pro Ala Ile Thr				
335	340	345	350	
ctg gaa tgg aag agg aag gtg gcc cag gaa gcc att gag agc ctc agc				1346
Leu Glu Trp Lys Arg Lys Val Ala Gln Glu Ala Ile Glu Ser Leu Ser				
351	356	361	366	
gcc tcc aaa ttg gct aag agc att tgc agc caa ttc cgg act cgg ctc				1394
Ala Ser Lys Leu Ala Lys Ser Ile Cys Ser Gln Phe Arg Thr Arg Leu				
367	372	377	382	
aat agt tcc cac gag gct ttt gca gcc tcc ttg cgg cag ctg gaa gct				1442
Asn Ser Ser His Glu Ala Phe Ala Ala Ser Leu Arg Gln Leu Glu Ala				
383	388	393	398	
ggc cac tca ggc cgg tta gag aaa acg gaa gat cta tgg ctg agg gtt				1490
Gly His Ser Gly Arg Leu Glu Lys Thr Glu Asp Leu Trp Leu Arg Val				
399	404	409	414	
cgg aaa gat cat gct ccc cgc ctg gcc cgc ctt tct ctg gaa agc cgt				1538
Arg Lys Asp His Ala Pro Arg Leu Ala Arg Leu Ser Leu Glu Ser Arg				
415	420	425	430	
tct tta cag gat gtc ttg ctt cat cgt aaa cct aaa ctg gga cag gaa				1586
Ser Leu Gln Asp Val Leu Leu His Arg Lys Pro Lys Leu Gly Gln Glu				
431	436	441	446	
ctg ggc cgg ggc cag tat ggt gtg gta tac ctg tgt gac aac tgg gga				1634
Leu Gly Arg Gly Gln Tyr Gly Val Val Tyr Leu Cys Asp Asn Trp Gly				
447	452	457	462	
gga cac ttc cct tgt gcc ctc aaa tca gtt gtc cct cca gat gag aag				1682
Gly His Phe Pro Cys Ala Leu Lys Ser Val Val Pro Pro Asp Glu Lys				
463	468	473	478	
cac tgg aat gat ctg gct ttg gaa ttt cac tat atg agg tct ctg ccg				1730
His Trp Asn Asp Leu Ala Leu Glu Phe His Tyr Met Arg Ser Leu Pro				
479	484	489	494	
aag cat gag cga ttg gtg gat ctc cat ggt tca gtc att gac tac aac				1778
Lys His Glu Arg Leu Val Asp Leu His Gly Ser Val Ile Asp Tyr Asn				
495	500	505	510	
tat ggt ggt ggc tcc agc att gct gtg ctc ctc att atg gag cgg cta				1826
Tyr Gly Gly Gly Ser Ser Ile Ala Val Leu Leu Ile Met Glu Arg Leu				
511	516	521	526	
cac cgg gat ctc tac aca ggg ctg aag gct ggg ctg acc ctg gag aca				1874
His Arg Asp Leu Tyr Thr Gly Leu Lys Ala Gly Leu Thr Leu Glu Thr				
527	532	537	542	

cgt ttg cag ata gca cta gat gtg gtg gag gga atc cgc ttc ctg cac	1922
Arg Leu Gln Ile Ala Leu Asp Val Val Glu Gly Ile Arg Phe Leu His	
543 548 553 558	
agc cag gga ctt gtc cat cgt gat atc aaa ctg aaa aat gtg ctg ctg	1970
Ser Gln Gly Leu Val His Arg Asp Ile Lys Leu Lys Asn Val Leu Leu	
559 564 569 574	
gat aag cag aac cgt gcc aag atc act gac tta gga ttc tgc aag cca	2018
Asp Lys Gln Asn Arg Ala Lys Ile Thr Asp Leu Gly Phe Cys Lys Pro	
575 580 585 590	
gag gcc atg atg tca ggc agc att gtg ggg aca cca atc cat atg gcc	2066
Glu Ala Met Met Ser Gly Ser Ile Val Gly Thr Pro Ile His Met Ala	
591 596 601 606	
cct gaa ctt ttc aca ggg aag tac gat aat tcc gtg gat gtc tac gct	2114
Pro Glu Leu Phe Thr Gly Lys Tyr Asp Asn Ser Val Asp Val Tyr Ala	
607 612 617 622	
ttt gga att ctt ttc tgg tat atc tgc tca ggc tct gtc aag ctc cct	2162
Phe Gly Ile Leu Phe Trp Tyr Ile Cys Ser Gly Ser Val Lys Leu Pro	
623 628 633 638	
gag gca ttt gag agg tgt gct agc aaa gac cat ctc tgg aac aat gtg	2210
Glu Ala Phe Glu Arg Cys Ala Ser Lys Asp His Leu Trp Asn Asn Val	
639 644 649 654	
cgg agg ggg gct cgc cca gaa cgt ctt cct gtg ttt gat gag gag tgc	2258
Arg Arg Gly Ala Arg Pro Glu Arg Leu Pro Val Phe Asp Glu Glu Cys	
655 660 665 670	
tgg cag ttg atg gaa gcc tgt tgg gat ggc gac ccc ttg aag agg cct	2306
Trp Gln Leu Met Glu Ala Cys Trp Asp Gly Asp Pro Leu Lys Arg Pro	
671 676 681 686	
ctc ttg ggc att gtc cat ccc atg ctc cag ggc atc atg aat cgg ctc	2354
Leu Leu Gly Ile Val His Pro Met Leu Gln Gly Ile Met Asn Arg Leu	
687 692 697 702	
tgc aag tcc aat tct gag cag cca aac aga gga cta gat gat tct act	2402
Cys Lys Ser Asn Ser Glu Gln Pro Asn Arg Gly Leu Asp Asp Ser Thr	
703 708 713 718	
tga aagc aaagaccttt ctctttcact ctctagttat ttccttcccc ctcaccattt	2459
*	
719	
ggccatgggg agaatttgac atttattcac tataggacac actocccaagg gaactggtgc	2519
ttgctgggaa acttggaacc ttcccaggca gggatgactc ctggacagtg aagagttgaa	2579
tgactgagca tattcagcag ctcaactgaag cgccaagcta tcccttttagc aaaaaagtgt	2639
ctcagatgtg taaaagctga ggaatgtggt gttctggctt cacaaatgaa aaggaggcag	2699

atgttaccat	tgtcttttca	ctgtatatac	ttctaagaca	gcaagcggga	cactgcagtg	2759
gcaatagtgt	taaaaaatct	cattctcatg	atTTTTggct	ctagctagga	atagttagt	2819
caggactcag	aaaatttgag	cttagttctg	ggattatgaa	aacatgggga	caaaaacaat	2879
aacttggtga	tgtctggttc	ctgctgtctg	cagccaggta	tctcagggtg	caatggtcag	2939
aagtcccagt	gagggagcta	gaaacagagc	tatctgttcc	tcatagtgcc	agtgtgttta	2999
catttatagg	accacatatc	cctggtttct	gggggagggt	ttcactgtta	catcaccaag	3059
aggccctgaa	aagaggaaaa	aaaaaaaaaa	agaggccggg	catgggggct	cacgcctgta	3119
atctcagcac	tttgggaggc	tgaggcgggc	ggatcacaag	gtccagagtt	caagagcagc	3179
ctggccaaca	tgttgaaacc	cgtctctac	taaagataca	aaaaattagc	cgggcgtggt	3239
ggtgcatgcc	tgtaatccaa	gatactcagg	aggctgaggc	aggagaatcg	cttgaacctg	3299
ggaggcggag	gttgacagtga	gccgagatca	tgccattgca	ctccagcctg	ggtgacagag	3359
tgagactctg	tctcaaaaaa	aaaaaaaaat	agaatgtgta	tgcataatatt	tgtgtgtata	3419
tgtatatatg	tgtgtgtgtc	tatatctcta	tctatataga	catacacaca	ggagttattg	3479
gatttagagt	tactgctaac	cccagaacag	aatctgttct	tttacctttg	agtcttttct	3539
tttgtttacc	tcttttcatc	tcaaagtggg	aaagctccag	ataacatggg	acttaggagt	3599
gagtgtctaa	gcaaaaacca	ccaatgcga	agtatttggg	tgagaactga	gaggtgggag	3659
atgattggag	gccatggcct	atgtacaaac	atactggaag	aaaaccagct	tgTTTTtaaa	3719
acttaacaca	atcagaaatt	tttctttttg	tgtttgaatc	taacacactg	acgtttggaa	3779
aacttgatca	atgagctttt	aaccacgatt	tctcccgcaa	tttgttcctt	ctttttacct	3839
ttttaaaaat	ctgttagaag	aaaaaaagca	gcagacgaaa	gagaaaaacc	ctcctctggt	3899
agttctgtgt	gtgcccctca	cccctgtgtg	ctagtgtctg	tgaagtttcc	ctgaaagggtg	3959
ggaggcgggt	gggtggtcct	ttggagggtt	cctcatgaag	tgtgcttgag	gaaagaaatt	4019
ctgattctag	gcagaggaag	gggaacaatt	taaatattgg	tgcatctcag	atgcacttga	4079
cttcaagcct	tctcaacca	aactggtcca	ttagattccg	aaaaacaggt	agacgaggaa	4139
gtagacagtg	gaagtgahta	gtctccctcc	atctgcctaa	tccccaataa	ctgtggtctg	4199
gccctgtgtg	tcagccccag	agtttgtaaa	acaggcccc	aggtaggtgt	ataagatgag	4259
ttgcaaatta	gcggggcatg	ctggcacgca	ccagtaatcc	cagctacttg	ggaggctgag	4319
gcaggagaat	cacttgaacc	cgagaggcag	aggctatggt	gagccgagat	cacgccactg	4379
cactccagcc	tgggcaacag	agcgagactc	tatcaaaaaa	aaaaaaca	aaaaaaaaac	4439

aaaaaacaaa gatgagtcgc acatctgctg ctgggatttt ctagggttgt ctatgacaga	4499
atgaccatct tttaaatatt aatggagtat aaatggagtc tataatgggt ctttcatata	4559
acttttaact ctttggtat cctgggctct gatcatgata tgtttgagca tagtagctcc	4619
ctaaactctt ggagcctttc agaaattcca tgtagtgcta ataacctttt tacttgcaaa	4679
tgataaagta actgactcag tgtctttggg ctctgcaggc tttagccttg ttttggtagg	4739
atgttcagta tattctcaga atttttacca cctatttagc tatacttcaa gtactctatt	4799
ctctgcacta acttactgtc cttctgggaa ctatgatggg gcttcaaggg agtcagggtgt	4859
caagaaagga ggggtaagta ctctctactt gctggaaaat cattgtaagt ctgttggtga	4919
tgaaatttta ggaaaagtct tatatagttc cctttccaga ctgttttctt ttgactctaa	4979
ctataatcat aagtctgtgc ttccattatg aaggtcacat tcctagcatt cttgggaagt	5039
attagctcat actctcattc acatatggga ggtagattt ttttcctcta cccagagtcc	5099
cttttttagt taccaccagg cttagtttgc tgtcagatac cagttctcta gcagattccc	5159
caacagtttt ttcccagtg gggaggggtg aagggaggga ctgatataag taaggagatg	5219
agtagttgtg ttacagttca ttttctttaa aaaaaagtac tttgagaaaa ggtgcaaaat	5279
attcttgaaa gtctctaggc cagccaaagt ccacatatgg atatttgggg atgttattta	5339
aatactcagc aggctgagtg caggtatacg tgtgtataga gtgtgtatac tttgcttttg	5399
ttttataaca ttgtcagcta attttggctt tgttcttttg catccattct tattataagt	5459
gatggaatgc catgaaatgt actgtattgt atattacttg ggaggacact aggttttcaa	5519
agaagtctgg cagcacttgg gttatagagg gctcagcatg accaaagtcc taaagatttt	5579
acctcccagc tttggttgta tgtgttcca agtggtgagg tgagattgtg gctggaggaa	5639
gaaaaaggat ggcataaag aatgaccctt attgtggtct gtccttctaa tcaacataat	5699
tagggcagct taccccaaca tgaaaatgat gacctggcca tttttaatgg ccagagcttg	5759
aagtctggtc tctcattttg tttcagaaat gagtgagagg ccttcttgca gagcagtcag	5819
gagaaatggg ggagcctggg gccctggaat ggctgaccct gtgcctagag agctgatggc	5879
aagggtctgc tggcatggct catttgggtg gggtttcccc aggcatacct tagttccctg	5939
atcctctgca aagagtagct cattgactga gcaagcgctt caggaggact gtgctggttg	5999
ttcccagacc aaagagagtc acttttgact ccatcaactt caaggggaca gagcctaggc	6059
agcagattct cctaattttt aacactaaaa ttcaaggaag cagtggagga aagaatgcat	6119

tactaccaca gatagaaata ggggactcat agaactctcg actagtacct gtcagctctc 6179
 agatgcattc ttgtgtcttt gcttgagctg ccaaagaagg gtcacaaagt gttcttcctc 6239
 atggaagaag tgcctcgggg ttgcagggt gcaaagtac aactgcactg aatgacactt 6299
 tattttttgg ctttggttta ttatttagca ctgggaggcc caggggaatt ggtgattaca 6359
 gtagcacttt gggaagttaa agcccccttt gggcttgctt tggagagatg atggcatgct 6419
 tggatttcca ttggataat caggaagcct cctagtcca tccatattgt gtcagagtgg 6479
 gattaacaac cctggaagag tccactgcc aagagtagt tgctttcctg gaatttccaa 6539
 agcttttgga ttttctggat caagtaacct actttttaa acctgaggtc aggagttcga 6599
 gaccagcctg gtaacatggt gaaaccccg ctctattaaa aatagaaaaa attagccagg 6659
 catggtggcg ggcacctata gtcccagcta ctcaggaggc tgaggtagga gaattgcttg 6719
 aaccaggag acagaggctg cattgagcca agatcacacc actgcactcc agcctgggca 6779
 gcagagcaag actccatctc 6799

<210> 300
 <211> 3721
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (22) .. (2517)

<400> 300
 ggtcggcggc attcggcggc g atg gag cgg ccc tgg gga gct gcg gac ggc 51
 Met Glu Arg Pro Trp Gly Ala Ala Asp Gly
 1 5
 ctc tcg cgc tgg ccc cat ggc ctc ggc ctc ctc ctc ctc ctg cag ctg 99
 Leu Ser Arg Trp Pro His Gly Leu Gly Leu Leu Leu Leu Leu Gln Leu
 11 16 21 26
 ctg ccg ccg tcg acc ctc agc cag gac cgg ctg gac gcg ccg ccg ccg 147
 Leu Pro Pro Ser Thr Leu Ser Gln Asp Arg Leu Asp Ala Pro Pro Pro
 27 32 37 42
 ccc gct gcg ccg ctg ccg cgc tgg tct ggc ccc atc ggg gtg agc tgg 195
 Pro Ala Ala Pro Leu Pro Arg Trp Ser Gly Pro Ile Gly Val Ser Trp
 43 48 53 58
 ggg ctg cgg gcg gcc gca gcc ggg ggc gcg ttt ccc cgc ggc ggc cgt 243
 Gly Leu Arg Ala Ala Ala Ala Gly Gly Ala Phe Pro Arg Gly Gly Arg
 59 64 69 74

tgg cgt cgc agc gcg ccg ggc gag gac gag gag tgc ggc cgg gtc cgg	291
Trp Arg Arg Ser Ala Pro Gly Glu Asp Glu Glu Cys Gly Arg Val Arg	
75 80 85 90	
gac ttc gtc gcc aag ctg gcc aac aac acg cac cag cat gtg ttt gat	339
Asp Phe Val Ala Lys Leu Ala Asn Asn Thr His Gln His Val Phe Asp	
91 96 101 106	
gat ctc aga ggc tca gta tcc ttg tcc tgg gtt gga gat agc act ggg	387
Asp Leu Arg Gly Ser Val Ser Leu Ser Trp Val Gly Asp Ser Thr Gly	
107 112 117 122	
gtc att cta gtc ttg act acc ttc cat gta cca ctg gta att atg act	435
Val Ile Leu Val Leu Thr Thr Phe His Val Pro Leu Val Ile Met Thr	
123 128 133 138	
ttt gga cag tcc aag cta tat cga agt gag gat tat ggg aag aac ttt	483
Phe Gly Gln Ser Lys Leu Tyr Arg Ser Glu Asp Tyr Gly Lys Asn Phe	
139 144 149 154	
aag gat att aca gat ctc atc aat aac acc ttt att cgg act gaa ttt	531
Lys Asp Ile Thr Asp Leu Ile Asn Asn Thr Phe Ile Arg Thr Glu Phe	
155 160 165 170	
ggc atg gct att ggt cct gag aac tct gga aag gtg gtg tta aca gca	579
Gly Met Ala Ile Gly Pro Glu Asn Ser Gly Lys Val Val Leu Thr Ala	
171 176 181 186	
gag gtg tct gga gga agt cgt gga gga aga atc ttc aga tca tca gat	627
Glu Val Ser Gly Gly Ser Arg Gly Gly Arg Ile Phe Arg Ser Ser Asp	
187 192 197 202	
ttt gcg aag aat ttt gtg caa aca gat ctc cct ttt cat cct ctc act	675
Phe Ala Lys Asn Phe Val Gln Thr Asp Leu Pro Phe His Pro Leu Thr	
203 208 213 218	
cag atg atg tat agc cct cag aat tct gat tat ctt tta gct ctc agc	723
Gln Met Met Tyr Ser Pro Gln Asn Ser Asp Tyr Leu Leu Ala Leu Ser	
219 224 229 234	
act gaa aat ggc ctg tgg gtg tcc aag aat ttt ggg gga aaa tgg gaa	771
Thr Glu Asn Gly Leu Trp Val Ser Lys Asn Phe Gly Gly Lys Trp Glu	
235 240 245 250	
gaa atc cac aaa gca gta tgt ttg gcc aaa tgg gga tca gac aac acc	819
Glu Ile His Lys Ala Val Cys Leu Ala Lys Trp Gly Ser Asp Asn Thr	
251 256 261 266	
atc ttc ttt aca acc tat gca aat ggc tcc tgc aaa gct gac ctt ggg	867
Ile Phe Phe Thr Thr Tyr Ala Asn Gly Ser Cys Lys Ala Asp Leu Gly	
267 272 277 282	
gct ctg gaa tta tgg aga act tca gac ttg gga aaa agc ttc aaa act	915
Ala Leu Glu Leu Trp Arg Thr Ser Asp Leu Gly Lys Ser Phe Lys Thr	
283 288 293 298	
att ggt gtg aaa atc tac tca ttt ggt ctt ggg gga cgt ttc ctt ttt	963

Ile Gly Val Lys Ile Tyr Ser Phe Gly Leu Gly Gly Arg Phe Leu Phe	
299 304 309 314	
gcc tct gtg atg gct gat aag gat aca aca aga agg atc cac gtt tca	1011
Ala Ser Val Met Ala Asp Lys Asp Thr Thr Arg Arg Ile His Val Ser	
315 320 325 330	
aca gat caa ggg gac aca tgg agc atg gcc cag ctc ccc tcc gtg gga	1059
Thr Asp Gln Gly Asp Thr Trp Ser Met Ala Gln Leu Pro Ser Val Gly	
331 336 341 346	
cag gaa cag ttc tat tct att ctg gca gca aat gat gac atg gta ttc	1107
Gln Glu Gln Phe Tyr Ser Ile Leu Ala Ala Asn Asp Asp Met Val Phe	
347 352 357 362	
atg cat gta gat gaa cct gga gac act ggg ttt ggc aca atc ttt acc	1155
Met His Val Asp Glu Pro Gly Asp Thr Gly Phe Gly Thr Ile Phe Thr	
363 368 373 378	
tca gat gat cga ggc att gtc tat tcc aag tct ttg gac cga cat ctc	1203
Ser Asp Asp Arg Gly Ile Val Tyr Ser Lys Ser Leu Asp Arg His Leu	
379 384 389 394	
tac act acc aca ggc gga gag acg gac ttt acc aac gtg acc tcc ctc	1251
Tyr Thr Thr Thr Gly Gly Glu Thr Asp Phe Thr Asn Val Thr Ser Leu	
395 400 405 410	
cgc ggc gtc tac ata aca agc gtg ctc tcc gaa gat aat tct atc cag	1299
Arg Gly Val Tyr Ile Thr Ser Val Leu Ser Glu Asp Asn Ser Ile Gln	
411 416 421 426	
acc atg atc act ttt gac caa gga gga agg tgg acg cac ctg agg aag	1347
Thr Met Ile Thr Phe Asp Gln Gly Gly Arg Trp Thr His Leu Arg Lys	
427 432 437 442	
cct gaa aac agt gaa tgt gat gct aca gca aaa aac aag aat gag tgc	1395
Pro Glu Asn Ser Glu Cys Asp Ala Thr Ala Lys Asn Lys Asn Glu Cys	
443 448 453 458	
agc ctt cat att cat gct tcc tac agc atc tcc cag aaa ctg aat gtt	1443
Ser Leu His Ile His Ala Ser Tyr Ser Ile Ser Gln Lys Leu Asn Val	
459 464 469 474	
cca atg gcc cca ctc tca gag ccg aat gcc gta ggc att gtc att gct	1491
Pro Met Ala Pro Leu Ser Glu Pro Asn Ala Val Gly Ile Val Ile Ala	
475 480 485 490	
cat ggt agc gtg ggg gat gcc atc tca gtg atg gtt cca gat gtg tac	1539
His Gly Ser Val Gly Asp Ala Ile Ser Val Met Val Pro Asp Val Tyr	
491 496 501 506	
atc tca gat gat ggg ggt tac tcc tgg aca aag atg ctg gaa gga ccc	1587
Ile Ser Asp Asp Gly Gly Tyr Ser Trp Thr Lys Met Leu Glu Gly Pro	
507 512 517 522	
cac tat tac acc atc ctg gat tct gga ggc atc att gtg gcc att gag	1635
His Tyr Tyr Thr Ile Leu Asp Ser Gly Gly Ile Ile Val Ala Ile Glu	

523	528	533	538	
cac agc agc cgt cct atc aat gtg att aag ttc tcc aca gac gaa ggt				1683
His Ser Ser Arg Pro Ile Asn Val Ile Lys Phe Ser Thr Asp Glu Gly				
539	544	549	554	
caa tgc tgg caa acc tac acg ttc acc agg gac ccc atc tat ttc act				1731
Gln Cys Trp Gln Thr Tyr Thr Phe Thr Arg Asp Pro Ile Tyr Phe Thr				
555	560	565	570	
ggc cta gct tca gaa cct gga gct agg tcc atg aat atc agc att tgg				1779
Gly Leu Ala Ser Glu Pro Gly Ala Arg Ser Met Asn Ile Ser Ile Trp				
571	576	581	586	
ggc ttc aca gaa tct ttc ctg acc agc cag tgg gtc tcc tac acc att				1827
Gly Phe Thr Glu Ser Phe Leu Thr Ser Gln Trp Val Ser Tyr Thr Ile				
587	592	597	602	
gat ttt aaa gat atc ctt gaa agg aac tgt gaa gag aag gac tat acc				1875
Asp Phe Lys Asp Ile Leu Glu Arg Asn Cys Glu Glu Lys Asp Tyr Thr				
603	608	613	618	
ata tgg ctg gca cac tcc aca gac cct gaa gat tat gaa gat ggc tgc				1923
Ile Trp Leu Ala His Ser Thr Asp Pro Glu Asp Tyr Glu Asp Gly Cys				
619	624	629	634	
att ttg ggc tac aaa gaa cag ttt ctg cgg cta cgc aag tca tcc gtg				1971
Ile Leu Gly Tyr Lys Glu Gln Phe Leu Arg Leu Arg Lys Ser Ser Val				
635	640	645	650	
tgt cag aat ggt cga gac tat gtt gtg acc aag cag ccc tcc atc tgc				2019
Cys Gln Asn Gly Arg Asp Tyr Val Val Thr Lys Gln Pro Ser Ile Cys				
651	656	661	666	
ctc tgt tcc ctg gag gac ttt ctc tgt gat ttt ggc tac tac cgt cca				2067
Leu Cys Ser Leu Glu Asp Phe Leu Cys Asp Phe Gly Tyr Tyr Arg Pro				
667	672	677	682	
gaa aat gac tcc aag tgt gtg gaa cag cca gaa ctg aag ggc cac gac				2115
Glu Asn Asp Ser Lys Cys Val Glu Gln Pro Glu Leu Lys Gly His Asp				
683	688	693	698	
ctg gag ttt tgt ctg tac gga aga gaa gaa cac cta aca aca aat ggg				2163
Leu Glu Phe Cys Leu Tyr Gly Arg Glu Glu His Leu Thr Thr Asn Gly				
699	704	709	714	
tac cgg aaa att cca ggg gac aaa tgc cag ggt ggg gta aat cca gtt				2211
Tyr Arg Lys Ile Pro Gly Asp Lys Cys Gln Gly Gly Val Asn Pro Val				
715	720	725	730	
cga gaa gta aaa gac ttg aaa aag aaa tgc aca agc aac ttt ttg agt				2259
Arg Glu Val Lys Asp Leu Lys Lys Lys Cys Thr Ser Asn Phe Leu Ser				
731	736	741	746	
ccg gaa aaa cag aat tcc aag tca aat tct gtt cca att atc ctg gcc				2307
Pro Glu Lys Gln Asn Ser Lys Ser Asn Ser Val Pro Ile Ile Leu Ala				
747	752	757	762	

atc gtg gga ttg atg ctg gtc aca gtc gta gca gga gtg ctc att gtg	2355
Ile Val Gly Leu Met Leu Val Thr Val Val Ala Gly Val Leu Ile Val	
763 768 773 778	
aag aaa tat gtc tgt ggg gga agg ttc ctg gtg cat cga tac tct gtg	2403
Lys Lys Tyr Val Cys Gly Gly Arg Phe Leu Val His Arg Tyr Ser Val	
779 784 789 794	
ctg cag cag cat gca gag gcc aat ggt gtg gat ggt gtg gat gct ttg	2451
Leu Gln Gln His Ala Glu Ala Asn Gly Val Asp Gly Val Asp Ala Leu	
795 800 805 810	
gac aca gcc tcc cac act aat aaa agt ggt tat cat gat gac tca gat	2499
Asp Thr Ala Ser His Thr Asn Lys Ser Gly Tyr His Asp Asp Ser Asp	
811 816 821 826	
gag gac ctc ttg gaa tag ctcttc agaggagctg gaccagcat ggatggtgga	2553
Glu Asp Leu Leu Glu *	
827 832	
accacagtac ctcttacact cctgtgggt ccaacttcag gaaataaatt tcccattgcg	2613
agggacccag ctctgtttct gctgcttcca tcaaagccaa aaggacctac actaaagaaa	2673
tgcagggtgg ggggtggggaa ccctgagcac ttttttaciaa ttggctctga gaaaaaggga	2733
gacattttaa attctttaac ttcttatttc tcgtcctgtc tctttgcaaa gtatgggctt	2793
ttgtttttgt tttttaaggg aaacgaaatg gaattcgaag ggaccttttc actaacccca	2853
cttctgtgtg ttctgcatgg tgcctgcccc agggcatctg ccaactccag tatcagctct	2913
cacagtgtac ttggtaccat ccctgggctc tgctggcgag acgaaacagc tgtagagatg	2973
aaaacaggct gcagaggctg gcacagctgg ccggcttttc tccatctggg gacagtccta	3033
ctccaagaac actgcacacc agctcctcac acagatccca cttacggcgc gcaacggggt	3093
ctaggctgca ggcagctcga ggacccgcgg ccccgccccg gctcggcctg gcagatagca	3153
gaggcagcag gccgtgccgg ggggggcatg ttgctgtaac cagtggccca ggggatgtta	3213
cggtggacag tgcacctgga gggcggggccc cgcagggtga accatgctgc agtggctgtc	3273
gggcacatggg tatactcctt cgggggttac tgctctggtg aagactatga gacactgcgt	3333
cagatagatg tgcacatttt caatgcagtg tccttgcggt ggacaaagct gccccgggtg	3393
aagtctgccca tccgtgggca agctcctgtg gtaccctaca tgcgtatgg acactcaacc	3453
gtcctcatcg acgacacagt cctccttttg ggcgggcgga atgacaccga agggcctgca	3513
atgtgctcta tgcctttgac gtcaatacgc acaagtgggt cacaccccca gtgtcaggga	3573
cagttcctgg ggccccggat ggacattcag cctgtgtcct aggcaagatc atgtacattt	3633

ttgggggcta cgagcagcag ggcactgttt ttccaatgac attcacaagc tagataccag 3693
caccatgaca tggactotta tctgtaca 3721

<210> 301
<211> 2592
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (133)..(2316)

<400> 301
aagctggtac gcctgcaggt accggtccgg aattcccggg tcgacccacg cgtccggacc 60
cggcctccta gggggtcgtc gtgggtgcaga cagtttagca gaacagcctc cgcggctccg 120
gggagaagca at atg tta agg ata cct gta aga aag gcc tta gta ggc 168
Met Leu Arg Ile Pro Val Arg Lys Ala Leu Val Gly
1 5 10
ctt tct aag tct cct aaa gga tgt gtt cga aca act gcc aca gca gca 216
Leu Ser Lys Ser Pro Lys Gly Cys Val Arg Thr Thr Ala Thr Ala Ala
13 18 23 28
agc aac ttg att gaa gta ttt gtt gat ggt cag tct gtc atg gtg gaa 264
Ser Asn Leu Ile Glu Val Phe Val Asp Gly Gln Ser Val Met Val Glu
29 34 39 44
ccg gga acg acc gtc ctc caa gct tgt gag aag gtt ggc atg cag atc 312
Pro Gly Thr Thr Val Leu Gln Ala Cys Glu Lys Val Gly Met Gln Ile
45 50 55 60
cct cga ttc tgt tat cat gaa agg ttg tct gtt gct gga aac tgc agg 360
Pro Arg Phe Cys Tyr His Glu Arg Leu Ser Val Ala Gly Asn Cys Arg
61 66 71 76
atg tgc ctt gtt gaa att gag aaa gcc cct aag gtt gta gct gct tgt 408
Met Cys Leu Val Glu Ile Glu Lys Ala Pro Lys Val Val Ala Ala Cys
77 82 87 92
gcc atg cca gta atg aag ggt tgg aat atc cta aca aac tca gaa aaa 456
Ala Met Pro Val Met Lys Gly Trp Asn Ile Leu Thr Asn Ser Glu Lys
93 98 103 108
tcc aaa aaa gcc agg gaa ggt gtg atg gag ttc tta tta gca aat cac 504
Ser Lys Lys Ala Arg Glu Gly Val Met Glu Phe Leu Leu Ala Asn His
109 114 119 124
cca ttg gac tgt cct att tgt gac cag gga ggt gaa tgt gat ctg cag 552
Pro Leu Asp Cys Pro Ile Cys Asp Gln Gly Gly Glu Cys Asp Leu Gln
125 130 135 140

gac cag tcc atg atg ttt gga aat gat agg agc cga ttt tta gag ggg	600
Asp Gln Ser Met Met Phe Gly Asn Asp Arg Ser Arg Phe Leu Glu Gly	
141 146 151 156	
aag cgt gct gtg gaa gac aag aac att ggg cca ttg gta aag acc atc	648
Lys Arg Ala Val Glu Asp Lys Asn Ile Gly Pro Leu Val Lys Thr Ile	
157 162 167 172	
atg aca aga tgt ata cag tgt act cgc tgc atc agg ttt gca agt gag	696
Met Thr Arg Cys Ile Gln Cys Thr Arg Cys Ile Arg Phe Ala Ser Glu	
173 178 183 188	
att gca gga gta gat gat ttg gga aca aca ggc aga gga aat gat atg	744
Ile Ala Gly Val Asp Asp Leu Gly Thr Thr Gly Arg Gly Asn Asp Met	
189 194 199 204	
caa gtt ggc aca tac att gaa aag atg ttc atg tct gaa ctg tct ggg	792
Gln Val Gly Thr Tyr Ile Glu Lys Met Phe Met Ser Glu Leu Ser Gly	
205 210 215 220	
aat atc att gat atc tgc cct gta ggt gcc cta acc tct aag ccc tat	840
Asn Ile Ile Asp Ile Cys Pro Val Gly Ala Leu Thr Ser Lys Pro Tyr	
221 226 231 236	
gcc ttt act gcc cgg cct tgg gaa aca aga aag aca gaa tcc att gat	888
Ala Phe Thr Ala Arg Pro Trp Glu Thr Arg Lys Thr Glu Ser Ile Asp	
237 242 247 252	
gta atg gat gcg gtt gga agt aat att gtg gtt agc aca aga act gga	936
Val Met Asp Ala Val Gly Ser Asn Ile Val Val Ser Thr Arg Thr Gly	
253 258 263 268	
gaa gtg atg agg att ttg cca cgt atg cat gag gac atc aat gaa gag	984
Glu Val Met Arg Ile Leu Pro Arg Met His Glu Asp Ile Asn Glu Glu	
269 274 279 284	
tgg atc tct gat aaa acc aga ttt gcc tat gat ggg cta aaa cgt caa	1032
Trp Ile Ser Asp Lys Thr Arg Phe Ala Tyr Asp Gly Leu Lys Arg Gln	
285 290 295 300	
aga ctt acc gag cca atg gtc aga aat gaa aaa ggg ctt tta acc tat	1080
Arg Leu Thr Glu Pro Met Val Arg Asn Glu Lys Gly Leu Leu Thr Tyr	
301 306 311 316	
act tct tgg gag gat gcg ctc tct cgc gta gct gga atg ttg cag agt	1128
Thr Ser Trp Glu Asp Ala Leu Ser Arg Val Ala Gly Met Leu Gln Ser	
317 322 327 332	
ttt caa ggc aaa gat gtg gca gca att gca ggt ggc ttg gtg gat gct	1176
Phe Gln Gly Lys Asp Val Ala Ala Ile Ala Gly Gly Leu Val Asp Ala	
333 338 343 348	
gaa gcc ctg gta gct ctc aaa gat ttg ctt aat aga gtg gac tct gac	1224
Glu Ala Leu Val Ala Leu Lys Asp Leu Leu Asn Arg Val Asp Ser Asp	
349 354 359 364	
acc tta tgc act gaa gag gtc ttc ccc act gca gga gct ggc aca gat	1272

Thr Leu Cys Thr Glu Glu Val Phe Pro Thr Ala Gly Ala Gly Thr Asp	
365 370 375 380	
ttg cgt tcc aat tat ctt ctt aat act aca att gct ggt gtg gaa gag	1320
Leu Arg Ser Asn Tyr Leu Leu Asn Thr Thr Ile Ala Gly Val Glu Glu	
381 386 391 396	
gca gat gtt gtt ctt ctg gtt ggt aca aac cca cgt ttt gag gca cca	1368
Ala Asp Val Val Leu Leu Val Gly Thr Asn Pro Arg Phe Glu Ala Pro	
397 402 407 412	
ctg ttt aat gct aga att cga aag agc tgg ctg cat aat gac tta aaa	1416
Leu Phe Asn Ala Arg Ile Arg Lys Ser Trp Leu His Asn Asp Leu Lys	
413 418 423 428	
gtg gcc ctt ata ggc agt cca gtg gac ctc act tac aca tat gac cac	1464
Val Ala Leu Ile Gly Ser Pro Val Asp Leu Thr Tyr Thr Tyr Asp His	
429 434 439 444	
ctg gga gac tcc ccc aaa att ctt caa gac att gct tcg gga agc cat	1512
Leu Gly Asp Ser Pro Lys Ile Leu Gln Asp Ile Ala Ser Gly Ser His	
445 450 455 460	
cca ttt agc cag gtc cta aag gaa gct aaa aaa cca atg gtg gtt tta	1560
Pro Phe Ser Gln Val Leu Lys Glu Ala Lys Lys Pro Met Val Val Leu	
461 466 471 476	
ggc agt tct gca ctc caa aga aat gat gga gca gca att ctt gca gct	1608
Gly Ser Ser Ala Leu Gln Arg Asn Asp Gly Ala Ala Ile Leu Ala Ala	
477 482 487 492	
gtt tct agc att gca caa aag att cgg atg act agt ggt gtt act ggt	1656
Val Ser Ser Ile Ala Gln Lys Ile Arg Met Thr Ser Gly Val Thr Gly	
493 498 503 508	
gat tgg aaa gtt atg aat atc ctt cat agg att gca agt caa gta gct	1704
Asp Trp Lys Val Met Asn Ile Leu His Arg Ile Ala Ser Gln Val Ala	
509 514 519 524	
gct ttg gac ctt ggc tat aag cct ggg gtg gaa gca att cgg aag aac	1752
Ala Leu Asp Leu Gly Tyr Lys Pro Gly Val Glu Ala Ile Arg Lys Asn	
525 530 535 540	
cct ccc aag gtg ctg ttt ctc ctg gga gca gat gga ggt tgt atc aca	1800
Pro Pro Lys Val Leu Phe Leu Leu Gly Ala Asp Gly Gly Cys Ile Thr	
541 546 551 556	
cga cag gat ttg cca aag gat tgt ttc att att tat caa gga cat cat	1848
Arg Gln Asp Leu Pro Lys Asp Cys Phe Ile Ile Tyr Gln Gly His His	
557 562 567 572	
ggg gat gtt ggg gct ccc ata gct gat gtt att ctc cca gga gct gct	1896
Gly Asp Val Gly Ala Pro Ile Ala Asp Val Ile Leu Pro Gly Ala Ala	
573 578 583 588	
tac aca gag aag tct gct aca tat gtc aac act gag ggt aga gct cag	1944
Tyr Thr Glu Lys Ser Ala Thr Tyr Val Asn Thr Glu Gly Arg Ala Gln	

589	594	599	604	
cag act aag gta gca gtg aca cct cct ggc ttg gca aga gaa gac tgg				1992
Gln Thr Lys Val Ala Val Thr Pro Pro Gly Leu Ala Arg Glu Asp Trp				
605	610	615	620	
aaa att ata aga gca ctc tct gag att gct gga atg act ctt cca tat				2040
Lys Ile Ile Arg Ala Leu Ser Glu Ile Ala Gly Met Thr Leu Pro Tyr				
621	626	631	636	
gat act ctg gat caa gta agg aac aga ttg gaa gaa ttc tct cct aat				2088
Asp Thr Leu Asp Gln Val Arg Asn Arg Leu Glu Glu Phe Ser Pro Asn				
637	642	647	652	
ctt gtt cga tat gat gat att gaa ggg gct aat tac ttc cag caa gca				2136
Leu Val Arg Tyr Asp Asp Ile Glu Gly Ala Asn Tyr Phe Gln Gln Ala				
653	658	663	668	
aat gag ctc tca aag cta gtg aac cag cag ctt ctt gct gac cca ctt				2184
Asn Glu Leu Ser Lys Leu Val Asn Gln Gln Leu Leu Ala Asp Pro Leu				
669	674	679	684	
gtt cca cct cag cta act cta aaa gac ttc tac atg aca gat tcg att				2232
Val Pro Pro Gln Leu Thr Leu Lys Asp Phe Tyr Met Thr Asp Ser Ile				
685	690	695	700	
agc aga gcc tca cag aca atg gcc aaa tgt gtc aaa gct gtc aca gag				2280
Ser Arg Ala Ser Gln Thr Met Ala Lys Cys Val Lys Ala Val Thr Glu				
701	706	711	716	
ggc gcc cag gca gta gag gaa cca tcc ata tgc tga agct tctactagga				2330
Gly Ala Gln Ala Val Glu Glu Pro Ser Ile Cys *				
717	722	727		
ccccagtttt gccgcagata attaattggac aactgtagtg cagtgatcct ttacaggttt				2390
atttcttttgt aaaaaaaaaa taataataat ttgaatcatg taatatttaa gggtatacta				2450
tgctattttg aaaatgatat tagttatcaa ctttgcagtt tgaaaaacat gtattgtgtg				2510
taaagggttaa ataacaaaac tatgcagatg ctcttaaaag cattgataac ctttgtgacg				2570
aacataaaga gatccttaaa tt				2592

<210> 302
 <211> 2571
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (404)..(1678)

 <400> 302

taagcttgcg ggcgcacaatt tttttttttt tttttttttt atgggtctctg acttttattat	60
taaatacata ggtgcaaata agaatttttca ttttaatctg tcaacgacaa tctgttgaaa	120
ccctgctgtg tgcccttgctc catgctgctc tgttagggga ctggggaggc caggacatgc	180
tgccagggag ctcccggctc agtgggaaag agtaaattgca gagtgccttg ctactggttt	240
aaaagaaaagg aacacaaaata tgattgcttt cttactctgg gtttgccctt ctggcatgtt	300
gcctgggtcc caagacgaag tctcggatgt gtacatattt gagagttcag tactgcagta	360
tctattcagt gaagtataaa cgaaagagca tttttcaaaa caa atg gta tgt aat	415
	Met Val Cys Asn
	1
att ttt gtc ttc ttt agg gct ctg gaa ctt cat cca ttc tct atg aaa	463
Ile Phe Val Phe Phe Arg Ala Leu Glu Leu His Pro Phe Ser Met Lys	
5 10 15 20	
cct ctt ctg agg cgg gcg atg gcc tat gaa act cta gag cag tat ggg	511
Pro Leu Leu Arg Arg Ala Met Ala Tyr Glu Thr Leu Glu Gln Tyr Gly	
21 26 31 36	
aaa gct tat gtg gat tat aaa aca gtg ttg cag ata gac tgt gga ctc	559
Lys Ala Tyr Val Asp Tyr Lys Thr Val Leu Gln Ile Asp Cys Gly Leu	
37 42 47 52	
cag cta gca aat gac agt gtt aac agg cta tca aga att tta atg gag	607
Gln Leu Ala Asn Asp Ser Val Asn Arg Leu Ser Arg Ile Leu Met Glu	
53 58 63 68	
ctg gat gga cca aat tgg cgg gag aag ctg tca ctt att cct gct gtg	655
Leu Asp Gly Pro Asn Trp Arg Glu Lys Leu Ser Leu Ile Pro Ala Val	
69 74 79 84	
cct gct tct gtg cca ctg caa gct tgg cat ccg gca aaa gag atg atc	703
Pro Ala Ser Val Pro Leu Gln Ala Trp His Pro Ala Lys Glu Met Ile	
85 90 95 100	
tca aaa caa gca gga gac tcc agc agc cat cgc cag cag ggc atc aca	751
Ser Lys Gln Ala Gly Asp Ser Ser Ser His Arg Gln Gln Gly Ile Thr	
101 106 111 116	
gat gaa aaa aca ttt aaa gcc ctt aag gaa gaa gga aat caa tgt gta	799
Asp Glu Lys Thr Phe Lys Ala Leu Lys Glu Glu Gly Asn Gln Cys Val	
117 122 127 132	
aat gac aaa aac tat aaa gac gcc ctc agt aaa tac agc gaa tgc tta	847
Asn Asp Lys Asn Tyr Lys Asp Ala Leu Ser Lys Tyr Ser Glu Cys Leu	
133 138 143 148	
aag att aac aat aag gaa tgt gcc ata tat aca aac aga gct ctc tgt	895
Lys Ile Asn Asn Lys Glu Cys Ala Ile Tyr Thr Asn Arg Ala Leu Cys	
149 154 159 164	
tac ttg aag ctg tgc cag ttt gaa gaa qca aag cag gac tgt gat cag	943

Tyr Leu Lys Leu Cys Gln Phe Glu Glu Ala Lys Gln Asp Cys Asp Gln	
165	170 175 180
gca ctt cag cta gct gat ggg aac gtg aaa gcc ttc tat aga cga gct	991
Ala Leu Gln Leu Ala Asp Gly Asn Val Lys Ala Phe Tyr Arg Arg Ala	
181	186 191 196
ctg gct cat aaa gga ctc aag aat tat cag aaa agc tta att gat ctc	1039
Leu Ala His Lys Gly Leu Lys Asn Tyr Gln Lys Ser Leu Ile Asp Leu	
197	202 207 212
aat aaa gtt atc cta cta gat cca agt att att gag gca aag atg gaa	1087
Asn Lys Val Ile Leu Leu Asp Pro Ser Ile Ile Glu Ala Lys Met Glu	
213	218 223 228
ctg gaa gag gta act aga ctc ctt aat ctt aag gat aag aca gca cca	1135
Leu Glu Glu Val Thr Arg Leu Leu Asn Leu Lys Asp Lys Thr Ala Pro	
229	234 239 244
ttc aac aaa gaa aag gag aga agg aaa att gag att caa gag gtg aat	1183
Phe Asn Lys Glu Lys Glu Arg Arg Lys Ile Glu Ile Gln Glu Val Asn	
245	250 255 260
gaa ggc aag gag gag cct gga aga cct gca ggg gag gtc tcc acg gga	1231
Glu Gly Lys Glu Glu Pro Gly Arg Pro Ala Gly Glu Val Ser Thr Gly	
261	266 271 276
tgc ctt gct tct gag aag gga ggc aaa agc agc agg tca cca gaa gac	1279
Cys Leu Ala Ser Glu Lys Gly Gly Lys Ser Ser Arg Ser Pro Glu Asp	
277	282 287 292
cct gag aaa ctt ccg ata gcc aag cct att aat gcc tat gaa ttt ggt	1327
Pro Glu Lys Leu Pro Ile Ala Lys Pro Ile Asn Ala Tyr Glu Phe Gly	
293	298 303 308
cag att ata aat gct ctc agt acc agg aag gat aaa gaa gcc tgt gca	1375
Gln Ile Ile Asn Ala Leu Ser Thr Arg Lys Asp Lys Glu Ala Cys Ala	
309	314 319 324
cat ctt tta gcc atc act gca cca aaa gat ttg ccg atg ttt tta agt	1423
His Leu Leu Ala Ile Thr Ala Pro Lys Asp Leu Pro Met Phe Leu Ser	
325	330 335 340
aac aaa ctt gaa ggg gat aca ttc ctt ctc ctc att cag tct ctg aaa	1471
Asn Lys Leu Glu Gly Asp Thr Phe Leu Leu Leu Ile Gln Ser Leu Lys	
341	346 351 356
aat aat ctt att gaa aaa gat ccc tca ttg gtg tat cag cat ctt tta	1519
Asn Asn Leu Ile Glu Lys Asp Pro Ser Leu Val Tyr Gln His Leu Leu	
357	362 367 372
tac ctg agt aaa gca gaa agg ttt aag atg atg ttg aca cta att agc	1567
Tyr Leu Ser Lys Ala Glu Arg Phe Lys Met Met Leu Thr Leu Ile Ser	
373	378 383 388
aag ggc caa aag gag cta att gaa cag ctg ttt gag gac ctt tcg gac	1615
Lys Gly Gln Lys Glu Leu Ile Glu Gln Leu Phe Glu Asp Leu Ser Asp	

389	394	399	404	
aca cca aac aac cat ttt act tta gaa gat ata cag gcc cta aaa agg				1663
Thr Pro Asn Asn His Phe Thr Leu Glu Asp Ile Gln Ala Leu Lys Arg				
405	410	415	420	
cag tat gag ctt taa atcaagataa ttgtagatt tcttccatgc atgtatgtgt				1718
Gln Tyr Glu Leu *				
421				
tccaggaatg ttaatgagat ggtattgtaa aagagttgca tggataaaac ttggcctaga				1778
aaagtttggg ctgcactata aaacatttta cttattttcc tacatagaac atgtatatcc				1838
tacaatctgc tttttattag ttgtaaatat tttcttatgt accagaacca aataagtata				1898
tttagaactt gttaaaaata cattttaatt tatgatatac atattatttt aattacttgt				1958
taaaattttg agttaagttg catttctttg ggctatgaag gagtcctctt aagtttgata				2018
gaaatgaatt tcttgtaaca ttctttttta aaagtggaag tcattaacag tgattattat				2078
atcacttata tcttgctaag atacacataa atcccatttt gtactagtac ctgtggatta				2138
cagtcagtta aaatgaaatg caacactgaa gtctataaca tgaaatgatt attaaattgt				2198
ttattaatth agagctataa gaggaactta ttttttctaa tacggaagca ttgcctaata				2258
attaagaaca aaaattgcc aaaaatttcta ccacttttta ctagatttta aaaagctact				2318
ttcttttata ttgcctatat aagcaaaaaa ccaaccactg tattaaagca aactaagcct				2378
gcatttatat ctgaattatt acctccatat ttaccaaac atttgaatgt ccccttccc				2438
ccttttttgt tttctgcttt tatgactgta tttattcctt tactgtaaaa gaatatgaag				2498
aactcataca tgttgaaagc tcctttgttg actgggtcaa agtgaaggaa tttcaatctc				2558
caaaaaaaaaaaa aaa				2571

<210> 303
 <211> 2089
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (765)..(1190)

<220>
 <221> misc_feature
 <222> (1)...(2089)
 <223> n = a,t,c or g

<400> 303

atttggccct cgagcagcaa ttcggcacga gtgaatggca tttgtatatt aaaacacttt	60
tttaaaggac agttgaaaag ggcaagagga aaccagggca gttctagagg agtgctggtg	120
actggatagc agttttaagt ggcgttcacc tagtcaacac gaccgcgtgt gttgcccctg	180
ccctgggctc cccgccatga catcttcact ttgcagcttg tgetgagact gacccaagtg	240
cagctagcac tgggacacag atccttgtct tcagcacctt ccaaggagcc aactttttatt	300
ccctttctc tctcccctcc ccacctcgct tcttccaat ttagtaactt agatgcttcc	360
agcacatacg taggtagcta cccagccgg tttggattac aggcctgtgc tggaacatca	420
tctcagttgg ccaccttcct ggcaggctgt agacctgaca ttttgagaca agcctagagt	480
caggagcagg gactttgact cttaggaaga gcacacatga gggcaaggct gctggcagac	540
gtctccattg tccttatggt gtctgtgttg ttttttttt tttttattga ccatggtgat	600
tattttttta aaccatcggt aatatactga agtgagctat agcacatata atgtgcttag	660
tttgttttatt tttctccatc tccccttggc ttcttagagt ttggacatat tccaggctaa	720
atgctttttac tcaagactac agaaagggtt gaagtagtgt gtgc atg gca tgc acg	776
Met Ala Cys Thr	
1	
tat gta agt aat ctg ggg aag aag caa aga tct gtt tca ttc tta gcc	824
Tyr Val Ser Asn Leu Gly Lys Lys Gln Arg Ser Val Ser Phe Leu Ala	
5 10 15 20	
tca ggc ctc atg agg gtc tcc aca ggg ccg gag ctc agg tta cac cac	872
Ser Gly Leu Met Arg Val Ser Thr Gly Pro Glu Leu Arg Leu His His	
21 26 31 36	
tcc ttc gtc ctt aca gga gat gta ggg aga aga atc tgc agg ctg ctt	920
Ser Phe Val Leu Thr Gly Asp Val Gly Arg Arg Ile Cys Arg Leu Leu	
37 42 47 52	
gta gga ctg ttc acc aag ggg gat acc agc agc aag aga gtg cac ccg	968
Val Gly Leu Phe Thr Lys Gly Asp Thr Ser Ser Lys Arg Val His Pro	
53 58 63 68	
ttt agc cct gga ccc tgt ttc tta ctg tgt gac ttg gct aga gtt ggg	1016
Phe Ser Pro Gly Pro Cys Phe Leu Leu Cys Asp Leu Ala Arg Val Gly	
69 74 79 84	
agt tcc ccc aaa ata aac gtg tcc cca ttt tac cag aac caa acc tca	1064
Ser Ser Pro Lys Ile Asn Val Ser Pro Phe Tyr Gln Asn Gln Thr Ser	
85 90 95 100	
aca cag cga agc tgt act gtc ttt gtg tgg caa aga tgt tcc ctt gta	1112
Thr Gln Arg Ser Cys Thr Val Phe Val Trp Gln Arg Cys Ser Leu Val	
101 106 111 116	

gccgccggc	atg agc cac atc cag atc ccg ccg ggg ctc acg gag ctg	228
	Met Ser His Ile Gln Ile Pro Pro Gly Leu Thr Glu Leu	
	1 5 10	
ctg cag ggc tac acg gtg gag gtg ctg cga cag cag ccg cct gac ctc	276	
Leu Gln Gly Tyr Thr Val Glu Val Leu Arg Gln Gln Pro Pro Asp Leu		
14 19 24 29		
gtc gaa ttc gca gtg gag tac ttc acc cgc ctg cgc gag gcc cgc gcc	324	
Val Glu Phe Ala Val Glu Tyr Phe Thr Arg Leu Arg Glu Ala Arg Ala		
30 35 40 45		
cca gcc tca gtc ctg ccc gcc gcc acc cca cgc cag agc ctg ggc cac	372	
Pro Ala Ser Val Leu Pro Ala Ala Thr Pro Arg Gln Ser Leu Gly His		
46 51 56 61		
ccc ccg cca gaa ccc ggc ccg gac cgt gtc gcc gac gcc aaa ggg gac	420	
Pro Pro Pro Glu Pro Gly Pro Asp Arg Val Ala Asp Ala Lys Gly Asp		
62 67 72 77		
agc gag tcg gag gag gac gag gac ttg gaa gtt cca gtt cct agc aga	468	
Ser Glu Ser Glu Glu Asp Glu Asp Leu Glu Val Pro Val Pro Ser Arg		
78 83 88 93		
ttt aat aga cga gta tca gtc tgt gct gag acc tat aac cct gat gag	516	
Phe Asn Arg Arg Val Ser Val Cys Ala Glu Thr Tyr Asn Pro Asp Glu		
94 99 104 109		
gaa gag gaa gat aca gat cca agg gtg att cat cct aaa act gat gaa	564	
Glu Glu Glu Asp Thr Asp Pro Arg Val Ile His Pro Lys Thr Asp Glu		
110 115 120 125		
cag aga tgc aga ctt cag gaa gct tgc aaa gat att ctc ctt ttc aaa	612	
Gln Arg Cys Arg Leu Gln Glu Ala Cys Lys Asp Ile Leu Leu Phe Lys		
126 131 136 141		
aat ctt gat cag gaa cag ctt tct caa gtt ctc gat gcc atg ttt gaa	660	
Asn Leu Asp Gln Glu Gln Leu Ser Gln Val Leu Asp Ala Met Phe Glu		
142 147 152 157		
agg ata gtc aaa gct gat gag cat gtc att gac caa gga gat gat gga	708	
Arg Ile Val Lys Ala Asp Glu His Val Ile Asp Gln Gly Asp Asp Gly		
158 163 168 173		
gac aac ttt tat gtc ata gaa cgg gga act tat gac att tta gta aca	756	
Asp Asn Phe Tyr Val Ile Glu Arg Gly Thr Tyr Asp Ile Leu Val Thr		
174 179 184 189		
aaa gat aat caa acc cgc tct gtt ggt caa tat gac aac cgt ggc agt	804	
Lys Asp Asn Gln Thr Arg Ser Val Gly Gln Tyr Asp Asn Arg Gly Ser		
190 195 200 205		
ttt gga gaa cta gct ctg atg tac aac acc ccg aga gct gct acc att	852	
Phe Gly Glu Leu Ala Leu Met Tyr Asn Thr Pro Arg Ala Ala Thr Ile		
206 211 216 221		
gtt gct acc tca gaa ggc tcc ctt tgg gga ctg gac cgg gtg act ttt	900	

Val Ala Thr Ser Glu Gly Ser Leu Trp Gly Leu Asp Arg Val Thr Phe	
222 227 232 237	
aga aga atc ata gtg aaa aat aat gca aag aag agg aag atg ttt gaa	948
Arg Arg Ile Ile Val Lys Asn Asn Ala Lys Lys Arg Lys Met Phe Glu	
238 243 248 253	
tca ttt att gag tct gtg ccc ctc ctt aaa tca cta gag gtg tca gaa	996
Ser Phe Ile Glu Ser Val Pro Leu Leu Lys Ser Leu Glu Val Ser Glu	
254 259 264 269	
cga atg aag att gtg gat gta ata gga gag aag atc tat aag gat gga	1044
Arg Met Lys Ile Val Asp Val Ile Gly Glu Lys Ile Tyr Lys Asp Gly	
270 275 280 285	
gaa cgc ata atc act cag ggt gaa aag gct gat agc ttt tac atc ata	1092
Glu Arg Ile Ile Thr Gln Gly Glu Lys Ala Asp Ser Phe Tyr Ile Ile	
286 291 296 301	
gag tct ggc gaa gtg agc atc ttg att aga agc agg act aaa tca aac	1140
Glu Ser Gly Glu Val Ser Ile Leu Ile Arg Ser Arg Thr Lys Ser Asn	
302 307 312 317	
aag gat ggt ggg aac cag gag gtc gag att gcc cgc tgc cat aag ggg	1188
Lys Asp Gly Gly Asn Gln Glu Val Glu Ile Ala Arg Cys His Lys Gly	
318 323 328 333	
cag tac ttt gga gag ctt gcc ctg gtc acc aac aaa ccc aga gct gcc	1236
Gln Tyr Phe Gly Glu Leu Ala Leu Val Thr Asn Lys Pro Arg Ala Ala	
334 339 344 349	
tca gct tat gca gtt gga gat gtc aaa tgc tta gtt atg gat gta caa	1284
Ser Ala Tyr Ala Val Gly Asp Val Lys Cys Leu Val Met Asp Val Gln	
350 355 360 365	
gca ttc gag agg ctt ctg ggg ccc tgc atg gac atc atg aag agg aac	1332
Ala Phe Glu Arg Leu Leu Gly Pro Cys Met Asp Ile Met Lys Arg Asn	
366 371 376 381	
atc tca cac tat gag gaa cag ctg gtg aag atg ttt ggc tcc agc gtg	1380
Ile Ser His Tyr Glu Glu Gln Leu Val Lys Met Phe Gly Ser Ser Val	
382 387 392 397	
gat ctg ggc aac ctc ggg cag tag gtgtgccaca cccagagcc ttcttagtgt	1434
Asp Leu Gly Asn Leu Gly Gln *	
398 403	
gacaccaaaa ccttctgggc agccacagaa cacatacaga aaacagacat gacagaactg	1494
ttcctgccgt tgccgccact gctgccattg ctgtgggttat gggcatttag aaaacttgaa	1554
agtcagcact aaaggatggg cagagggttca acccacacct ccactttgct tctgaaggcc	1614
cattcattag accacttgta aagattactc caaccagtt tttatatctt tggttcaaaa	1674
cggcattgtct ctccaacaat ttaagtgcct gatacaaagt ccaaagtata aacatgctcc	1734

tttctctctt taaaaaaaaa aaa

1757

<210> 305
<211> 2080
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (518)..(1633)

<400> 305

agtcccggtcc ggaattcccg ggtcgaccca cgcgtccgca ggtggagggt ttgggccaga 60

tcctgggtca gggaccacat tgccagccag acgcctccct gtcccccgac cctcttttga 120

tgccctcagca agtgaagagg aggaagaaga ggaggaggag gaggatgaag atgaagagga 180

ggaagtggca gcttggaggc tgcccccaag atggagtcag ctgggaacct cccagcggcc 240

ccgcccttcc cgcgccactc atcgaaaaac ctgctcacag cgcgcgccgc gagccatgag 300

agccttccgg atgctgctct actcaaaaag cacctcgctg acattccact ggaagctttg 360

ggggcgccac cggggcgggc ggcggggcct cgcacacccc aagaaccatc tttcacccca 420

gcaagggggg gcgacgccac aggtgccatc cccctgttgt cgttttgact cccccgggg 480

gccacctcca ccccggtgg gtctgctagg tgctctc atg gct gag gat ggg gtg 535
Met Ala Glu Asp Gly Val

1

aga ggg tct cca cca gtg ccc tct ggg ccc ccc atg gag gaa gat gga 583
Arg Gly Ser Pro Pro Val Pro Ser Gly Pro Pro Met Glu Glu Asp Gly
7 12 17 22

ctc agg tgg act cca aag tct cct ctg gac cct gac tcg ggc ctc ctt 631
Leu Arg Trp Thr Pro Lys Ser Pro Leu Asp Pro Asp Ser Gly Leu Leu
23 28 33 38

tca tgt act ctg ccc aac ggt ttt ggg gga caa tct ggg cca gaa ggg 679
Ser Cys Thr Leu Pro Asn Gly Phe Gly Gly Gln Ser Gly Pro Glu Gly
39 44 49 54

gag cgc agc ttg gca ccc cct gat gcc agc atc ctc atc agc aat gtg 727
Glu Arg Ser Leu Ala Pro Pro Asp Ala Ser Ile Leu Ile Ser Asn Val
55 60 65 70

tgc agc atc ggg gac cat gtg gcc cag gag ctt ttt cag ggc tca gat 775
Cys Ser Ile Gly Asp His Val Ala Gln Glu Leu Phe Gln Gly Ser Asp
71 76 81 86

ttg ggc atg gca gaa gag gca gag agg cct ggg gag aaa gcc ggc cag 823
Leu Gly Met Ala Glu Glu Ala Glu Arg Pro Gly Glu Lys Ala Gly Gln

87	92	97	102	
cac agc ccc ctg cga gag gag cat gtg acc tgc gta cag agc atc ttg His Ser Pro Leu Arg Glu Glu His Val Thr Cys Val Gln Ser Ile Leu 103 108 113 118				871
gac gaa ttc ctt caa acg tat ggc agc ctc ata ccc ctc agc act gat Asp Glu Phe Leu Gln Thr Tyr Gly Ser Leu Ile Pro Leu Ser Thr Asp 119 124 129 134				919
gag gta gta gag aag ctg gag gac att ttc cag cag gag ttt tcc acc Glu Val Val Glu Lys Leu Glu Asp Ile Phe Gln Gln Glu Phe Ser Thr 135 140 145 150				967
cct tcc agg aag ggc ctg gtg ttg cag ctg atc cag tct tac cag cgg Pro Ser Arg Lys Gly Leu Val Leu Gln Leu Ile Gln Ser Tyr Gln Arg 151 156 161 166				1015
atg cca ggc aat gcc atg gtg agg ggc ttc cga gtg gct tat aag cgg Met Pro Gly Asn Ala Met Val Arg Gly Phe Arg Val Ala Tyr Lys Arg 167 172 177 182				1063
cac gtg ctg acc atg gat gac ttg ggg acc ttg tat gga cag aac tgg His Val Leu Thr Met Asp Asp Leu Gly Thr Leu Tyr Gly Gln Asn Trp 183 188 193 198				1111
ctc aat gac cag gtg atg aac atg tat gga gac ctg gtc atg gac aca Leu Asn Asp Gln Val Met Asn Met Tyr Gly Asp Leu Val Met Asp Thr 199 204 209 214				1159
gtc cct gaa aag gtg cat ttc ttc aat agt ttc ttc tat gat aaa ctc Val Pro Glu Lys Val His Phe Phe Asn Ser Phe Phe Tyr Asp Lys Leu 215 220 225 230				1207
cgt acc aag ggt tat gat ggg gtg aaa agg tgg acc aaa aac gtg gac Arg Thr Lys Gly Tyr Asp Gly Val Lys Arg Trp Thr Lys Asn Val Asp 231 236 241 246				1255
atc ttc aat aag gag cta ctg cta atc ccc atc cac ctg gag gtg cat Ile Phe Asn Lys Glu Leu Leu Leu Ile Pro Ile His Leu Glu Val His 247 252 257 262				1303
tgg tcc ctc atc tct gtt gat gtg agg cga cgc acc atc acc tat ttt Trp Ser Leu Ile Ser Val Asp Val Arg Arg Arg Thr Ile Thr Tyr Phe 263 268 273 278				1351
gac tgc cag cgt acc cta aac cgc cgc tgc cct aag cat att gcc aag Asp Ser Gln Arg Thr Leu Asn Arg Arg Cys Pro Lys His Ile Ala Lys 279 284 289 294				1399
tat cta cag gca gag gcg gta aag aaa gac cga ctg gat ttc cac cag Tyr Leu Gln Ala Glu Ala Val Lys Lys Asp Arg Leu Asp Phe His Gln 295 300 305 310				1447
ggc tgg aaa ggt tac ttc aaa atg aat gtg gcc agg cag aat aat gac Gly Trp Lys Gly Tyr Phe Lys Met Asn Val Ala Arg Gln Asn Asn Asp 311 316 321 326				1495

agt gac tgt ggt gct ttt gtg ttg cag tac tgc aag cat ctg gcc ctg 1543
 Ser Asp Cys Gly Ala Phe Val Leu Gln Tyr Cys Lys His Leu Ala Leu
 327 332 337 342

tct cag cca ttc agc ttc acc cag cag gac atg ccc aaa ctt cgt cgg 1591
 Ser Gln Pro Phe Ser Phe Thr Gln Gln Asp Met Pro Lys Leu Arg Arg
 343 348 353 358

cag atc tac aag gag ctg tgt cac tgc aaa ctc act gtg tga gcctcgt 1640
 Gln Ile Tyr Lys Glu Leu Cys His Cys Lys Leu Thr Val *
 359 364 369

acccagacc ccaagcccat aaatgggaag ggagacatgg gagtcccttc ccaagaaact 1700

ccagttcctt tcctctcttg cctcttccca ctcacttccc ttggttttt catatttaaa 1760

tggttcaatt tctgtatttt tttttctttg agagaataact tgttgatttc tgatgtgcag 1820

ggggtggcta cagaaaagcc cctttcttcc tctgtttgca ggggagtgtg gccctgtggc 1880

ctgggtggag cagtcacct ccccttccc cgtgcaggga gcaggaaatc agtgctgggg 1940

gtgggtggcg gacaatagga tcaactgcctg ccagatcttc aaacttttat atatatatat 2000

atatatatat atatatatat aaaaatatat aaatgccacg gtcctgctct ggtcaataaa 2060

ggatcctttg ttgatacgta 2080

<210> 306
 <211> 2029
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (518)..(1582)

<400> 306
 agtcccgtcc ggaattcccg ggtcgacca cgcgtccgca ggtggagggt ttgggccaga 60
 tcctgggtca gggaccacat tgccagccag acgcctccct gtcccccgac cctcttttga 120
 tgccctcagca agtgaagagg aggaagaaga ggaggaggag gaggatgaag atgaagagga 180
 ggaagtggca gcttggaggc tgcccccaag atggagtcag ctgggaacct ccagcggcc 240
 ccgccccttc cgcgccactc atcgaaaaac ctgctcacag cgccgcgccc gagccatgag 300
 agccttcccg atgctgctct actcaaaaag cacctcgtg acattccact ggaagctttg 360
 ggggcccac cggggccggc ggcggggcct cgcacacccc aagaaccatc tttcaccca 420
 gcaagggggg gcgaogccac aggtgccatc cccctgttgt cgttttgact cccccgggg 480

gccacctcca ccccggtctg gtctgctagg tgctctc atg gct gag gat ggg gtg 535
Met Ala Glu Asp Gly Val

1

aga ggg tct cca cca gtg ccc tct ggg ccc ccc atg gag gaa gat gga 583
Arg Gly Ser Pro Pro Val Pro Ser Gly Pro Pro Met Glu Glu Asp Gly
7 12 17 22

ctc agg tgg act cca aag tct cct ctg gac cct gac tcg ggc ctc ctt 631
Leu Arg Trp Thr Pro Lys Ser Pro Leu Asp Pro Asp Ser Gly Leu Leu
23 28 33 38

tca tgt act ctg ccc aac ggt ttt ggg gga caa tct ggg cca gaa ggg 679
Ser Cys Thr Leu Pro Asn Gly Phe Gly Gly Gln Ser Gly Pro Glu Gly
39 44 49 54

gag cgc agc ttg gca ccc cct gat gcc agc atc ctc atc agc aat gtg 727
Glu Arg Ser Leu Ala Pro Pro Asp Ala Ser Ile Leu Ile Ser Asn Val
55 60 65 70

tgc agc atc ggg gac cat gtg gcc cag gag ctt ttt cag ggc tca gat 775
Cys Ser Ile Gly Asp His Val Ala Gln Glu Leu Phe Gln Gly Ser Asp
71 76 81 86

ttg ggc atg gca gaa gag gca gag agg cct ggg gag aaa gcc ggc cag 823
Leu Gly Met Ala Glu Glu Ala Glu Arg Pro Gly Glu Lys Ala Gly Gln
87 92 97 102

cac agc ccc ctg cga gag gag cat gtg acc tgc gta cag agc atc ttg 871
His Ser Pro Leu Arg Glu Glu His Val Thr Cys Val Gln Ser Ile Leu
103 108 113 118

gac gaa ttc ctt caa acg tat ggc agc ctc ata ccc ctc agc act gat 919
Asp Glu Phe Leu Gln Thr Tyr Gly Ser Leu Ile Pro Leu Ser Thr Asp
119 124 129 134

gag gta gta gag aag ctg gag gac att ttc cag cag gag ttt tcc acc 967
Glu Val Val Glu Lys Leu Glu Asp Ile Phe Gln Gln Glu Phe Ser Thr
135 140 145 150

cct tcc agg aag ggc ctg gtg ttg cag ctg atc cag tct tac cag cgg 1015
Pro Ser Arg Lys Gly Leu Val Leu Gln Leu Ile Gln Ser Tyr Gln Arg
151 156 161 166

atg cca ggc aat gcc atg gtg agg ggc ttc cga gtg gct tat aag cgg 1063
Met Pro Gly Asn Ala Met Val Arg Gly Phe Arg Val Ala Tyr Lys Arg
167 172 177 182

cac gtg ctg acc atg gat gac ttg ggg acc ttg tat gga cag aac tgg 1111
His Val Leu Thr Met Asp Asp Leu Gly Thr Leu Tyr Gly Gln Asn Trp
183 188 193 198

ctc aat gac cag gtg atg aac atg tat gga gac ctg gtc atg gac aca 1159
Leu Asn Asp Gln Val Met Asn Met Tyr Gly Asp Leu Val Met Asp Thr
199 204 209 214

gtc cct gaa aag gtg cat ttc ttc aat agt ttc ttc tat gat aaa ctc	1207
Val Pro Glu Lys Val His Phe Phe Asn Ser Phe Phe Tyr Asp Lys Leu	
215 220 225 230	
cgt acc aag ggt tat gat ggg gtg aaa agg tgg acc aaa aac gtg gac	1255
Arg Thr Lys Gly Tyr Asp Gly Val Lys Arg Trp Thr Lys Asn Val Asp	
231 236 241 246	
atc ttc aat aag gag cta ctg cta atc ccc atc cac ctg gag gtg cat	1303
Ile Phe Asn Lys Glu Leu Leu Leu Ile Pro Ile His Leu Glu Val His	
247 252 257 262	
tgg tcc ctc atc tct gtt gat gtg agg cga cgc acc atc acc tat ttt	1351
Trp Ser Leu Ile Ser Val Asp Val Arg Arg Arg Thr Ile Thr Tyr Phe	
263 268 273 278	
gac tcg cag cgt acc cta aac cgc cgc tgc cct aag cat att gcc aag	1399
Asp Ser Gln Arg Thr Leu Asn Arg Arg Cys Pro Lys His Ile Ala Lys	
279 284 289 294	
tat cta cag gca gag gcg gta aag aaa gac cga ctg gat ttc cac cag	1447
Tyr Leu Gln Ala Glu Ala Val Lys Lys Asp Arg Leu Asp Phe His Gln	
295 300 305 310	
ggc tgg aaa ggt tac ttc aaa atg tac tgc aag cat ctg gcc ctg tct	1495
Gly Trp Lys Gly Tyr Phe Lys Met Tyr Cys Lys His Leu Ala Leu Ser	
311 316 321 326	
cag cca ttc agc ttc acc cag cag gac atg ccc aaa ctt cgt cgg cag	1543
Gln Pro Phe Ser Phe Thr Gln Gln Asp Met Pro Lys Leu Arg Arg Gln	
327 332 337 342	
atc tac aag gag ctg tgt cac tgc aaa ctc act gtg tga gcctcgtagc	1592
Ile Tyr Lys Glu Leu Cys His Cys Lys Leu Thr Val *	
343 348 353	
ccagacccca agcccataaa tgggaagggga gacatgggag tcccttccca agaaactcca	1652
gttcctttcc tctcttgcc tttccactc acttcccttt gggttttcat atttaaatgt	1712
ttcaatttct gtattttttt ttctttgaga gaataacttgt tgatttctga tgtgcagggg	1772
gtggctacag aaaagccct ttcttccctc gtttgagggg gagggtggcc ctgtggcctg	1832
gggtggagcag tcactctccc cttccccgt gcagggagca ggaaatcagt gctgggggtg	1892
gtgggcggac aataggatca ctgcctgcca gatottcaaa cttttatata tatatatata	1952
tatatatata tatatatataa aatatataaa tgccacgggc ctgctctggt caataaagga	2012
tcctttgttg atacgta	2029

<210> 307
<211> 2982

```
<220>
<221> CDS
<222> (198)..(2474)
```

cqgaattccc gqgtcgaacga ttctgtgcga tggcgcgacc tcggctcact gcaagctccg 60

aatttttttgt attttttagta qggacggggt ttcaccatgt tggtcaggct ggtctcaaac 180

att gga gcc tac gat cag cag ata tgg gaa aag tca atc gaa cag act 278
Ile Gly Ala Tyr Asp Gln Gln Ile Trp Glu Lys Ser Ile Glu Gln Thr
12 17 22 27

cga gac ttg att gac gtt gac tta atc aga ggg tca aca ttt gcc aaa 374
Pro Asp Leu Ile Asp Val Asp Leu Ile Arg Gly Ser Thr Phe Ala Lys
44 49 54 59

cga gtt gta ttt ttt cca ttg ttc agc aat tgg tgg att cag gtt acc 470
Arg Val Val Phe Phe Pro Leu Phe Ser Asn Trp Trp Ile Gln Val Thr
76 81 86 91

ata gca att gtc tta tat ttg atg atg cct att gtg aac ata agt gaa 566
Ile Ala Ile Val Leu Tyr Leu Met Met Pro Ile Val Asn Ile Ser Glu
108 113 118 123

```

caa att gtg tct act cag ata aca aga cca tca gga aac aat gga aat      662
Gln Ile Val Ser Thr Gln Ile Thr Arg Pro Ser Gly Asn Asn Gly Asn
140                      145                      150                      155

```

1085

gaa aat gga aat aac tcc tct gat aaa gtc aga gga ata gaa act ttg	758
Glu Asn Gly Asn Asn Ser Ser Asp Lys Val Arg Gly Ile Glu Thr Leu	
172 177 182 187	
gaa tct gta ccc att att ggt ggt ttt tgg gag act atc ttt ggc aac	806
Glu Ser Val Pro Ile Ile Gly Gly Phe Trp Glu Thr Ile Phe Gly Asn	
188 193 198 203	
agg att aaa aga gta aaa tta ata tct aac aaa ggg act gaa act gac	854
Arg Ile Lys Arg Val Lys Leu Ile Ser Asn Lys Gly Thr Glu Thr Asp	
204 209 214 219	
aat gac cca agt tgt gtc cat cct atc att aag agg aga caa tgt cga	902
Asn Asp Pro Ser Cys Val His Pro Ile Ile Lys Arg Arg Gln Cys Arg	
220 225 230 235	
cca gag att aga atg tgc caa aca aga gag aaa cca aaa ttt tca gat	950
Pro Glu Ile Arg Met Cys Gln Thr Arg Glu Lys Pro Lys Phe Ser Asp	
236 241 246 251	
gga gaa aag tgc cgt agg gag gct ttt agg cgt ttg ggt aat ggg gtg	998
Gly Glu Lys Cys Arg Arg Glu Ala Phe Arg Arg Leu Gly Asn Gly Val	
252 257 262 267	
tct gat gac ctg tca agt gaa gaa gat ggt gaa gca cgg aca cag atg	1046
Ser Asp Asp Leu Ser Ser Glu Glu Asp Gly Glu Ala Arg Thr Gln Met	
268 273 278 283	
ata tta ttg cgt agg agt gtg gaa ggg gcc tca agt gac aat ggt tgt	1094
Ile Leu Leu Arg Arg Ser Val Glu Gly Ala Ser Ser Asp Asn Gly Cys	
284 289 294 299	
gaa gtt aag aat aga aaa tca ata ctt tca agg cac cta aac tct cag	1142
Glu Val Lys Asn Arg Lys Ser Ile Leu Ser Arg His Leu Asn Ser Gln	
300 305 310 315	
gta aag aaa acc act aca agg tgg tgt cat att gtg cgg gat tca gat	1190
Val Lys Lys Thr Thr Thr Arg Trp Cys His Ile Val Arg Asp Ser Asp	
316 321 326 331	
agt ctg gct gaa tca gaa ttt gaa tca gca gcc ttc agc cag ggc tct	1238
Ser Leu Ala Glu Ser Glu Phe Glu Ser Ala Ala Phe Ser Gln Gly Ser	
332 337 342 347	
aga tcg ggt gtg agt ggt ggc tct cga agc ctc aac atg tca aga aga	1286
Arg Ser Gly Val Ser Gly Gly Ser Arg Ser Leu Asn Met Ser Arg Arg	
348 353 358 363	
gac tca gaa agc acc cgc cat gac tcg gag act gag gac atg tta tgg	1334
Asp Ser Glu Ser Thr Arg His Asp Ser Glu Thr Glu Asp Met Leu Trp	
364 369 374 379	
gac gac ctg cta cat ggc cca gag tgc cgg tca tct gtc acc agt gac	1382
Asp Asp Leu Leu His Gly Pro Glu Cys Arg Ser Ser Val Thr Ser Asp	
380 385 390 395	

agt gag ggg gcc cat gtg aat acc ctt cac tca ggg acc aaa cgt gac	1430
Ser Glu Gly Ala His Val Asn Thr Leu His Ser Gly Thr Lys Arg Asp	
396 401 406 411	
ccc aaa gag gat gtt ttt cag cag aat cat tta ttc tgg ctt cag aat	1478
Pro Lys Glu Asp Val Phe Gln Gln Asn His Leu Phe Trp Leu Gln Asn	
412 417 422 427	
tca agt cct tcc tct gat cga gtt agt gca ata atc tgg gag ggg aat	1526
Ser Ser Pro Ser Ser Asp Arg Val Ser Ala Ile Ile Trp Glu Gly Asn	
428 433 438 443	
gag tgc aaa aag atg gat atg tct gtg ttg gaa ata agt ggc atc atc	1574
Glu Cys Lys Lys Met Asp Met Ser Val Leu Glu Ile Ser Gly Ile Ile	
444 449 454 459	
atg agc agg gtc aat gcc tat cag caa gga gta ggt tat cag atg ctg	1622
Met Ser Arg Val Asn Ala Tyr Gln Gln Gly Val Gly Tyr Gln Met Leu	
460 465 470 475	
gga aat gtt gtc act att gga tta gca ttt ttt cca ttc tta cat cga	1670
Gly Asn Val Val Thr Ile Gly Leu Ala Phe Phe Pro Phe Leu His Arg	
476 481 486 491	
ctt ttc cgt gag aag agc ctt gac caa cta aag tcc att tca gct gag	1718
Leu Phe Arg Glu Lys Ser Leu Asp Gln Leu Lys Ser Ile Ser Ala Glu	
492 497 502 507	
gag atc ttg act ctc ttt tgt ggg gca cca cct gtt aca cct att att	1766
Glu Ile Leu Thr Leu Phe Cys Gly Ala Pro Pro Val Thr Pro Ile Ile	
508 513 518 523	
gtt ttg tcg ata att aat ttt ttt gaa aga ttg tgt ctt act tgg atg	1814
Val Leu Ser Ile Ile Asn Phe Phe Glu Arg Leu Cys Leu Thr Trp Met	
524 529 534 539	
ttt ttt ttc atg atg tgt gtg gca gag aga aca tat aaa cag aga ttt	1862
Phe Phe Phe Met Met Cys Val Ala Glu Arg Thr Tyr Lys Gln Arg Phe	
540 545 550 555	
tta ttt gca aaa ctc ttc agc cat att act tct gcc agg aaa gct agg	1910
Leu Phe Ala Lys Leu Phe Ser His Ile Thr Ser Ala Arg Lys Ala Arg	
556 561 566 571	
aaa tat gaa ata cct cat ttc aga ctt aag aag gtg gag aat att aaa	1958
Lys Tyr Glu Ile Pro His Phe Arg Leu Lys Lys Val Glu Asn Ile Lys	
572 577 582 587	
ata tgg tta tca ctg cgt tcc tat cta aag aga cgg ggg cca cag cgt	2006
Ile Trp Leu Ser Leu Arg Ser Tyr Leu Lys Arg Arg Gly Pro Gln Arg	
588 593 598 603	
tca gtt gat gtg gtt gta tcc tcg gtt ttc cta ctg aca ctt tcg att	2054
Ser Val Asp Val Val Val Ser Ser Val Phe Leu Leu Thr Leu Ser Ile	
604 609 614 619	
gct ttc att tgt tgt gct cag gtt ctc caa gga cat aaa act ttc ctg	2102

Ala Phe Ile Cys Cys Ala Gln Val Leu Gln Gly His Lys Thr Phe Leu	
620 625 630 635	
aat gat gct tat aac tgg gag ttt ttg atc tgg gaa aca gct tta cta	2150
Asn Asp Ala Tyr Asn Trp Glu Phe Leu Ile Trp Glu Thr Ala Leu Leu	
636 641 646 651	
ctt ttt tta ttg cgt ctg gcc tca ctg ggg tct gaa acc aat aag aaa	2198
Leu Phe Leu Leu Arg Leu Ala Ser Leu Gly Ser Glu Thr Asn Lys Lys	
652 657 662 667	
tac agc aat gtt tca ata tta ctt aca gaa cag att aat tta tat ctt	2246
Tyr Ser Asn Val Ser Ile Leu Leu Thr Glu Gln Ile Asn Leu Tyr Leu	
668 673 678 683	
aag atg gaa aaa aag cca aat aag aaa gaa cag ctt act cta gta aac	2294
Lys Met Glu Lys Lys Pro Asn Lys Lys Glu Gln Leu Thr Leu Val Asn	
684 689 694 699	
aat gta tta aag ctg tcc acc aag ttg ttg aaa gag ctg gac aca cca	2342
Asn Val Leu Lys Leu Ser Thr Lys Leu Leu Lys Glu Leu Asp Thr Pro	
700 705 710 715	
ttt aga ctc tat gga ctg aca atg aat ccc tta atc tac aat atc aca	2390
Phe Arg Leu Tyr Gly Leu Thr Met Asn Pro Leu Ile Tyr Asn Ile Thr	
716 721 726 731	
aga gta gtt atc ctt tct gct gtc tca ggt gtt ata agt gat ctt cta	2438
Arg Val Val Ile Leu Ser Ala Val Ser Gly Val Ile Ser Asp Leu Leu	
732 737 742 747	
gga ttt aat ata aga ctg tgg aaa att aaa tca taa gctg agttaaagtc	2488
Gly Phe Asn Ile Arg Leu Trp Lys Ile Lys Ser *	
748 753 758	
ctggactctc ccctggctgg tatcaaaact tacctatcaa ggaaagtgat gactgcagaa	2548
accagtgaga taccacactg cttgttcaca tgcacaggtg ctctcagctc tgccaaagcg	2608
aatgaatggt gtttccggag gagcaagtcc ttttccaact ggggtgtgcat gctaaaaacc	2668
tgtattttca tgcttttcaa acaacatgaa tagtcagctg actaaagact gtgtgtgttg	2728
tggtaacaca aagacaattt tgtaagtttg cgcttcagta ctgtgacagt tatgtttact	2788
ggacatagtc ttttgggcaa ctatgataga tgcccaaagc atgaagcaaa tatcttttat	2848
tggaatatg caaattcaat acttttccat tatagtctat agaactggag atttcatttc	2908
tctatcaaag agagatcaag cgaactattt taggttaaact ccgaataaaa gaactttact	2968
ggaaaaaaaaaaaa	2982

<210> 308

<211> 1354
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (226)..(1251)

<400> 308

```

ttctcccaat ctctatttca tcgttgctct gttctatttc ttacttctc tttatatact      60
cttcatacct ccactgtatc gcgaacacac aaaattgtac gcttggagta ccgttccgga      120
attcccgggt cgaccacgc gtccgggtga ggcggccgaa atcgtaggac ttccgaaagc      180
agcgggtggcg tttgcttcac tgcttgggaag tgtgagtgcg cgaag      atg cga aag      234
                                     Met Arg Lys
                                     1

gtg gtt ttg atc acc ggg gct agc agt ggc att ggc ctg gcc ctc tgc      282
Val Val Leu Ile Thr Gly Ala Ser Ser Gly Ile Gly Leu Ala Leu Cys
  4              9              14              19

aag cgg ctg ctg gcg gaa gat gat gag ctt cat ctg tgt ttg gcg tgc      330
Lys Arg Leu Leu Ala Glu Asp Asp Glu Leu His Leu Cys Leu Ala Cys
  20              25              30              35

agg aac atg agc aag gca gaa gct gtc tgt gct gct ctg ctg gcc tct      378
Arg Asn Met Ser Lys Ala Glu Ala Val Cys Ala Ala Leu Leu Ala Ser
  36              41              46              51

cac ccc act gct gag gtc acc att gtc cag gtg gat gtc agc aac ctg      426
His Pro Thr Ala Glu Val Thr Ile Val Gln Val Asp Val Ser Asn Leu
  52              57              62              67

cag tcg gtc ttc cgg gcc tcc aag gaa ctt aag caa agg ttt cag aga      474
Gln Ser Val Phe Arg Ala Ser Lys Glu Leu Lys Gln Arg Phe Gln Arg
  68              73              78              83

tta gac tgt ata tat cta aat gct ggg atc atg cct aat cca caa cta      522
Leu Asp Cys Ile Tyr Leu Asn Ala Gly Ile Met Pro Asn Pro Gln Leu
  84              89              94              99

aat atc aaa gca ctt ttc ttt ggc ctc ttt tca aga aaa gtg att cat      570
Asn Ile Lys Ala Leu Phe Phe Gly Leu Phe Ser Arg Lys Val Ile His
  100              105              110              115

atg ttc tcc aca gct gaa ggc ctg ctg acc cag ggt gat aag atc act      618
Met Phe Ser Thr Ala Glu Gly Leu Leu Thr Gln Gly Asp Lys Ile Thr
  116              121              126              131

gct gat gga ctt cag gag gtg ttt gag acc aat gtc ttt ggc cat ttt      666
Ala Asp Gly Leu Gln Glu Val Phe Glu Thr Asn Val Phe Gly His Phe
  132              137              142              147

atc ctg att cgg gaa ctg gag cct ctc ctc tgt cac agt gac aat cca      714
Ile Leu Ile Arg Glu Leu Glu Pro Leu Leu Cys His Ser Asp Asn Pro

```

148	153	158	163	
tct cag ctc atc tgg aca tca tct cgc agt gca agg aaa tct aat ttc				762
Ser Gln Leu Ile Trp Thr Ser Ser Arg Ser Ala Arg Lys Ser Asn Phe				
164	169	174	179	
agc ctc gag gac ttc cag cac agc aaa ggc aag gaa ccc tac agc tct				810
Ser Leu Glu Asp Phe Gln His Ser Lys Gly Lys Glu Pro Tyr Ser Ser				
180	185	190	195	
tcc aaa tat gcc act gac ctt ttg agt gtg gct ttg aac agg aac ttc				858
Ser Lys Tyr Ala Thr Asp Leu Leu Ser Val Ala Leu Asn Arg Asn Phe				
196	201	206	211	
aac cag cag ggt ctc tat tcc aat gtg gcc tgt cca ggt aca gca ttg				906
Asn Gln Gln Gly Leu Tyr Ser Asn Val Ala Cys Pro Gly Thr Ala Leu				
212	217	222	227	
acc aat ttg aca tat gga att ctg cct ccg ttt ata tgg acg ctg ttg				954
Thr Asn Leu Thr Tyr Gly Ile Leu Pro Pro Phe Ile Trp Thr Leu Leu				
228	233	238	243	
atg ccg gca ata ttg cta ctt cgc ttt ttt gca aat gca ttc act ttg				1002
Met Pro Ala Ile Leu Leu Leu Arg Phe Phe Ala Asn Ala Phe Thr Leu				
244	249	254	259	
aca cca tat aat gga aca gaa gct ctg gta tgg ctt ttc cac caa aag				1050
Thr Pro Tyr Asn Gly Thr Glu Ala Leu Val Trp Leu Phe His Gln Lys				
260	265	270	275	
cct gaa tct ctc aat cct ctg atc aaa tat ctg agt gcc acc act ggc				1098
Pro Glu Ser Leu Asn Pro Leu Ile Lys Tyr Leu Ser Ala Thr Thr Gly				
276	281	286	291	
ttt gga aga aat tat att atg acc cag aag atg gac cta gat gaa gac				1146
Phe Gly Arg Asn Tyr Ile Met Thr Gln Lys Met Asp Leu Asp Glu Asp				
292	297	302	307	
act gct gaa aaa ttt tat caa aag tta ctg gaa ctg gaa aag cac att				1194
Thr Ala Glu Lys Phe Tyr Gln Lys Leu Leu Glu Leu Glu Lys His Ile				
308	313	318	323	
agg gtc act att caa aaa aca gat aat cag gcc agg ctc agt ggc tca				1242
Arg Val Thr Ile Gln Lys Thr Asp Asn Gln Ala Arg Leu Ser Gly Ser				
324	329	334	339	
tgc cta taa ttccagc actttgggag gccaaaggcag aaggatcact tgagaccagg				1298
Cys Leu *				
340				
agttcgagac cagcctgaga aacatagtga gcccttgtct ctacaaaaaa aaaaaa				1354

<210> 309

<211> 2769

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (248)..(2659)

<400> 309

```
cgctagcgtt taaacttaag cttggtaccg agctcggatc cactagtcca gtgtggtgga      60
attcatggcg gcgccctttg tctgctctgg agtgccgtcc ccggccttct cgcggccgtg      120
atgcacctcc ctctgcggtg gggtcgggga catggcaggt aatgagccgg acgaggggag      180
ccaagctgga gtttacacag gcaaactgtc agaaaagagt agcctgggct gtctggaaat      240
ctgagcc  atg gac ttt ccc cag cac agc cag cat gtc ttg gaa cag ctg      289
          Met Asp Phe Pro Gln His Ser Gln His Val Leu Glu Gln Leu
          1             5             10

aac cag cag cgg cag ctg ggg ctt ctc tgt gac tgc acc ttt gtg gtg      337
Asn Gln Gln Arg Gln Leu Gly Leu Leu Cys Asp Cys Thr Phe Val Val
  15             20             25             30

gac ggt gtt cac ttt aag gct cat aaa gca gtg ctg gcg gcc tgc agc      385
Asp Gly Val His Phe Lys Ala His Lys Ala Val Leu Ala Ala Cys Ser
  31             36             41             46

gag tac ttc aag atg ctc ttc gtg gac cag aag gac gtg gtg cac ctg      433
Glu Tyr Phe Lys Met Leu Phe Val Asp Gln Lys Asp Val Val His Leu
  47             52             57             62

gac atc agt aac gcg gca ggc ctg ggg cag gtg ctg gag ttt atg tac      481
Asp Ile Ser Asn Ala Ala Gly Leu Gly Gln Val Leu Glu Phe Met Tyr
  63             68             73             78

acg gcc aag ctg agc ctg agc cct gag aac gtg gat gat gtg ctg gcc      529
Thr Ala Lys Leu Ser Leu Ser Pro Glu Asn Val Asp Asp Val Leu Ala
  79             84             89             94

gtg gcc act ttc ctc caa atg cag gac atc atc acg gcc tgc cat gcc      577
Val Ala Thr Phe Leu Gln Met Gln Asp Ile Ile Thr Ala Cys His Ala
  95             100            105            110

ctc aag tca ctt gct gag ccg gct acc agc cct ggg gga aat gcg gag      625
Leu Lys Ser Leu Ala Glu Pro Ala Thr Ser Pro Gly Gly Asn Ala Glu
 111             116            121            126

gcc ttg gcc aca gaa gga ggg gac aag aga gcc aaa gag gag aag gtg      673
Ala Leu Ala Thr Glu Gly Gly Asp Lys Arg Ala Lys Glu Glu Lys Val
 127             132            137            142

gcc acc agc acg ctg agc agg ctg gag cag gca gga cgc agc aca ccc      721
Ala Thr Ser Thr Leu Ser Arg Leu Glu Gln Ala Gly Arg Ser Thr Pro
 143             148            153            158

ata ggc ccc agc agg gac ctc aag gag gag cgc ggc ggt cag gcc cag      769
```

Ile Gly Pro Ser Arg Asp Leu Lys Glu Glu Arg Gly Gly Gln Ala Gln	
159 164 169 174	
agc gcg gcc agc ggt gca gag cag aca gag aaa gcc gat gcg ccc cgg	817
Ser Ala Ala Ser Gly Ala Glu Gln Thr Glu Lys Ala Asp Ala Pro Arg	
175 180 185 190	
gag ccg ccg cct gtg gag ctc aag cca gac ccc acg agt ggc atg gct	865
Glu Pro Pro Pro Val Glu Leu Lys Pro Asp Pro Thr Ser Gly Met Ala	
191 196 201 206	
gcc gca gaa gct gag gcc gct ttg tcc gag agc tcg gag caa gaa atg	913
Ala Ala Glu Ala Glu Ala Ala Leu Ser Glu Ser Ser Glu Gln Glu Met	
207 212 217 222	
gag gtg gag ccc gcc cgg aaa ggg gaa gag gag caa aag gag caa gag	961
Glu Val Glu Pro Ala Arg Lys Gly Glu Glu Glu Gln Lys Glu Gln Glu	
223 228 233 238	
gag caa gag gag gag ggc gca ggg cca gct gag gtc aag gag gag ggt	1009
Glu Gln Glu Glu Glu Gly Ala Gly Pro Ala Glu Val Lys Glu Glu Gly	
239 244 249 254	
tcc cag ctg gag aac gga gag gcc ccc gag gag aac gag aat gag gag	1057
Ser Gln Leu Glu Asn Gly Glu Ala Pro Glu Glu Asn Glu Asn Glu Glu	
255 260 265 270	
tca gcg ggc aca gac tcg ggg cag gag ctc ggc tcc gag gcc cgg ggc	1105
Ser Ala Gly Thr Asp Ser Gly Gln Glu Leu Gly Ser Glu Ala Arg Gly	
271 276 281 286	
ctg cgc tca ggc acc tac ggc gac cgc acg gag tcc aag gcc tac ggc	1153
Leu Arg Ser Gly Thr Tyr Gly Asp Arg Thr Glu Ser Lys Ala Tyr Gly	
287 292 297 302	
tcc gtc atc cac aag tgc gag gac tgt ggg aag gag ttc acg cac acg	1201
Ser Val Ile His Lys Cys Glu Asp Cys Gly Lys Glu Phe Thr His Thr	
303 308 313 318	
ggg aac ttc aag cgg cac atc cgc atc cac acg ggg gag aag ccc ttc	1249
Gly Asn Phe Lys Arg His Ile Arg Ile His Thr Gly Glu Lys Pro Phe	
319 324 329 334	
tcg tgc cgg gag tgc agc aag gcc ttt tcc gac ccg gcc gcg tgc aag	1297
Ser Cys Arg Glu Cys Ser Lys Ala Phe Ser Asp Pro Ala Ala Cys Lys	
335 340 345 350	
gcc cat gag aag acg cac agc cct ctg aag ccc tac ggc tgc gag gag	1345
Ala His Glu Lys Thr His Ser Pro Leu Lys Pro Tyr Gly Cys Glu Glu	
351 356 361 366	
tgc ggg aag agc tac cgc ctc atc agc ctg ctg aac ctg cac aag aag	1393
Cys Gly Lys Ser Tyr Arg Leu Ile Ser Leu Leu Asn Leu His Lys Lys	
367 372 377 382	
cgg cac tcg ggc gag gcg cgc tac cgc tgc gag gac tgc ggc aag ctc	1441
Arg His Ser Gly Glu Ala Arg Tyr Arg Cys Glu Asp Cys Gly Lys Leu	

383	388	393	398	
ttc acc acc tcg ggc aac ctc aag cgc cac cag ctg gtg cac agc ggc				1489
Phe Thr Thr Ser Gly Asn Leu Lys Arg His Gln Leu Val His Ser Gly				
399	404	409	414	
gag aag ccc tac cag tgc gac tac tgc ggc cgc tcc ttc tcc gac ccc				1537
Glu Lys Pro Tyr Gln Cys Asp Tyr Cys Gly Arg Ser Phe Ser Asp Pro				
415	420	425	430	
act tcc aag atg cgc cac ctg gag acc cac gac acg gac aag gag cac				1585
Thr Ser Lys Met Arg His Leu Glu Thr His Asp Thr Asp Lys Glu His				
431	436	441	446	
aag tgc cca cac tgc gac aag aag ttc aac cag gta ggg aac ctg aag				1633
Lys Cys Pro His Cys Asp Lys Lys Phe Asn Gln Val Gly Asn Leu Lys				
447	452	457	462	
gcc cac ctg aag atc cac atc gct gac ggc ccc ctc aag tgc cga gag				1681
Ala His Leu Lys Ile His Ile Ala Asp Gly Pro Leu Lys Cys Arg Glu				
463	468	473	478	
tgt ggg aag cag ttc acc acc tca ggg aac ctg aag cgg cac ctt cgg				1729
Cys Gly Lys Gln Phe Thr Thr Ser Gly Asn Leu Lys Arg His Leu Arg				
479	484	489	494	
atc cac agc ggg gag aag ccc tac gtg tgc atc cac tgc cag cga cag				1777
Ile His Ser Gly Glu Lys Pro Tyr Val Cys Ile His Cys Gln Arg Gln				
495	500	505	510	
ttt gca gac ccc ggc gct ctg cag cgg cac gtc cgc att cac aca ggt				1825
Phe Ala Asp Pro Gly Ala Leu Gln Arg His Val Arg Ile His Thr Gly				
511	516	521	526	
gag aag cca tgc cag tgt gtg atg tgc ggt aag gcc ttc acc cag gcc				1873
Glu Lys Pro Cys Gln Cys Val Met Cys Gly Lys Ala Phe Thr Gln Ala				
527	532	537	542	
agc tcc ctc atc gcc cac gtg cgc cag cac acc ggg gag aag ccc tac				1921
Ser Ser Leu Ile Ala His Val Arg Gln His Thr Gly Glu Lys Pro Tyr				
543	548	553	558	
gtc tgc gag cgc tgc ggc aag aga ttc gtc cag tcc agc cag ttg gcc				1969
Val Cys Glu Arg Cys Gly Lys Arg Phe Val Gln Ser Ser Gln Leu Ala				
559	564	569	574	
aat cat att cgc cac cac gac aac atc cgc cca cac aag tgc agc gtg				2017
Asn His Ile Arg His His Asp Asn Ile Arg Pro His Lys Cys Ser Val				
575	580	585	590	
tgc agc aag gcc ttc gtg aac gtg ggg gac ctg tcc aag cac atc atc				2065
Cys Ser Lys Ala Phe Val Asn Val Gly Asp Leu Ser Lys His Ile Ile				
591	596	601	606	
att cac act gga gag aag cct tac ctg tgt gat aag tgt ggg cgt ggc				2113
Ile His Thr Gly Glu Lys Pro Tyr Leu Cys Asp Lys Cys Gly Arg Gly				
607	612	617	622	

ttc aac cgg gta gac aac ctg cgc tcc cac gtg aag acc gtg cac cag	2161
Phe Asn Arg Val Asp Asn Leu Arg Ser His Val Lys Thr Val His Gln	
623 628 633 638	
ggc aag gca ggc atc aag atc ctg gag ccc gag gag ggc agt gag gtc	2209
Gly Lys Ala Gly Ile Lys Ile Leu Glu Pro Glu Glu Gly Ser Glu Val	
639 644 649 654	
agc gtg gtc act gtg gat gac atg gtc acg ctg gct acc gag gca ctg	2257
Ser Val Val Thr Val Asp Asp Met Val Thr Leu Ala Thr Glu Ala Leu	
655 660 665 670	
gca gcg aca gcc gtc act cag ctc aca gtg gtg ccg gtg gga gct gca	2305
Ala Ala Thr Ala Val Thr Gln Leu Thr Val Val Pro Val Gly Ala Ala	
671 676 681 686	
gtg aca gcc gat gag acg gaa gtc ctg aag gcc gag atc agc aaa gct	2353
Val Thr Ala Asp Glu Thr Glu Val Leu Lys Ala Glu Ile Ser Lys Ala	
687 692 697 702	
gtg aag caa gtg cag gaa gaa gac ccc aac act cac atc ctc tac gcc	2401
Val Lys Gln Val Gln Glu Glu Asp Pro Asn Thr His Ile Leu Tyr Ala	
703 708 713 718	
tgt gac tcc tgt ggg gac aag ttt ctg gat gcc aac agc ctg gct cag	2449
Cys Asp Ser Cys Gly Asp Lys Phe Leu Asp Ala Asn Ser Leu Ala Gln	
719 724 729 734	
cat gtg cga atc cac aca gcc cag gca ctg gtc atg ttc cag aca gac	2497
His Val Arg Ile His Thr Ala Gln Ala Leu Val Met Phe Gln Thr Asp	
735 740 745 750	
gcg gac ttc tat cag cag tat ggg cca ggt ggc acg tgg cct gcc ggg	2545
Ala Asp Phe Tyr Gln Gln Tyr Gly Pro Gly Gly Thr Trp Pro Ala Gly	
751 756 761 766	
cag gtg ctg cag gct ggg gag ctg gtc ttc cgc cct cgc gac ggg gct	2593
Gln Val Leu Gln Ala Gly Glu Leu Val Phe Arg Pro Arg Asp Gly Ala	
767 772 777 782	
gag ggc cag ccc gca ctg gca gag acc tcc cct aca gct cct gaa tgt	2641
Glu Gly Gln Pro Ala Leu Ala Glu Thr Ser Pro Thr Ala Pro Glu Cys	
783 788 793 798	
ccc ccg cct gcc gag tga gctggc ggcccttctg actgtttatt taaggatgga	2695
Pro Pro Pro Ala Glu *	
799 804	
tggcaccctg gaaccgggaa ggggtggcctg ttccctagag agaataaatt ggattatttt	2755
ctaaaaaaaaaaaa	2769

<210> 310

<211> 5006
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (191)..(4699)

<400> 310

```

ttttgtcccc ggtccggact ctggcggggg agcccgcggc agtgggtggg gaagtcgaag      60
ccaagcgccg tatgggactt tgggcgctgt gagcggcggc gagcaggtgc tgctgcatga      120
ggaggcgggt gattctggct ttgtcagtct ctctcggtcg ggcccatctc tgagggacaa      180
ggacctggaa  atg gag gag cta atg ctg cag gat gag aca ctg ctg ggg      229
              Met Glu Glu Leu Met Leu Gln Asp Glu Thr Leu Leu Gly
                1             5             10

acc atg cag agc tac atg gat gcc tcc ctt atc tcc ctc att gag gat      277
Thr Met Gln Ser Tyr Met Asp Ala Ser Leu Ile Ser Leu Ile Glu Asp
  14             19             24             29

ttt ggg agc ctt gga gag gtt gaa atg tct ctt cca gat ccc tct tgg      325
Phe Gly Ser Leu Gly Glu Val Glu Met Ser Leu Pro Asp Pro Ser Trp
  30             35             40             45

gac ttc tcc cca ccc tct ttc tta gag acc tct tcc ccc aag ctt cct      373
Asp Phe Ser Pro Pro Ser Phe Leu Glu Thr Ser Ser Pro Lys Leu Pro
  46             51             56             61

agc tgg aga ccc cca aga tca aga cca cgc tgg ggc caa tcc cca cct      421
Ser Trp Arg Pro Pro Arg Ser Arg Pro Arg Trp Gly Gln Ser Pro Pro
  62             67             72             77

ccc cag cag cgc agt gat gga gaa gaa gag gag gag gtg gcc agc ttc      469
Pro Gln Gln Arg Ser Asp Gly Glu Glu Glu Glu Glu Val Ala Ser Phe
  78             83             88             93

agt ggc cag att ctt gcc ggg gag ctt gac aac tgt gtg agc agt atc      517
Ser Gly Gln Ile Leu Ala Gly Glu Leu Asp Asn Cys Val Ser Ser Ile
  94             99             104            109

ccg gac ttc ccc atg cat ttg gcc tgc cct gag gag gaa gat aaa gca      565
Pro Asp Phe Pro Met His Leu Ala Cys Pro Glu Glu Glu Asp Lys Ala
 110             115             120             125

aca gca gca gag atg gca gtg cca gca gct ggt gat gag agc atc tcc      613
Thr Ala Ala Glu Met Ala Val Pro Ala Ala Gly Asp Glu Ser Ile Ser
 126             131             136             141

tcc ctg agt gag ctg gtg cgg gcc atg cac cca tac tgc ctg ccc aac      661
Ser Leu Ser Glu Leu Val Arg Ala Met His Pro Tyr Cys Leu Pro Asn
 142             147             152             157

ctc acc cac ctg gca tca ctt gag gat gag ctt cag gag cag cca gat      709
Leu Thr His Leu Ala Ser Leu Glu Asp Glu Leu Gln Glu Gln Pro Asp

```


158	163	168	173	
gat ttg aca ctg cct gag ggc tgc gta gtg ctg gag att gtg ggg cag				757
Asp Leu Thr Leu Pro Glu Gly Cys Val Val Leu Glu Ile Val Gly Gln				
174	179	184	189	
gca gcc aca gct ggc gat gac ctg gag atc cca gtt gtg gtg cga cag				805
Ala Ala Thr Ala Gly Asp Asp Leu Glu Ile Pro Val Val Val Arg Gln				
190	195	200	205	
gtc tct cct gga ccc cgg cct gtg ctc ctg gat gac tcg cta gag act				853
Val Ser Pro Gly Pro Arg Pro Val Leu Leu Asp Asp Ser Leu Glu Thr				
206	211	216	221	
agt tct gcc ttg cag ctg ctt atg cct aca ctg gag tca gag aca gag				901
Ser Ser Ala Leu Gln Leu Leu Met Pro Thr Leu Glu Ser Glu Thr Glu				
222	227	232	237	
gct gct gtg ccc aag gta acc ctc tgc tct gag aaa gag ggg ttg tca				949
Ala Ala Val Pro Lys Val Thr Leu Cys Ser Glu Lys Glu Gly Leu Ser				
238	243	248	253	
ttg aac tca gag gag aag ctg gac tca gcc tgc tta ttg aag ccc agg				997
Leu Asn Ser Glu Glu Lys Leu Asp Ser Ala Cys Leu Leu Lys Pro Arg				
254	259	264	269	
gag gtc gtg gag ccg gtg gtg ccc aag gag cct cag aac cca cct gcc				1045
Glu Val Val Glu Pro Val Val Pro Lys Glu Pro Gln Asn Pro Pro Ala				
270	275	280	285	
aat gca gca cca ggt tcc cag aga gct cga aag ggc agg aag aag aag				1093
Asn Ala Ala Pro Gly Ser Gln Arg Ala Arg Lys Gly Arg Lys Lys Lys				
286	291	296	301	
agc aag gag cag cca gca gcc tgt gtg gaa ggc tat gcc agg agg ctg				1141
Ser Lys Glu Gln Pro Ala Ala Cys Val Glu Gly Tyr Ala Arg Arg Leu				
302	307	312	317	
agg tca tct tct cgc ggg cag tct act gta ggt aca gaa gtg acc tct				1189
Arg Ser Ser Ser Arg Gly Gln Ser Thr Val Gly Thr Glu Val Thr Ser				
318	323	328	333	
cag gta gac aac ttg cag aaa cag cct cag gaa gaa ctt caa aaa gag				1237
Gln Val Asp Asn Leu Gln Lys Gln Pro Gln Glu Glu Leu Gln Lys Glu				
334	339	344	349	
tct ggg cct ctc cag ggt aag ggg aag ccc cgg gct tgg gct cgg gcc				1285
Ser Gly Pro Leu Gln Gly Lys Gly Lys Pro Arg Ala Trp Ala Arg Ala				
350	355	360	365	
tgg gca gct gcc ttg gag aat tct agc cct aag aac ttg gag aga agt				1333
Trp Ala Ala Ala Leu Glu Asn Ser Ser Pro Lys Asn Leu Glu Arg Ser				
366	371	376	381	
gct gga caa agt agt cct gct aaa gaa ggc cct cta gac ctc tac cca				1381
Ala Gly Gln Ser Ser Pro Ala Lys Glu Gly Pro Leu Asp Leu Tyr Pro				
382	387	392	397	

aag ctg gct gac act atc caa acc aat cct ata cca acc cat ctc tca	1429
Lys Leu Ala Asp Thr Ile Gln Thr Asn Pro Ile Pro Thr His Leu Ser	
398 403 408 413	
ttg gtc gac tct gcc caa gcc agc ccc atg cca gtt gac tct gtt gaa	1477
Leu Val Asp Ser Ala Gln Ala Ser Pro Met Pro Val Asp Ser Val Glu	
414 419 424 429	
gct gat ccc act gca gtt ggc cct gtt cta gct ggc cct gta cct gtt	1525
Ala Asp Pro Thr Ala Val Gly Pro Val Leu Ala Gly Pro Val Pro Val	
430 435 440 445	
gac cct ggg ttg gtt gac ctt gct tca acc agc tca gaa ctg gtt gag	1573
Asp Pro Gly Leu Val Asp Leu Ala Ser Thr Ser Ser Glu Leu Val Glu	
446 451 456 461	
cct ctc ccg gct gag cca gtg ctg atc aac cca gtc ctg gct gac tca	1621
Pro Leu Pro Ala Glu Pro Val Leu Ile Asn Pro Val Leu Ala Asp Ser	
462 467 472 477	
gca gca gtt gac cct gca gtg gtt ccc atc tca gat aac ttg cca cca	1669
Ala Ala Val Asp Pro Ala Val Val Pro Ile Ser Asp Asn Leu Pro Pro	
478 483 488 493	
gtt gat gct gtc ccg tct ggc cca gca cca gtt gat cta gca ctg gtt	1717
Val Asp Ala Val Pro Ser Gly Pro Ala Pro Val Asp Leu Ala Leu Val	
494 499 504 509	
gac cct gtt cct aat gac ctg act cca gtt gac cca gtg cta gtt aag	1765
Asp Pro Val Pro Asn Asp Leu Thr Pro Val Asp Pro Val Leu Val Lys	
510 515 520 525	
tcc aga cca act gat ccc aga cgt ggt gca gtg tca tca gcc ctg ggg	1813
Ser Arg Pro Thr Asp Pro Arg Arg Gly Ala Val Ser Ser Ala Leu Gly	
526 531 536 541	
ggg tca gca ccc cag ctc ctc gtg gag tca gag tcc ttg gac cca cca	1861
Gly Ser Ala Pro Gln Leu Leu Val Glu Ser Glu Ser Leu Asp Pro Pro	
542 547 552 557	
aag acc atc atc cct gaa gtc aaa gag gtt gtg gat tct ctg aaa att	1909
Lys Thr Ile Ile Pro Glu Val Lys Glu Val Val Asp Ser Leu Lys Ile	
558 563 568 573	
gaa agt ggt acc agt gct aca acc cat gaa gcc aga cct cgg cct ctc	1957
Glu Ser Gly Thr Ser Ala Thr Thr His Glu Ala Arg Pro Arg Pro Leu	
574 579 584 589	
agc tta tct gag tac cgg cga cga agg cag caa cgc caa gca gaa aca	2005
Ser Leu Ser Glu Tyr Arg Arg Arg Arg Gln Gln Arg Gln Ala Glu Thr	
590 595 600 605	
gaa gag aga agt cca cag ccc cca act ggg aag tgg cct agc ctt cca	2053
Glu Glu Arg Ser Pro Gln Pro Pro Thr Gly Lys Trp Pro Ser Leu Pro	
606 611 616 621	

gag act ccc aca ggg ctg gca gac atc cct tgt ctt gtc atc cca cca	2101
Glu Thr Pro Thr Gly Leu Ala Asp Ile Pro Cys Leu Val Ile Pro Pro	
622 627 632 637	
gcc cca gcc aag aag aca gct ctg cag aga agc cct gaa aca ccc ctt	2149
Ala Pro Ala Lys Lys Thr Ala Leu Gln Arg Ser Pro Glu Thr Pro Leu	
638 643 648 653	
gag att tgc ctt gtg cct gta ggt ccc agc cct gct tct cct agt cct	2197
Glu Ile Cys Leu Val Pro Val Gly Pro Ser Pro Ala Ser Pro Ser Pro	
654 659 664 669	
gag cca cct gta agc aaa cct gtg gcc tca tct ccc act gag cag gtg	2245
Glu Pro Pro Val Ser Lys Pro Val Ala Ser Ser Pro Thr Glu Gln Val	
670 675 680 685	
cca tcc cag gag atg cca ctg ttg gcg aga cct tcc cct cct gtg cag	2293
Pro Ser Gln Glu Met Pro Leu Leu Ala Arg Pro Ser Pro Pro Val Gln	
686 691 696 701	
tct gtg tcc cct gct gtg ccc aca cct ccc tgc atg tct gct gcc ctg	2341
Ser Val Ser Pro Ala Val Pro Thr Pro Pro Ser Met Ser Ala Ala Leu	
702 707 712 717	
cct ttc cct gca ggt ggg ctt ggc atg ccc ccc agt ctg ccc cca cct	2389
Pro Phe Pro Ala Gly Gly Leu Gly Met Pro Pro Ser Leu Pro Pro Pro	
718 723 728 733	
ccc ttg cag cct cct agt ctt cca ttg tct atg ggg cca gta cta cct	2437
Pro Leu Gln Pro Pro Ser Leu Pro Leu Ser Met Gly Pro Val Leu Pro	
734 739 744 749	
gat ccg ttt act cac tat gcc ccc ttg cca tcc tgg cct tgt tat cct	2485
Asp Pro Phe Thr His Tyr Ala Pro Leu Pro Ser Trp Pro Cys Tyr Pro	
750 755 760 765	
cat gtg tcc cct tct ggc tat cct tgc ctg ccc ccc cca cca acg gtg	2533
His Val Ser Pro Ser Gly Tyr Pro Cys Leu Pro Pro Pro Pro Thr Val	
766 771 776 781	
ccc cta gtg tct ggt act cct ggt gcc tat gcc gtg cct ccc act tgc	2581
Pro Leu Val Ser Gly Thr Pro Gly Ala Tyr Ala Val Pro Pro Thr Cys	
782 787 792 797	
agt gtg cct tgg gca ccc cct cct gcc cca gtc tca cct tac agt tcc	2629
Ser Val Pro Trp Ala Pro Pro Pro Ala Pro Val Ser Pro Tyr Ser Ser	
798 803 808 813	
aca tgt acc tat ggg ccc ttg gga tgg ggc cca ggg cct caa cat gct	2677
Thr Cys Thr Tyr Gly Pro Leu Gly Trp Gly Pro Gly Pro Gln His Ala	
814 819 824 829	
cca ttc tgg tct act gtt ccc cca cct cct ttg cct cca gcc tcc att	2725
Pro Phe Trp Ser Thr Val Pro Pro Pro Pro Leu Pro Pro Ala Ser Ile	
830 835 840 845	
ggg aga gct gtt ccc caa cct aaa atg gag tct agg ggc act cca gct	2773

Gly	Arg	Ala	Val	Pro	Gln	Pro	Lys	Met	Glu	Ser	Arg	Gly	Thr	Pro	Ala		
846					851					856					861		
ggc	cct	cct	gaa	aat	gta	ctt	ccc	ttg	tcg	atg	gct	cct	ccc	ctc	agt	2821	
Gly	Pro	Pro	Glu	Asn	Val	Leu	Pro	Leu	Ser	Met	Ala	Pro	Pro	Leu	Ser		
862					867					872					877		
ctt	ggg	cta	cct	ggc	cat	gga	gct	cct	cag	aca	gag	cct	acc	aag	gtg	2869	
Leu	Gly	Leu	Pro	Gly	His	Gly	Ala	Pro	Gln	Thr	Glu	Pro	Thr	Lys	Val		
878					883					888					893		
gag	gtc	aag	cca	gtg	cct	gca	tct	ccc	cat	ccg	aaa	cac	aag	gtg	tct	2917	
Glu	Val	Lys	Pro	Val	Pro	Ala	Ser	Pro	His	Pro	Lys	His	Lys	Val	Ser		
894					899					904					909		
gcc	ctg	gtg	caa	agt	ccc	cag	atg	aag	gct	cta	gca	tgt	gtg	tct	gct	2965	
Ala	Leu	Val	Gln	Ser	Pro	Gln	Met	Lys	Ala	Leu	Ala	Cys	Val	Ser	Ala		
910					915					920					925		
gaa	ggg	gtg	act	gtt	gag	gag	cct	gca	tca	gag	agg	cta	aag	cct	gag	3013	
Glu	Gly	Val	Thr	Val	Glu	Glu	Pro	Ala	Ser	Glu	Arg	Leu	Lys	Pro	Glu		
926					931					936					941		
acc	caa	gag	acc	agg	ccc	agg	gag	aag	ccc	ccc	ttg	cct	gct	acc	aag	3061	
Thr	Gln	Glu	Thr	Arg	Pro	Arg	Glu	Lys	Pro	Pro	Leu	Pro	Ala	Thr	Lys		
942					947					952					957		
gct	gtt	ccc	aca	cca	agg	cag	agc	act	gtc	ccc	aag	ctg	cct	gct	gtc	3109	
Ala	Val	Pro	Thr	Pro	Arg	Gln	Ser	Thr	Val	Pro	Lys	Leu	Pro	Ala	Val		
958					963					968					973		
cac	cca	gcc	cgt	cta	agg	aag	ctg	tcc	ttc	ctg	cct	acc	cca	cgt	act	3157	
His	Pro	Ala	Arg	Leu	Arg	Lys	Leu	Ser	Phe	Leu	Pro	Thr	Pro	Arg	Thr		
974					979					984					989		
cag	ggg	tct	gaa	gat	gtg	gta	cag	gct	ttc	atc	agt	gag	att	gga	att	3205	
Gln	Gly	Ser	Glu	Asp	Val	Val	Gln	Ala	Phe	Ile	Ser	Glu	Ile	Gly	Ile		
990					995					1000					1005		
gag	gca	tcg	gac	ctg	tcc	agt	ctg	ctg	gag	cag	ttt	gag	aaa	tca	gaa	3253	
Glu	Ala	Ser	Asp	Leu	Ser	Ser	Leu	Leu	Glu	Gln	Phe	Glu	Lys	Ser	Glu		
1006					1011					1016					1021		
gcc	aaa	aag	gag	tgt	cct	cct	ccg	gct	cct	gct	gac	agc	ttg	gct	gta	3301	
Ala	Lys	Lys	Glu	Cys	Pro	Pro	Pro	Ala	Pro	Ala	Asp	Ser	Leu	Ala	Val		
1022					1027					1032					1037		
gga	aac	tca	ggc	ggc	gtt	gac	att	ccc	cag	gag	aag	agg	ccc	cta	gac	3349	
Gly	Asn	Ser	Gly	Gly	Val	Asp	Ile	Pro	Gln	Glu	Lys	Arg	Pro	Leu	Asp		
1038					1043					1048					1053		
cgg	tta	caa	gcc	cca	gaa	ctg	gcc	aac	gtg	gca	ggg	ctc	acc	cct	cca	3397	
Arg	Leu	Gln	Ala	Pro	Glu	Leu	Ala	Asn	Val	Ala	Gly	Leu	Thr	Pro	Pro		
1054					1059					1064					1069		
gct	acc	cct	ccc	cac	cag	tta	tgg	aag	ccc	ctg	gct	gct	gtc	tca	ctg	3445	
Ala	Thr	Pro	Pro	His	Gln	Leu	Trp	Lys	Pro	Leu	Ala	Ala	Val	Ser	Leu		

1070	1075	1080	1085	
ctg gcc aaa gcc aaa tct cct aag tcc acc gcc cag gag gga acc ctg				3493
Leu Ala Lys Ala Lys Ser Pro Lys Ser Thr Ala Gln Glu Gly Thr Leu				
1086	1091	1096	1101	
aag cct gaa gga gtt acg gag gcc aaa cat cca gct gca gtt cgc ctc				3541
Lys Pro Glu Gly Val Thr Glu Ala Lys His Pro Ala Ala Val Arg Leu				
1102	1107	1112	1117	
caa gaa ggg gtc cat ggc cct agt cga gtc cat gtg ggc tct ggg gac				3589
Gln Glu Gly Val His Gly Pro Ser Arg Val His Val Gly Ser Gly Asp				
1118	1123	1128	1133	
cat gac tat tgt gtc cgg agc agg acc ccc cca aaa aag atg cct gcc				3637
His Asp Tyr Cys Val Arg Ser Arg Thr Pro Pro Lys Lys Met Pro Ala				
1134	1139	1144	1149	
cta gtc att cca gag gtg ggc tcc cga tgg aat gtc aag cgc cat cag				3685
Leu Val Ile Pro Glu Val Gly Ser Arg Trp Asn Val Lys Arg His Gln				
1150	1155	1160	1165	
gac atc acc atc aaa cct gtc ttg tcc ttg ggc cca gct gcc cct ccg				3733
Asp Ile Thr Ile Lys Pro Val Leu Ser Leu Gly Pro Ala Ala Pro Pro				
1166	1171	1176	1181	
ccc cca tgc ata gct gcc tcc cgg gag ccg ctt gat cac agg act agc				3781
Pro Pro Cys Ile Ala Ala Ser Arg Glu Pro Leu Asp His Arg Thr Ser				
1182	1187	1192	1197	
agt gag cag gca gat ccc tca gca ccc tgc ctt gcc cca tcc agc ttg				3829
Ser Glu Gln Ala Asp Pro Ser Ala Pro Cys Leu Ala Pro Ser Ser Leu				
1198	1203	1208	1213	
ctg tcc cct gag gcc tca ccc tgc cgg aat gac atg aac act agg act				3877
Leu Ser Pro Glu Ala Ser Pro Cys Arg Asn Asp Met Asn Thr Arg Thr				
1214	1219	1224	1229	
ccc cct gaa ccc tca gcc aag cag cgg tca atg cgc tgt tac cga aaa				3925
Pro Pro Glu Pro Ser Ala Lys Gln Arg Ser Met Arg Cys Tyr Arg Lys				
1230	1235	1240	1245	
gcc tgc agg tca gcc agc ccc tca agc cag ggc tgg cag ggc cgc cga				3973
Ala Cys Arg Ser Ala Ser Pro Ser Ser Gln Gly Trp Gln Gly Arg Arg				
1246	1251	1256	1261	
ggc cgc aac agc cgt tct gtc agc tct ggg tcc aac cgg act agc gaa				4021
Gly Arg Asn Ser Arg Ser Val Ser Ser Gly Ser Asn Arg Thr Ser Glu				
1262	1267	1272	1277	
gca tct tcc tca tcc tca tca tgc tct tcc tca tcc cga tct cgg tcc				4069
Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Arg Ser Arg Ser				
1278	1283	1288	1293	
agg tcc ctc tcc ccc cca cac aag agg tgg cga agg tcc agc tgt agt				4117
Arg Ser Leu Ser Pro Pro His Lys Arg Trp Arg Arg Ser Ser Cys Ser				
1294	1299	1304	1309	

122	127	132	137	
gag tat ttg aaa gct gtg ata act cca gag tgt ctt ctg ata tta gat				603
Glu Tyr Leu Lys Ala Val Ile Thr Pro Glu Cys Leu Leu Ile Leu Asp				
138	143	148	153	
tat cgt aat tta aac tta gag caa tgg ctg ttc cgg gaa ctc cct tca				651
Tyr Arg Asn Leu Asn Leu Glu Gln Trp Leu Phe Arg Glu Leu Pro Ser				
154	159	164	169	
cag ttg tct gga gag ggt caa ctc gtt aca tac cct tta cct ttt gag				699
Gln Leu Ser Gly Glu Gly Gln Leu Val Thr Tyr Pro Leu Pro Phe Glu				
170	175	180	185	
ttt aga gct ata gaa gca ctc ctg caa tat tgg atc aac acc ctt cag				747
Phe Arg Ala Ile Glu Ala Leu Leu Gln Tyr Trp Ile Asn Thr Leu Gln				
186	191	196	201	
ggg aaa ctt agc att ttg cag cca ctg atc ctt gag acc ttg gat gct				795
Gly Lys Leu Ser Ile Leu Gln Pro Leu Ile Leu Glu Thr Leu Asp Ala				
202	207	212	217	
ttg gtg gac ccc aaa cat tct tct gta gac aga agc aaa ctg cac att				843
Leu Val Asp Pro Lys His Ser Ser Val Asp Arg Ser Lys Leu His Ile				
218	223	228	233	
tta cta cag aat ggc aaa agt cta tca gag tta gaa aca gat att aaa				891
Leu Leu Gln Asn Gly Lys Ser Leu Ser Glu Leu Glu Thr Asp Ile Lys				
234	239	244	249	
att ttc aaa gag tca att ttg gag atc ttg gat gag gaa gag ttg cta				939
Ile Phe Lys Glu Ser Ile Leu Glu Ile Leu Asp Glu Glu Glu Leu Leu				
250	255	260	265	
gaa gag ctc tgt gta tca aaa tgg agt gac cca caa gtc ttt gaa aag				987
Glu Glu Leu Cys Val Ser Lys Trp Ser Asp Pro Gln Val Phe Glu Lys				
266	271	276	281	
agc agt gct ggg att gac cat gca gaa gag atg gag ttg ctg ttg gaa				1035
Ser Ser Ala Gly Ile Asp His Ala Glu Glu Met Glu Leu Leu Leu Glu				
282	287	292	297	
aac tac tac cga ttg gct gac gat ctc tcc aat gca gct cgt gag ctt				1083
Asn Tyr Tyr Arg Leu Ala Asp Asp Leu Ser Asn Ala Ala Arg Glu Leu				
298	303	308	313	
agg gtg ctg att gat gat tca caa agt att att ttc att aat ctg gac				1131
Arg Val Leu Ile Asp Asp Ser Gln Ser Ile Ile Phe Ile Asn Leu Asp				
314	319	324	329	
agc cac cga aac gtg atg atg agg ttg aat cta cag ctg acc atg gga				1179
Ser His Arg Asn Val Met Met Arg Leu Asn Leu Gln Leu Thr Met Gly				
330	335	340	345	
acc ttc tct ctt tcg ctc ttt gga cta atg gga gtt gct ttt gga atg				1227
Thr Phe Ser Leu Ser Leu Phe Gly Leu Met Gly Val Ala Phe Gly Met				
346	351	356	361	

aat ttg gaa tct tcc ctt gaa gag gac cat aga att ttt tgg ctg att 1275
 Asn Leu Glu Ser Ser Leu Glu Glu Asp His Arg Ile Phe Trp Leu Ile
 362 367 372 377

aca gga att atg ttc atg gga agt ggc ctc atc tgg agg cgc ctg ctt 1323
 Thr Gly Ile Met Phe Met Gly Ser Gly Leu Ile Trp Arg Arg Leu Leu
 378 383 388 393

tca ttc ctt gga cga cag cta gaa gct cca ttg cct cct atg atg gct 1371
 Ser Phe Leu Gly Arg Gln Leu Glu Ala Pro Leu Pro Pro Met Met Ala
 394 399 404 409

tct tta cct aaa aag act ctt ctg gca gat aga agc atg gaa ttg aaa 1419
 Ser Leu Pro Lys Lys Thr Leu Leu Ala Asp Arg Ser Met Glu Leu Lys
 410 415 420 425

aat agc ctc aga ctg gat gga ctt gga tca gga agg agc atc cta aca 1467
 Asn Ser Leu Arg Leu Asp Gly Leu Gly Ser Gly Arg Ser Ile Leu Thr
 426 431 436 441

aac cgt tag gaacagc cccgtggata ctgaagtttt ttttatggta gttacaggaa 1523
 Asn Arg *
 442

acttctgata ctctttttat tattttcttg tatagagtca gacacttgaa aaaaaaaaaa 1583
 a 1584

<210> 312
 <211> 1051
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (79)..(558)

<400> 312
 atttggccct cgaggccaag aattcggcac gaggggcagg caacagagtg gcggccgcta 60

cgggccctgta acagggcc atg gag aag ctg cgg cga gtc ctg agc ggc cag 111
 Met Glu Lys Leu Arg Arg Val Leu Ser Gly Gln
 1 5

gac gac gag gag cag ggc ctg act gcg cag gtc ctg gat gcc tca tcc 159
 Asp Asp Glu Glu Gln Gly Leu Thr Ala Gln Val Leu Asp Ala Ser Ser
 12 17 22 27

ctt agt ttc aac acc aga ttg aaa tgg ttt gcc atc tgc ttc gta tgt 207
 Leu Ser Phe Asn Thr Arg Leu Lys Trp Phe Ala Ile Cys Phe Val Cys
 28 33 38 43

ggc gtt ttc ttt tct att ctt gga act gga ttg ctg tgg ctt ccg ggc 255

Gly	Val	Phe	Phe	Ser	Ile	Leu	Gly	Thr	Gly	Leu	Leu	Trp	Leu	Pro	Gly	
44					49					54					59	
ggc	ata	aag	ctt	ttt	gca	gtg	ttt	tat	acc	ctc	ggc	aat	ctt	gct	gcg	303
Gly	Ile	Lys	Leu	Phe	Ala	Val	Phe	Tyr	Thr	Leu	Gly	Asn	Leu	Ala	Ala	
60					65					70					75	
tta	gcc	agt	aca	tgc	ttt	tta	atg	gga	cct	gtg	aag	caa	ctg	aag	aaa	351
Leu	Ala	Ser	Thr	Cys	Phe	Leu	Met	Gly	Pro	Val	Lys	Gln	Leu	Lys	Lys	
76					81					86					91	
atg	ttt	gaa	gca	aca	aga	ttg	ctt	gca	aca	att	gtt	atg	ctt	ttg	tgt	399
Met	Phe	Glu	Ala	Thr	Arg	Leu	Leu	Ala	Thr	Ile	Val	Met	Leu	Leu	Cys	
92					97					102					107	
ttc	ata	ttt	acc	ctg	tgt	gct	gct	ctt	tgg	tgg	cat	aag	aag	gga	ctg	447
Phe	Ile	Phe	Thr	Leu	Cys	Ala	Ala	Leu	Trp	Trp	His	Lys	Lys	Gly	Leu	
108					113					118					123	
gct	gtg	tta	ttc	tgc	ata	ttg	cag	ttc	ttg	tca	atg	acc	tgg	tat	agc	495
Ala	Val	Leu	Phe	Cys	Ile	Leu	Gln	Phe	Leu	Ser	Met	Thr	Trp	Tyr	Ser	
124					129					134					139	
ctg	tcg	tac	atc	cca	tat	gca	agg	gat	gca	gtt	att	aaa	tgc	tgt	tct	543
Leu	Ser	Tyr	Ile	Pro	Tyr	Ala	Arg	Asp	Ala	Val	Ile	Lys	Cys	Cys	Ser	
140					145					150					155	
tct	ctc	cta	agt	tga	aaatcagaaa	cttgtggaaa	agagcacttg	aatgttggtg								598
Ser	Leu	Leu	Ser	*												
156																
ctctatg	ttt	ggtgaag	ttt	gcttttcccc	ataaaacact	ccaggaacaa	ctgacgtgac									658
agttgaagac	cg	ttttgtac	taagtctcat	tttgtatact	ggtaaaaact	acatgcttga										718
ttaaaccatt	aatgctt	gt	aactttaaat	tcattatgtg	tcattaatat	acttttccaa										778
agataagatt	tttaatcact	gccagttgta	aattattttt	agccaattttt	taaatctttt											838
caaagcagct	ttgaaatgtg	aatattttaa	ggtagacctg	tgctgcaaga	taattaaact											898
tttttgcttt	taaaaaatgt	ctgcattttt	aagatttttt	ttacttttaa	tgtgaaactt											958
attttaagct	aaaaattgct	tatttatatgt	aataaaaaata	atatataaat	ctttacaatt											1018
ttgaaataaa	cccatccttg	gaaaaaaaaa	aaa													1051

<210> 313
 <211> 1825
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (234) .. (1235)

<400> 313

accggaacgg aattccccggg gcgagccacg cgtccggcct gggggtcctg gctgaactgg	60
tctggtgtta agggggcccc ctgaccccct tgaagagggg gctgggctgg gtgagggggg	120
gtggccaacc ccagccagg ttcccaggca ggatgagctg gggttggggg ggctaggccg	180
agggccttgg gagctgggca gtctgggctg ggctgggctg ggcagggcgc cac atg Met 1	236
gaa gct gga gga gca acg gga gcg ctg ggc gtg ggg tgc aaa ttg ccc Glu Ala Gly Gly Ala Thr Gly Ala Leu Gly Val Gly Cys Lys Leu Pro 2 7 12 17	284
agt gcc ttc tgt ttc cca ggc agc tct gtg gcc atg gat atg ttc cag Ser Ala Phe Cys Phe Pro Gly Ser Ser Val Ala Met Asp Met Phe Gln 18 23 28 33	332
aag gta gag aag atc gga gag ggc acc tat ggg gtg gtg tac aag gcc Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly Val Val Tyr Lys Ala 34 39 44 49	380
aag aac agg gag aca ggg cag ctg gtg gcc ctg aag aag atc aga ctg Lys Asn Arg Glu Thr Gly Gln Leu Val Ala Leu Lys Lys Ile Arg Leu 50 55 60 65	428
gat ttg gag atg gag ggg gtc cca agc act gcc atc agg gag atc tcg Asp Leu Glu Met Glu Gly Val Pro Ser Thr Ala Ile Arg Glu Ile Ser 66 71 76 81	476
ctg ctc aag gaa ctg aag cac ccc aac atc gtc cga ctg ctg gac gtg Leu Leu Lys Glu Leu Lys His Pro Asn Ile Val Arg Leu Leu Asp Val 82 87 92 97	524
gtg cac aac gag agg aag ctc tat ctg gtg ttt gag ttc ctc agc cag Val His Asn Glu Arg Lys Leu Tyr Leu Val Phe Glu Phe Leu Ser Gln 98 103 108 113	572
gac ctg aag aag tac atg gac tcc acc cca ggc tca gag ctc ccc ctg Asp Leu Lys Lys Tyr Met Asp Ser Thr Pro Gly Ser Glu Leu Pro Leu 114 119 124 129	620
cac ctc atc aag agc tac ctc ttc cag ctg ctg cag ggg gtg agt ttc His Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu Gln Gly Val Ser Phe 130 135 140 145	668
tgc cac tca cat cgg gtc atc cac cga gac ctg aag ccc cag aac ctg Cys His Ser His Arg Val Ile His Arg Asp Leu Lys Pro Gln Asn Leu 146 151 156 161	716
ctc atc aat gag ttg ggt gcc atc aag ctg gct gac ttc ggc ctg gct Leu Ile Asn Glu Leu Gly Ala Ile Lys Leu Ala Asp Phe Gly Leu Ala 162 167 172 177	764

cgc gcc ttc ggg gtg ccc ctg cgc acc tac acc cat gag gtg gtg aca	812
Arg Ala Phe Gly Val Pro Leu Arg Thr Tyr Thr His Glu Val Val Thr	
178 183 188 193	
ctg tgg tat cgc gcc ccc gag att ctc ttg ggc agc aag ttc tat acc	860
Leu Trp Tyr Arg Ala Pro Glu Ile Leu Leu Gly Ser Lys Phe Tyr Thr	
194 199 204 209	
aca gct gtg gat atc tgg agc att ggt tgc atc ttt gca gag atg gtg	908
Thr Ala Val Asp Ile Trp Ser Ile Gly Cys Ile Phe Ala Glu Met Val	
210 215 220 225	
act cga aaa gcc ctg ttt cct ggt gac tct gag att gac cag ctc ttt	956
Thr Arg Lys Ala Leu Phe Pro Gly Asp Ser Glu Ile Asp Gln Leu Phe	
226 231 236 241	
cgt atc ttt cgt atg ctg ggg aca ccc agc gaa gac aca tgg ccc ggg	1004
Arg Ile Phe Arg Met Leu Gly Thr Pro Ser Glu Asp Thr Trp Pro Gly	
242 247 252 257	
gtc acc cag ctg cct gac tat aag ggc agc ttc cct aag tgg acc agg	1052
Val Thr Gln Leu Pro Asp Tyr Lys Gly Ser Phe Pro Lys Trp Thr Arg	
258 263 268 273	
aag gga ctg gaa gag att gtg ccc aat ctg gag cca gag ggc agg gac	1100
Lys Gly Leu Glu Glu Ile Val Pro Asn Leu Glu Pro Glu Gly Arg Asp	
274 279 284 289	
ctg ctc atg caa ctc ctg cag tat gac ccc agc cag cgg atc aca gcc	1148
Leu Leu Met Gln Leu Leu Gln Tyr Asp Pro Ser Gln Arg Ile Thr Ala	
290 295 300 305	
aag act gcc ctg gcc cac cgg tac ttc tca tcc cct gag ccc tcc cca	1196
Lys Thr Ala Leu Ala His Pro Tyr Phe Ser Ser Pro Glu Pro Ser Pro	
306 311 316 321	
gct gcc cgc cag tat gtg ctg cag cga ttc cgc cat tga gaatgtcaag	1245
Ala Ala Arg Gln Tyr Val Leu Gln Arg Phe Arg His *	
322 327 332	
gccacactca gatcctttct cgagcagcag ctgctgcccc agctgcctcc taccattgc	1305
caagagagga tgcattctggg gagagcaaag cactaaggaa ttcagcatca gcctgcagag	1365
ggctgagtct gggttagtcc tgcccgagg ttagcgagat cctgtgttgt tttttgggtt	1425
ggacggtgcc gtttcaaaat agaggcacag atgctccatg cagcaggggt ccccgggcac	1485
tggaacaagt gccaaattga aggcaggggg cctgccagag ctgggtgtgg gtattcaggc	1545
cctcacctgc cctgectgca gggccagacc ctgaggaaag ggcgccccct gctggtcttt	1605
ttggatttaa aatgtttggg ggaagagttg agttccagtt cagtcccaag ttaaacagga	1665
gggagtgagg gagaggagag agggcgttcc ccgatccca ggagagctgg gctatgactg	1725
caataaggag ttgttccttc acctgagatg tgcttctttt gggttcatttc tggcttgaca	1785

acaagaaata aacgtggtat gttcctgaaa aaaaaaaaaa

1825

<210> 314
<211> 3394
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (417)..(1934)

<400> 314

ggaaatctgg gaggagtgtc ctttgggcag cattttaaaa gggggaggga actgcggcta 60
aagagacgtt cggatgatggg agcgcaatgt atgaggggat acagtgcctc aggtttaaaa 120
gagcaggaag ctgagtgaga ggttgcagaa aaagtgtctt cgctcggcag aggttacagg 180
tggcatctca gaaagagctt tgaggctaca ggctgtagtc gggaagggga tcggagaact 240
gtgtgaaggg acagcttagg gactagcgtc ctgggactag ggggaagttc gcgactttct 300
gaagactggc aggaatgtgc ctcttgccc tcgatgcttc cccctgagg ggaggcatcg 360
tgagggactg tggcaggctt cactgaacgc tgagccgggg aggtccaact ccacgt 416
atg gat ccg ggg aat gag aat tca gcc aca gag gct gcc gcg atc ata 464
Met Asp Pro Gly Asn Glu Asn Ser Ala Thr Glu Ala Ala Ala Ile Ile
1 5 10 15
gac cta gat ccc gac ttc gaa ccc cag agc cgt ccc cgc tcc tgc acc 512
Asp Leu Asp Pro Asp Phe Glu Pro Gln Ser Arg Pro Arg Ser Cys Thr
17 22 27 32
tgg ccc ctt ccc cga cca gag atc gct aac cag ccg tcc aag ccg ccc 560
Trp Pro Leu Pro Arg Pro Glu Ile Ala Asn Gln Pro Ser Lys Pro Pro
33 38 43 48
gag gtg gag cca gat ctg ggg gaa aag gta cac acg gag ggg cgc tca 608
Glu Val Glu Pro Asp Leu Gly Glu Lys Val His Thr Glu Gly Arg Ser
49 54 59 64
gag ccg atc ctg ttg ccc tct cgg ctc cca gag ccg gcc ggg gcc ccc 656
Glu Pro Ile Leu Leu Pro Ser Arg Leu Pro Glu Pro Ala Gly Ala Pro
65 70 75 80
cag ccc gga atc ctg ggg gct gta aca ggt cct cgg aag gga ggc tcc 704
Gln Pro Gly Ile Leu Gly Ala Val Thr Gly Pro Arg Lys Gly Gly Ser
81 86 91 96
cgc cgg aat gcc tgg gga aat cag tca tat gca gaa ctc atc agc cag 752
Arg Arg Asn Ala Trp Gly Asn Gln Ser Tyr Ala Glu Leu Ile Ser Gln
97 102 107 112

gcc att gaa agc gcc ccg gag aag cga ctg aca ctt gcc cag atc tac	800
Ala Ile Glu Ser Ala Pro Glu Lys Arg Leu Thr Leu Ala Gln Ile Tyr	
113 118 123 128	
gag tgg atg gtc cgt act gta ccc tac ttc aag gac aag ggt gac agc	848
Glu Trp Met Val Arg Thr Val Pro Tyr Phe Lys Asp Lys Gly Asp Ser	
129 134 139 144	
aac agc tca gca gga tgg aag aac tcg atc cgc cac aac ctg tcc ctg	896
Asn Ser Ser Ala Gly Trp Lys Asn Ser Ile Arg His Asn Leu Ser Leu	
145 150 155 160	
cac agc aag ttc atc aag gtt cac aac gag gcc acc ggc aaa agc tct	944
His Ser Lys Phe Ile Lys Val His Asn Glu Ala Thr Gly Lys Ser Ser	
161 166 171 176	
tgg tgg atg ctg aac cct gag gga ggc aag agc ggc aaa gcc ccc cgc	992
Trp Trp Met Leu Asn Pro Glu Gly Gly Lys Ser Gly Lys Ala Pro Arg	
177 182 187 192	
cgc cgg gcc gcc tcc atg gat agc agc agc aag ctg ctc cgg ggc cgc	1040
Arg Arg Ala Ala Ser Met Asp Ser Ser Ser Lys Leu Leu Arg Gly Arg	
193 198 203 208	
agt aaa gcc ccc aag aag aaa cca tct gtg ctg cca gct cca ccc gaa	1088
Ser Lys Ala Pro Lys Lys Lys Pro Ser Val Leu Pro Ala Pro Pro Glu	
209 214 219 224	
ggc gcc act cca acg agc cct gtc ggc cac ttt gcc aag tgg tca ggc	1136
Gly Ala Thr Pro Thr Ser Pro Val Gly His Phe Ala Lys Trp Ser Gly	
225 230 235 240	
agc ccc tgc tct cga aac cgt gaa gaa gcc gat atg tgg acc acc ttc	1184
Ser Pro Cys Ser Arg Asn Arg Glu Glu Ala Asp Met Trp Thr Thr Phe	
241 246 251 256	
cgt cca cga agc agt tca aat gcc agc agt gtc agc acc cgg ctg tcc	1232
Arg Pro Arg Ser Ser Ser Asn Ala Ser Ser Val Ser Thr Arg Leu Ser	
257 262 267 272	
ccc ttg agg cca gag tct gag gtg ctg gcg gag gaa ata cca gct tca	1280
Pro Leu Arg Pro Glu Ser Glu Val Leu Ala Glu Glu Ile Pro Ala Ser	
273 278 283 288	
gtc agc agt tat gca ggg ggt gtc cct ccc acc ctc aat gaa ggt cta	1328
Val Ser Ser Tyr Ala Gly Gly Val Pro Pro Thr Leu Asn Glu Gly Leu	
289 294 299 304	
gag ctg tta gat ggg ctc aat ctc acc tct tcc cat tcc ctg cta tct	1376
Glu Leu Leu Asp Gly Leu Asn Leu Thr Ser Ser His Ser Leu Leu Ser	
305 310 315 320	
cgg agt ggt ctc tct ggc ttc tct ttg cag cat cct ggg gtt acc ggc	1424
Arg Ser Gly Leu Ser Gly Phe Ser Leu Gln His Pro Gly Val Thr Gly	
321 326 331 336	
ccc tta cac acc tac agc agc tcc ctt ttc agc cca gca gag ggg ccc	1472

Pro Leu His Thr Tyr Ser Ser Ser Leu Phe Ser Pro Ala Glu Gly Pro	
337 342 347 352	
ctg tca gca gga gaa ggg tgc ttc tcc agc tcc cag gct ctg gag gcc	1520
Leu Ser Ala Gly Glu Gly Cys Phe Ser Ser Ser Gln Ala Leu Glu Ala	
353 358 363 368	
ctg ctc acc tct gat acg cca cca ccc cct gct gac gtc ctc atg acc	1568
Leu Leu Thr Ser Asp Thr Pro Pro Pro Pro Ala Asp Val Leu Met Thr	
369 374 379 384	
cag gta gat ccc att ctg tcc cag gct ccg act ctt ctg ttg ctg ggg	1616
Gln Val Asp Pro Ile Leu Ser Gln Ala Pro Thr Leu Leu Leu Leu Gly	
385 390 395 400	
ggg ctt cct tcc tcc agt aag ctg gcc acg ggc gtc ggc ctg tgt ccc	1664
Gly Leu Pro Ser Ser Ser Lys Leu Ala Thr Gly Val Gly Leu Cys Pro	
401 406 411 416	
aag ccc cta gag gct cca ggc ccc agc agt ctg gtt ccc acc ctt tct	1712
Lys Pro Leu Glu Ala Pro Gly Pro Ser Ser Leu Val Pro Thr Leu Ser	
417 422 427 432	
atg ata gca cca cct cca gtc atg gca agt gcc ccc atc ccc aag gct	1760
Met Ile Ala Pro Pro Pro Val Met Ala Ser Ala Pro Ile Pro Lys Ala	
433 438 443 448	
ctg ggg act cct gtg ctc aca ccc cct act gaa gct gca agc caa gac	1808
Leu Gly Thr Pro Val Leu Thr Pro Pro Thr Glu Ala Ala Ser Gln Asp	
449 454 459 464	
aga atg cct cag gat cta gat ctt gat atg tat atg gag aac ctg gag	1856
Arg Met Pro Gln Asp Leu Asp Leu Asp Met Tyr Met Glu Asn Leu Glu	
465 470 475 480	
tgt gac atg gat aac atc atc agt gac ctc atg gat gag ggc gag gga	1904
Cys Asp Met Asp Asn Ile Ile Ser Asp Leu Met Asp Glu Gly Glu Gly	
481 486 491 496	
ctg gac ttc aac ttt gag cca gat ccc tga g tcatgcctgg aagctttgtc	1955
Leu Asp Phe Asn Phe Glu Pro Asp Pro *	
497 502	
ccctgcttca gatgtggagc caggcgtgtt catatctact ctttaccctt gagccctccc	2015
caggaatttg ggaccctgct ttagagctag ggtgggggtct ggtcacacac aggtgttgaa	2075
gaaattataa agataaagct gcccacatctg gggacgatat ggggagggag atgggagggg	2135
aaaggggaga gggtttttct cactgtgcca attaggggggt aaggccccct ctcaggagcc	2195
atcatcggtt ttccccattc ctaccactt aggcctttgta gcaagatgag caatgctgtt	2255
ggaaatgtga agtcaccagt ggccttacct ctgcctttgg gagcaggatt tttttgtaga	2315
gagtcttata tgagctgagc caggctagct ggagcctggg atttctatgc agtggccccct	2375

taggccagtg atgtgcggtg ggtgggctgt ttaggggatc tggaagggcc aaggtctgag	2435
cactggagtg gctcgccagg ccaaatacacc cttagaaggc tgcagataac agaaaggctt	2495
tttataaact tttaaagaaa tataaacaca aatatagaga ttttttaacc atggcagggg	2555
gctagtggtg ggcagaatgc ttttttttct ttctgaaggc tttgtgatag tgacatgata	2615
caaacactac agacaataaa tattaggaga cacagggag tggggagagg tggggagtaa	2675
tagtaaacac aggggaagagc tcccctacgg accaggtata gagaaaggtc tatgcagaaa	2735
taggttagag tttccctaac aaaaaagcta acccaggtcc cctcattcct tcaacttggt	2795
cctgggagtg tgtggtgtta ggggtgcagcc acagtcttct atgaccagc atgggttagt	2855
gctatggtgg gagagtacat tgaaggcctg gaattagctt ggggccaggg aagggactgg	2915
gaggggagag aagagaagga ggggaaggatt taggatggta aagttaggta cagagacctc	2975
cctgttcaag gccctgaca gctgtccctg cccttcttcc ccttccctga ctgcaggggt	3035
tatgtggaag tgtgtgtggc agcaggcagc ggggagggga ggaacagggg agggggagct	3095
ggggagcttg gctgagggtc tgggaaatga gcagggatgg ggggggatgt ggatcaggtt	3155
tactagcacc tgccaggag gccatctggg gctccttctc cccccagcc cccaaagcag	3215
cccttcccc agtgccctt gcacgtccc ctccccacc cctgctgtgg gttcccatca	3275
tttctgtgt cagcgcttg cctaccaga ttgtatcatg tgctagattg gagtggggaa	3335
gtgtgtcaaa tcaataaatg aataaattca ataatgcct ataaccaaaa aaaaaaaaa	3394

<210> 315
 <211> 3398
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (130)..(2286)

<400> 315	
taagcttgcg gccgcccggg cccgggcccg cgtcgggcgc ctggctctgt acgcgagccc	60
ggggatctgc ggcttcctg cccccctcc cgggaggagc gtggagcggc ggcggcggcg	120
gcggcagaa atg atg gaa gaa ttg cat agc ctg gac cca cga cgg cag	168
Met Met Glu Glu Leu His Ser Leu Asp Pro Arg Arg Gln	
1 5 10	
gaa tta ttg gag gcc agg ttt act gga gta ggt gtt agt aag gga cca	216
Glu Leu Leu Glu Ala Arg Phe Thr Gly Val Gly Val Ser Lys Gly Pro	

14	19	24	29	
ctt aat agt gag tct tcc aac cag agc ttg tgc agc gtc gga tcc ttg				264
Leu Asn Ser Glu Ser Ser Asn Gln Ser Leu Cys Ser Val Gly Ser Leu				
30	35	40	45	
agt gat aaa gaa gta gag act ccc gag aaa aag cag aat gac cag cga				312
Ser Asp Lys Glu Val Glu Thr Pro Glu Lys Lys Gln Asn Asp Gln Arg				
46	51	56	61	
aat cgg aaa aga aaa gct gaa cca tat gaa act agc caa ggg aaa ggc				360
Asn Arg Lys Arg Lys Ala Glu Pro Tyr Glu Thr Ser Gln Gly Lys Gly				
62	67	72	77	
act cct agg gga cat aaa att agt gat tac ttt gag cga cga gta gaa				408
Thr Pro Arg Gly His Lys Ile Ser Asp Tyr Phe Glu Arg Arg Val Glu				
78	83	88	93	
cag ccc ctc tat ggt tta gat ggc agt gct gca aag gag gca acg gag				456
Gln Pro Leu Tyr Gly Leu Asp Gly Ser Ala Ala Lys Glu Ala Thr Glu				
94	99	104	109	
gag cag tct gct ctg cca acc ctc atg tca gtg atg cta gca aaa cct				504
Glu Gln Ser Ala Leu Pro Thr Leu Met Ser Val Met Leu Ala Lys Pro				
110	115	120	125	
cgg ctt gac aca gag cag ctg gcg caa agg gga gct ggc ctc tgc ttc				552
Arg Leu Asp Thr Glu Gln Leu Ala Gln Arg Gly Ala Gly Leu Cys Phe				
126	131	136	141	
act ttt gtt tca gct cag caa aac agt ccc tca tct acg gga tct ggc				600
Thr Phe Val Ser Ala Gln Gln Asn Ser Pro Ser Ser Thr Gly Ser Gly				
142	147	152	157	
aac aca gag cat tcc tgc agc tcc caa aaa cag atc tcc atc cag cac				648
Asn Thr Glu His Ser Cys Ser Ser Gln Lys Gln Ile Ser Ile Gln His				
158	163	168	173	
aga cag acc cag tcc gac ctc aca ata gaa aaa ata tct gca cta gaa				696
Arg Gln Thr Gln Ser Asp Leu Thr Ile Glu Lys Ile Ser Ala Leu Glu				
174	179	184	189	
aac agt aag aat tct gac tta gag aag aag gag gga aga ata gat gat				744
Asn Ser Lys Asn Ser Asp Leu Glu Lys Lys Glu Gly Arg Ile Asp Asp				
190	195	200	205	
tta tta aga gcc aac tgt gat ttg aga cgg cag att gat gaa cag caa				792
Leu Leu Arg Ala Asn Cys Asp Leu Arg Arg Gln Ile Asp Glu Gln Gln				
206	211	216	221	
aag atg cta gag aaa tac aag gaa cga tta aat aga tgt gtg aca atg				840
Lys Met Leu Glu Lys Tyr Lys Glu Arg Leu Asn Arg Cys Val Thr Met				
222	227	232	237	
agc aag aaa ctc ctt ata gaa aag tca aaa caa gag aag atg gcg tgt				888
Ser Lys Lys Leu Leu Ile Glu Lys Ser Lys Gln Glu Lys Met Ala Cys				
238	243	248	253	

aga gat aag agc atg caa gac cgc ttg aga ctg ggc cac ttt act act	936
Arg Asp Lys Ser Met Gln Asp Arg Leu Arg Leu Gly His Phe Thr Thr	
254 259 264 269	
gtc cga cac gga gcc tca ttt act gaa cag tgg aca gat ggt tat gct	984
Val Arg His Gly Ala Ser Phe Thr Glu Gln Trp Thr Asp Gly Tyr Ala	
270 275 280 285	
ttt cag aat ctt atc aag caa cag gaa agg ata aat tca cag agg gaa	1032
Phe Gln Asn Leu Ile Lys Gln Gln Glu Arg Ile Asn Ser Gln Arg Glu	
286 291 296 301	
gag ata gaa aga caa cgg aaa atg tta gca aag cgg aaa cct cct gcc	1080
Glu Ile Glu Arg Gln Arg Lys Met Leu Ala Lys Arg Lys Pro Pro Ala	
302 307 312 317	
atg ggt cag gcc cct cct gca acc aat gag cag aaa cag cgg aaa agc	1128
Met Gly Gln Ala Pro Pro Ala Thr Asn Glu Gln Lys Gln Arg Lys Ser	
318 323 328 333	
aag acc aat gga gct gaa aat gaa acg tta acg tta gca gaa tac cat	1176
Lys Thr Asn Gly Ala Glu Asn Glu Thr Leu Thr Leu Ala Glu Tyr His	
334 339 344 349	
gaa caa gaa gaa atc ttc aaa ctc aga tta ggt cat ctt aaa aag gag	1224
Glu Gln Glu Glu Ile Phe Lys Leu Arg Leu Gly His Leu Lys Lys Glu	
350 355 360 365	
gaa gca gag atc cag gca gag ctg gag aga cta gaa agg gtt aga aat	1272
Glu Ala Glu Ile Gln Ala Glu Leu Glu Arg Leu Glu Arg Val Arg Asn	
366 371 376 381	
cta cat atc agg gaa cta aaa agg ata cat aat gaa gat aat tca caa	1320
Leu His Ile Arg Glu Leu Lys Arg Ile His Asn Glu Asp Asn Ser Gln	
382 387 392 397	
ttt aaa gat cat cca acg cta aat gac aga tat ttg ttg tta cat ctt	1368
Phe Lys Asp His Pro Thr Leu Asn Asp Arg Tyr Leu Leu Leu His Leu	
398 403 408 413	
ttg ggt aga gga ggt ttc agt gaa gtt tac aag gca ttt gat cta aca	1416
Leu Gly Arg Gly Gly Phe Ser Glu Val Tyr Lys Ala Phe Asp Leu Thr	
414 419 424 429	
gag caa aga tac gta gct gtg aaa att cac cag tta aat aaa aac tgg	1464
Glu Gln Arg Tyr Val Ala Val Lys Ile His Gln Leu Asn Lys Asn Trp	
430 435 440 445	
aga gat gag aaa aag gag aat tac cac aag cat gca tgt agg gaa tac	1512
Arg Asp Glu Lys Lys Glu Asn Tyr His Lys His Ala Cys Arg Glu Tyr	
446 451 456 461	
cgg att cat aaa gag ctg gat cat ccc aga ata gtt aag ctg tat gat	1560
Arg Ile His Lys Glu Leu Asp His Pro Arg Ile Val Lys Leu Tyr Asp	
462 467 472 477	

tac ttt tca ctg gat act gac tcg ttt tgt aca gta tta gaa tac tgt	1608
Tyr Phe Ser Leu Asp Thr Asp Ser Phe Cys Thr Val Leu Glu Tyr Cys	
478 483 488 493	
gag gga aat gat ctg gac ttc tac ctg aaa cag cac aaa tta atg tcg	1656
Glu Gly Asn Asp Leu Asp Phe Tyr Leu Lys Gln His Lys Leu Met Ser	
494 499 504 509	
gag aaa gag gcc cgg tcc att atc atg cag att gtg aat gct tta aag	1704
Glu Lys Glu Ala Arg Ser Ile Ile Met Gln Ile Val Asn Ala Leu Lys	
510 515 520 525	
tac tta aat gaa ata aaa cct ccc atc ata cac tat gac ctc aaa cca	1752
Tyr Leu Asn Glu Ile Lys Pro Pro Ile Ile His Tyr Asp Leu Lys Pro	
526 531 536 541	
ggg aat att ctt tta gta aat ggt aca gcg tgt gga gag ata aaa att	1800
Gly Asn Ile Leu Leu Val Asn Gly Thr Ala Cys Gly Glu Ile Lys Ile	
542 547 552 557	
aca gat ttt ggt ctt tcg aag atc atg gat gat gat agc tac aat tca	1848
Thr Asp Phe Gly Leu Ser Lys Ile Met Asp Asp Asp Ser Tyr Asn Ser	
558 563 568 573	
gtg gat ggc atg gag cta aca tca caa ggt gct ggt act tat tgg tat	1896
Val Asp Gly Met Glu Leu Thr Ser Gln Gly Ala Gly Thr Tyr Trp Tyr	
574 579 584 589	
tta cca ccg gag tgt ttt gtg gtt ggg aaa gaa cca cca aag atc tca	1944
Leu Pro Pro Glu Cys Phe Val Val Gly Lys Glu Pro Pro Lys Ile Ser	
590 595 600 605	
aat aaa gtt gat gtg tgg tcg gtg ggt gtg atc ttc tat cag tgt ctt	1992
Asn Lys Val Asp Val Trp Ser Val Gly Val Ile Phe Tyr Gln Cys Leu	
606 611 616 621	
tat gga agg aag cct ttt ggc cat aac cag tct cag caa gac atc cta	2040
Tyr Gly Arg Lys Pro Phe Gly His Asn Gln Ser Gln Gln Asp Ile Leu	
622 627 632 637	
caa gag aat acg att ctt aaa gct act gaa gtg cag ttc ccg cca aag	2088
Gln Glu Asn Thr Ile Leu Lys Ala Thr Glu Val Gln Phe Pro Pro Lys	
638 643 648 653	
cca gta gta aca cct gaa gca aag gcg ttt att cga cga tgc ttg gcc	2136
Pro Val Val Thr Pro Glu Ala Lys Ala Phe Ile Arg Arg Cys Leu Ala	
654 659 664 669	
tac cga aag gag gac cgc att gat gtc cag cag ctg gcc tgt gat ccc	2184
Tyr Arg Lys Glu Asp Arg Ile Asp Val Gln Gln Leu Ala Cys Asp Pro	
670 675 680 685	
tac ttg ttg cct cac atc cga aag tca gtc tct aca agt agc cct gct	2232
Tyr Leu Leu Pro His Ile Arg Lys Ser Val Ser Thr Ser Ser Pro Ala	
686 691 696 701	
gga gct gct att gca tca acc tct ggg gcg tcc aat aac agt tct tct	2280

Gly Ala Ala Ile Ala Ser Thr Ser Gly Ala Ser Asn Asn Ser Ser Ser
 702 707 712 717

aat tga gactgactcc aaggccacaa actgttcaac acacacaaag tggacaaatg 2336
 Asn *
 718

gcgttcagca gcgggtttgg aacatagcga atccgaatgg atctgatgaa acctgtacca 2396

ggtgctttta ttttcttgct tttttcccat ccatagagca tgacagcatc gattctcatt 2456

gaggagaaac cttgggcagc tccggccagg ccttgtagga aaaggccccc ccogaggttc 2516

cagcgtcaac ggccaactgtg tgtggctgct ctgagtggag aaaaaattaa aaagaaaaac 2576

tggttccatg tactgtgaac ttgaaaactt gcagactcag gggggtccct gatgcagtgc 2636

ttcagatgaa gaatgtggac ttgaaaatac agactgggct agtccagtgt ctatatattaa 2696

acttgttctt ttcttttaaat aaagtttagg taacatctcc tgaaaagctt gtagcacaaa 2756

ggctcagctg gggatggtgt ttgacttcgg aggaaaaaag ttgctattgc ccgttaaagg 2816

cactagagtt agtggttttat ccctaaataa tttcaatttt taaaaacatg cagcttcctt 2876

ctcccctttt ttatttttga aagaatacat ttggtcataa agtgaaaccc gtattagcaa 2936

gtacgtggca atgttcattc caatcagatg cagctttctc ctccgtctgg tctcctgttt 2996

gcaattgctt cctcatctc agtagggaaa aaattgagtg ggagtactga gatgtgtggg 3056

tttttgccat tggacaaaga atgagggttag aagactgcag cttggagtct ctctaggttt 3116

tcaactatctt cttcacaatt tgaacacttg acggttgtcc cttttaattt atttgaagtg 3176

ctatctttttt aaataaaggt tcatctgtcc atgcagtcct cttggattct ctgaatgtag 3236

taactatgaa gctatgccaa aggtaggcag aaaatgggct tgggagccag acactccagg 3296

gatcagtagt tctacccat agtctttgtg tgcttgctaa atggtgtaca tttcttgcta 3356

accacgttat taaaacttga tcagcacata aaaaaaaaaa aa 3398

<210> 316

<211> 872

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (61) .. (639)

<400> 316

atttggccct cgaggccaag aattcggcac gaggaccagc aggcagcct ccttgggtctc 60

atg ttg acc tta gag ttt ggg att ctg gaa ttc gat cct tca tgg ata	108
Met Leu Thr Leu Glu Phe Gly Ile Leu Glu Phe Asp Pro Ser Trp Ile	
1 5 10 15	
ggc agc tgg aca cag agg tcg tgg gtg agc tgg agg agc agg ccc gga	156
Gly Ser Trp Thr Gln Arg Ser Trp Val Ser Trp Arg Ser Arg Pro Gly	
17 22 27 32	
tgt gag ctg ttc tcc ata gtg gtg ttc ggc tcc atc gtg aac gag ggc	204
Cys Glu Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly	
33 38 43 48	
tac ctc aac agc gcc tcc gag ggg gag gag ttc tgc atc tac aac cgc	252
Tyr Leu Asn Ser Ala Ser Glu Gly Glu Glu Phe Cys Ile Tyr Asn Arg	
49 54 59 64	
aac ccc aac gcc tgc agc tat ggc gtg gcc gtg ggc gtg ctc gcc ttc	300
Asn Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe	
65 70 75 80	
ctc acc tgc ctg ctg tac ctg gcc ctg gac gtg tac ttc ccg cag atc	348
Leu Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile	
81 86 91 96	
agc agc gtc aag gac cgc aag aaa gcc gtc ctg tcc gac atc ggt gtc	396
Ser Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val	
97 102 107 112	
tcg gcc ttc tgg gct ttc ctc tgg ttc gtg gga ttc tgc tac ctg gcc	444
Ser Ala Phe Trp Ala Phe Leu Trp Phe Val Gly Phe Cys Tyr Leu Ala	
113 118 123 128	
aac cag tgg cag gtc tcc aag ccc aag gac aac cca ctg aac gaa ggg	492
Asn Gln Trp Gln Val Ser Lys Pro Lys Asp Asn Pro Leu Asn Glu Gly	
129 134 139 144	
acg gac gca gcc cgg gcc gcc atc gcc ttc tcc ttt ttc tcc atc ttc	540
Thr Asp Ala Ala Arg Ala Ala Ile Ala Phe Ser Phe Phe Ser Ile Phe	
145 150 155 160	
acc tgg agc ctg acc gca gcc ctg gcc gtg cgg aga ttc aag gac cta	588
Thr Trp Ser Leu Thr Ala Ala Leu Ala Val Arg Arg Phe Lys Asp Leu	
161 166 171 176	
agc ttc cag gag gag tac agc aca ctg ttc cct gcc tcg gca cag ccg	636
Ser Phe Gln Glu Glu Tyr Ser Thr Leu Phe Pro Ala Ser Ala Gln Pro	
177 182 187 192	
tag gcct ccccggttg cagaggccgg cagccctgta tcaccctgg cagtgggtg	693
*	
193	
gcaggagcag cctagtgcc gaaatgtcca agatgccagg gcatgcaggg cagtggaagg	753
ctggetttag gaaccaattc aggttctcca ctgactcatt cattccttca ccgcctcctt	813

cattgattct tcatgcgttc attcattcag taaacattta ttgagcaaaa aaaaaaaaaa 872

<210> 317
 <211> 1639
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (93)..(668)

<400> 317

tttgacacgc ctgcggtacc ggtccggaat tcccgggtcg acccacgcgt ccgccccacgc 60

gtccggggggg gcaccgcgcg ggtgcagcca cg atg gaa ggg ggt gcg tac gga 113
 Met Glu Gly Gly Ala Tyr Gly
 1 5

gcg ggc aaa gcc ggg ggc gcc ttc gac ccc tac acc ctg gtc cgg cag 161
 Ala Gly Lys Ala Gly Gly Ala Phe Asp Pro Tyr Thr Leu Val Arg Gln
 8 13 18 23

cgc cac acc atc ctg cgc gtc gtg tct tgg ctg ttc tcc ata gtg gtg 209
 Pro His Thr Ile Leu Arg Val Val Ser Trp Leu Phe Ser Ile Val Val
 24 29 34 39

ttc ggc tcc atc gtg aac gag ggc tac ctc aac agc gcc tcc gag ggg 257
 Phe Gly Ser Ile Val Asn Glu Gly Tyr Leu Asn Ser Ala Ser Glu Gly
 40 45 50 55

gag gag ttc tgc atc tac aac cgc aac ccc aac gcc tgc agc tat ggc 305
 Glu Glu Phe Cys Ile Tyr Asn Arg Asn Pro Asn Ala Cys Ser Tyr Gly
 56 61 66 71

gtg gcc gtg ggc gtg ctc gcc ttc ctc acc tgc ctg ctg tac ctg gcc 353
 Val Ala Val Gly Val Leu Ala Phe Leu Thr Cys Leu Leu Tyr Leu Ala
 72 77 82 87

ctg gac gtg tac ttc ccg cag atc agc agc gtc aag gac cgc aag aaa 401
 Leu Asp Val Tyr Phe Pro Gln Ile Ser Ser Val Lys Asp Arg Lys Lys
 88 93 98 103

gcc gtc ctg tcc gac atc ggt gtc tgc gcc ttc tgg gct ttc ctc tgg 449
 Ala Val Leu Ser Asp Ile Gly Val Ser Ala Phe Trp Ala Phe Leu Trp
 104 109 114 119

ttc gtg gga ttc tgc tac ctg gcc aac cag tgg cag gtc tcc aag ccc 497
 Phe Val Gly Phe Cys Tyr Leu Ala Asn Gln Trp Gln Val Ser Lys Pro
 120 125 130 135

aag gac aac cca ctg aac gaa ggg acg gac gca gcc cgg gcc gcc atc 545
 Lys Asp Asn Pro Leu Asn Glu Gly Thr Asp Ala Ala Arg Ala Ala Ile
 136 141 146 151

gcc ttc tcc ttt ttc tcc atc ttc acc tgg agc ctg acc gca gcc ctg	593
Ala Phe Ser Phe Phe Ser Ile Phe Thr Trp Ser Leu Thr Ala Ala Leu	
152 157 162 167	
gcc gtg cgg aga ttc aag gac cta agc ttc cag gag gag tac agc aca	641
Ala Val Arg Arg Phe Lys Asp Leu Ser Phe Gln Glu Glu Tyr Ser Thr	
168 173 178 183	
ctg ttc cct gcc tcg gca cag ccg tag gcctc cccggcttgc agaggccggc	693
Leu Phe Pro Ala Ser Ala Gln Pro *	
184 189	
agccctgtat cacccttggc agtgaggtgg caggagcagc ctagtgccag aaatgtccaa	753
gatgccaggg catgcagggc agtggaaaggc tggcttgagg aaccaattca ggttctccac	813
tgactcattc attccttcac cgctccttc attgattctt catgcgttca ttcattcagt	873
aaacatttat tgagcagctg ttttgtgcct agtgatgaat taggtggggc ccttggctcc	933
aggagcccac aggctgggga ggagaaaaca aacacatcaa tatctcttcc aaatggacag	993
ccgtggacag ttaccaggta ggtagcggcc ccatacatgg gctgcctaga ggcgttcag	1053
gtccccattg ctgagctgtg ggtgcagagc aatagcctct ccttcacag cggtgtgaag	1113
agtgacctca ctgtccttag ggtagcctc ctggccgagg atgtcacagg gctcctggtc	1173
tggctctgtc ctcatgtgct atgtgacct gacaaacccg tgcacctctc tcagcctcag	1233
tccacttacc tgaactgagg ggtgataatg gaccaacctc tcaaggctgt tgtgccaatg	1293
aaacaaaggc cagcccaggc cttagcacia gcatgctcaa taaatgtaag ctcttttgtt	1353
cattcattca ttcattcatt cattcattct tctctccaga gagtcagggg cacctccaga	1413
atctctactt tgagagtaat tctcatgtga tgaatccttg ttctccaaa ggattttggt	1473
ctctggttct acacagggtt cctgcttggg gccccagct gcctgggcag gaactcacc	1533
attcctccac tctctgctgg agttgaggag gctggaggag cacagacagt tccccaaag	1593
caatgcctca accctgcgag ggctgagca catcgagagt gagctt	1639

<210> 318
 <211> 842
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (61) .. (609)

<400> 318

atttggccct cgaggccaag aattcggcac gaggaccagc aggcattgcct ccttggtctc	60
atg ttg acc tta gag ttt ggg att ctg gaa ttc gat cct tca tgg ata	108
Met Leu Thr Leu Glu Phe Gly Ile Leu Glu Phe Asp Pro Ser Trp Ile	
1 5 10 15	
ggc agc tgg aca cag agg tcg tgg ctg ttc tcc ata gtg gtg ttc ggc	156
Gly Ser Trp Thr Gln Arg Ser Trp Leu Phe Ser Ile Val Val Phe Gly	
17 22 27 32	
tcc atc gtg aac gag ggc tac ctc aac agc gcc tcc gag ggg gag gag	204
Ser Ile Val Asn Glu Gly Tyr Leu Asn Ser Ala Ser Glu Gly Glu Glu	
33 38 43 48	
ttc tgc atc tac aac cgc aac ccc aac gcc tgc agc tat ggc gtg gcc	252
Phe Cys Ile Tyr Asn Arg Asn Pro Asn Ala Cys Ser Tyr Gly Val Ala	
49 54 59 64	
gtg ggc gtg ctc gcc ttc ctc acc tgc ctg ctg tac ctg gcc ctg gac	300
Val Gly Val Leu Ala Phe Leu Thr Cys Leu Leu Tyr Leu Ala Leu Asp	
65 70 75 80	
gtg tac ttc ccg cag atc agc agc gtc aag gac cgc aag aaa gcc gtc	348
Val Tyr Phe Pro Gln Ile Ser Ser Val Lys Asp Arg Lys Lys Ala Val	
81 86 91 96	
ctg tcc gac atc ggt gtc tcg gcc ttc tgg gct ttc ctc tgg ttc gtg	396
Leu Ser Asp Ile Gly Val Ser Ala Phe Trp Ala Phe Leu Trp Phe Val	
97 102 107 112	
gga ttc tgc tac ctg gcc aac cag tgg cag gtc tcc aag ccc aag gac	444
Gly Phe Cys Tyr Leu Ala Asn Gln Trp Gln Val Ser Lys Pro Lys Asp	
113 118 123 128	
aac cca ctg aac gaa ggg acg gac gca gcc cgg gcc gcc atc gcc ttc	492
Asn Pro Leu Asn Glu Gly Thr Asp Ala Ala Arg Ala Ala Ile Ala Phe	
129 134 139 144	
tcc ttt ttc tcc atc ttc acc tgg agc ctg acc gca gcc ctg gcc gtg	540
Ser Phe Phe Ser Ile Phe Thr Trp Ser Leu Thr Ala Ala Leu Ala Val	
145 150 155 160	
cgg aga ttc aag gac cta agc ttc cag gag gag tac agc aca ctg ttc	588
Arg Arg Phe Lys Asp Leu Ser Phe Gln Glu Glu Tyr Ser Thr Leu Phe	
161 166 171 176	
cct gcc tcg gca cag ccg tag gc ctccccggct tgcagaggcc ggcagccctg	641
Pro Ala Ser Ala Gln Pro *	
177 182	
tatcaccctt ggcagtgagg tggcaggagc agcctagtgc cagaaatgtc caagatgcc	701
gggcatgcag ggcagtggaa ggctggcttg aggaaccaat tcaggttctc cactgactca	761
ttcattcctt caccgcctcc ttcattgatt cttcatgcgt tcattcattc agtaaacatt	821
tattgagcaa aaaaaaaaaa a	842

<210> 319
 <211> 6757
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (182)..(1957)

<400> 319

```
gcacgagcgg ccgtggcctc gaggcaggcg ggacgtgctt tgcctccacc gatctccctg      60
tggggccctca tgtgctgtgc tcgctgacac ccgaagtccg cggctttccg cacacgggtgg      120
ggctgtcaga cccgctgccc ttggcggtcg aagtcgtcgt gggggcccgc ggcggccgcc      180
c   atg gag aag gcc agg aga ggc ggg gat ggc gtc ccc cgg ggg ccc      226
    Met Glu Lys Ala Arg Arg Gly Gly Asp Gly Val Pro Arg Gly Pro
      1             5             10

gta ctg cac atc gtg gtg gtc gga ttt cac cac aag aag ggc tgc cag      274
Val Leu His Ile Val Val Val Gly Phe His His Lys Lys Gly Cys Gln
  16             21             26             31

gtt gaa ttc tct tac ccg ccc ctg att cca gga gat gga cat gac agc      322
Val Glu Phe Ser Tyr Pro Pro Leu Ile Pro Gly Asp Gly His Asp Ser
  32             37             42             47

cac act tta cct gaa gaa tgg aag tat ttg ccc ttc ctt gcc tta cca      370
His Thr Leu Pro Glu Glu Trp Lys Tyr Leu Pro Phe Leu Ala Leu Pro
  48             53             58             63

gat ggc gca cac aac tac cag gaa gat act gtg ttt ttt cac ttg cca      418
Asp Gly Ala His Asn Tyr Gln Glu Asp Thr Val Phe Phe His Leu Pro
  64             69             74             79

ccc aga aat gga aat gga gcc aca gta ttt ggt atc tct tgc tat cga      466
Pro Arg Asn Gly Asn Gly Ala Thr Val Phe Gly Ile Ser Cys Tyr Arg
  80             85             90             95

caa att gaa gcc aag gca ctg aaa gta agg caa gca gat atc acc aga      514
Gln Ile Glu Ala Lys Ala Leu Lys Val Arg Gln Ala Asp Ile Thr Arg
  96             101            106            111

gag act gtt cag aaa agt gtc tgt gtt cta agc aag ctg cct ctg tat      562
Glu Thr Val Gln Lys Ser Val Cys Val Leu Ser Lys Leu Pro Leu Tyr
 112            117            122            127

ggg tta ctt caa gca aaa ctt caa ctc att aca cat gca tat ttt gaa      610
Gly Leu Leu Gln Ala Lys Leu Gln Leu Ile Thr His Ala Tyr Phe Glu
 128            133            138            143

gag aag gat ttt tcc caa att tct att cta aag gag ctt tat gaa cat      658
```

Glu Lys Asp Phe Ser Gln Ile Ser Ile Leu Lys Glu Leu Tyr Glu His	
144 149 154 159	
atg aat agt tcc ttg gga ggt gct tca tta gaa gga tcc caa gta tat	706
Met Asn Ser Ser Leu Gly Gly Ala Ser Leu Glu Gly Ser Gln Val Tyr	
160 165 170 175	
ctt ggt ctg tca cct cga gat ctt gtc ctt cat ttt cga cac aag gtc	754
Leu Gly Leu Ser Pro Arg Asp Leu Val Leu His Phe Arg His Lys Val	
176 181 186 191	
tta atc cta ttt aag cta att ctt ctt gaa aaa aag gtt ctt ttt tat	802
Leu Ile Leu Phe Lys Leu Ile Leu Leu Glu Lys Lys Val Leu Phe Tyr	
192 197 202 207	
att tct cca gtg aat aaa ttg gtg ggt gca ctg atg act gtg tta tcc	850
Ile Ser Pro Val Asn Lys Leu Val Gly Ala Leu Met Thr Val Leu Ser	
208 213 218 223	
ctt ttt cca ggc atg att gaa cat ggt ctc agt gac tgt tct cag tat	898
Leu Phe Pro Gly Met Ile Glu His Gly Leu Ser Asp Cys Ser Gln Tyr	
224 229 234 239	
aga ccc cgg aaa agt atg tct gaa gat ggt ggg ctt cag gaa agt aac	946
Arg Pro Arg Lys Ser Met Ser Glu Asp Gly Gly Leu Gln Glu Ser Asn	
240 245 250 255	
cca tgt gca gat gat ttt gtt tct gca tcc act gct gat gtt tca cat	994
Pro Cys Ala Asp Asp Phe Val Ser Ala Ser Thr Ala Asp Val Ser His	
256 261 266 271	
acc aac ttg gga act atc agg aaa gtc atg gca gga aac cat gga gaa	1042
Thr Asn Leu Gly Thr Ile Arg Lys Val Met Ala Gly Asn His Gly Glu	
272 277 282 287	
gat gct gcc atg aag act gag gag cct ttg ttc caa gtg gaa gac agc	1090
Asp Ala Ala Met Lys Thr Glu Glu Pro Leu Phe Gln Val Glu Asp Ser	
288 293 298 303	
agc aaa ggg cag gaa ccc aat gat acc aat caa tat ttg aaa cct cca	1138
Ser Lys Gly Gln Glu Pro Asn Asp Thr Asn Gln Tyr Leu Lys Pro Pro	
304 309 314 319	
tct cgc cca tct cca gat tct tca gaa agt gac tgg gaa act ttg gat	1186
Ser Arg Pro Ser Pro Asp Ser Ser Glu Ser Asp Trp Glu Thr Leu Asp	
320 325 330 335	
cct agt gtc tta gag gac ccc aac ttg aaa gaa agg gaa cag ctg gga	1234
Pro Ser Val Leu Glu Asp Pro Asn Leu Lys Glu Arg Glu Gln Leu Gly	
336 341 346 351	
tca gac cag aca aat ttg ttt cca aag gac tct gtc ccc tca gag agt	1282
Ser Asp Gln Thr Asn Leu Phe Pro Lys Asp Ser Val Pro Ser Glu Ser	
352 357 362 367	
ctt cca att act gta caa cct caa gct aat acg gga cag gta gtc ctg	1330
Leu Pro Ile Thr Val Gln Pro Gln Ala Asn Thr Gly Gln Val Val Leu	

368	373	378	383	
ata cca ggg ctc att tgc ggt ttg gaa gag gat cag tat ggc atg ccc				1378
Ile Pro Gly Leu Ile Ser Gly Leu Glu Glu Asp Gln Tyr Gly Met Pro				
384	389	394	399	
ctg gcc atc ttc aca aag gga tat ctg tgt ttg cct tac atg gca ttg				1426
Leu Ala Ile Phe Thr Lys Gly Tyr Leu Cys Leu Pro Tyr Met Ala Leu				
400	405	410	415	
cag cag cat cat ctt ctc tcc gat gtc acc gtt cgg ggg ttt gtt gct				1474
Gln Gln His His Leu Leu Ser Asp Val Thr Val Arg Gly Phe Val Ala				
416	421	426	431	
gga gct act aac atc ctt ttt cga caa cag aaa cac ctc agt gat gcc				1522
Gly Ala Thr Asn Ile Leu Phe Arg Gln Gln Lys His Leu Ser Asp Ala				
432	437	442	447	
att gtg gaa gta gaa gaa gct ctg atc cag atc cat gat cca gaa ctc				1570
Ile Val Glu Val Glu Glu Ala Leu Ile Gln Ile His Asp Pro Glu Leu				
448	453	458	463	
agg aag ctg ctt aac cca acc act gca gac cta agg ttc gca gac tac				1618
Arg Lys Leu Leu Asn Pro Thr Thr Ala Asp Leu Arg Phe Ala Asp Tyr				
464	469	474	479	
cta gtg agg cac gtg act gag aat cgg gat gac gtc ttc cta gat ggc				1666
Leu Val Arg His Val Thr Glu Asn Arg Asp Asp Val Phe Leu Asp Gly				
480	485	490	495	
acg ggc tgg gag gga ggt gac gaa tgg atc cgg gcc cag ttt gcg gtc				1714
Thr Gly Trp Glu Gly Gly Asp Glu Trp Ile Arg Ala Gln Phe Ala Val				
496	501	506	511	
tac att cat gcc ctg ctg gct gcc acg ctg caa tta gtt ctg ttc aga				1762
Tyr Ile His Ala Leu Leu Ala Ala Thr Leu Gln Leu Val Leu Phe Arg				
512	517	522	527	
ata gtg aac gtg gca aaa aaa att gga aac gtc atg gtc aca act agc				1810
Ile Val Asn Val Ala Lys Lys Ile Gly Asn Val Met Val Thr Thr Ser				
528	533	538	543	
cgg aat gtt gta caa aca gga aaa gct gtt ggc cag tca gtt gga gga				1858
Arg Asn Val Val Gln Thr Gly Lys Ala Val Gly Gln Ser Val Gly Gly				
544	549	554	559	
gct ttt tcc agt gca aag aca gct atg tct tca tgg ctt tcc act ttc				1906
Ala Phe Ser Ser Ala Lys Thr Ala Met Ser Ser Trp Leu Ser Thr Phe				
560	565	570	575	
acc act tcc acc tcc caa agt ctc act gag cca cca gat gag aag cct				1954
Thr Thr Ser Thr Ser Gln Ser Leu Thr Glu Pro Pro Asp Glu Lys Pro				
576	581	586	591	
tga gcaa ggcgtcagag gctgctattg ctttctgagg tttaagtgtc cctgtctgt				2011
*				
592				

ctgctgctcc caggctgtta ctagccacag atccacagca ggggaccata tgtcgaactg 2071
tttacaatgga tgttgctcta agtgaatgtt tgggatgccc gaaatgatga aatcacagcc 2131
atagcagggga tggctttcca ggttgggggtt tcaattgact acttttattt cagtctgagc 2191
ctgattaataa catacagtga acctttctaata gaattttgag ttttgatatt gtacattggt 2251
ttactttaga agagttttta cttatgtaaa ttttgttctg ttttggtggt tgaatatcta 2311
gatggtcact gtaatttata cttgctaaaa ttaatttata ttaccatttt ctctaaagtt 2371
ggccttaaaa cgtgcttata aagtgaaggg gtcatacagt tgggccttca ttattttgct 2431
gaattatgtg atgatttttt tgctttctac ccacaaaaca tttattaatt cacttcctcc 2491
cagaaacatg aaagttagag gtggtagttc tgaggattgg gtgttttggt ttacgttttt 2551
agtttgttct tccacatcc ttaaaaactt ggtttcagac atcaaggagt atcactgtgc 2611
tttctcctc tttataactg tgcaggtggg tgtgcagaga aatagcagag tgatgggtcg 2671
atgatactga agcagtttaa catgaatgtg tctgtagggc aatactttca aagaagacct 2731
atgtgtttat ttttcaaccg cagtcatgtt gcagtcttac aagcactttt tttttattcc 2791
agagtttggt ccactgtttt ctcttttttt ttgggggggg gggggggcgg ggtctcactc 2851
tatcgccag gctggagtgc agtgggtgcca tctcggtcca ctgcaacctc catctcccg 2911
gttcaagcaa ttcttgtaac tcagcctccc aagtagctgg gattatggac atgcgccacc 2971
atgcccggct aagtttttgt attttagtag agacgggggt tcaccatgtt ggccaggatg 3031
gtctcgatct cctgacctcg tgatccacc accccggcct cccaaagtgc tgggattaca 3091
ggcatgagcc actgcgcccg gcctgtttct tttttaaaca gttttctatt ggggtgttgc 3151
agacctacag cttttctcgt agtcttattc ataaagcttt tcaaagcact tagtcttcta 3211
cttcctaac tgaaagtct cctataatca atccctacc cttctagaa gtatcttaaa 3271
agaaaagcaa ggtgattgta agtattaaat agaaatctca tcttagttta tattcagcaa 3331
agtaagaggc aagagaagaa aactgcagcc ttgacatctg tcatctgaga aaggacatct 3391
ggtttcatgt taggcacata catgcatgtg tgtgccatct actgatgatt tgtacacagc 3451
tggaacctcg gtgtttgcca tgctcagctc tcatttgctt ttcaaggata cctgggatgg 3511
ctgttctcag agagtactta cggggaacag actgcctttt agtaacaagg gatacttggg 3571
aaatacattg tgagtatgat ctatcccaga ttgctgggga aataaaggag ggccctgatt 3631
atatttggtt tattcctcac taaatgttta agaagtaa atgtcccaagg catttgaaat 3691

gaacatagaa acataatcta aatgtctcta aattttccac tttgtgtttt ctaaacacaa 3751
 attgtattac tcatttgagc ataactcaag aattcagcga tgataaattg aagggctgaa 3811
 tgtgagaact ccattaatc cacttcttcc aagaaagtta acctcaggaa atactgtttg 3871
 aagagaagaa agtagtacca aacaaaaacc ttaaacagta cttgaatctt ttttgcgctg 3931
 agactataaa gaattcattc taacatcttg tttcataagg gccacatcat tcgttgagc 3991
 atgatagtgt gatttgtgta caattgttac ctctcagctg ctgaagttca cacttcaagg 4051
 atctaggagc tctgtgaggg gtcgtccagc aagatgctga tttgtcttcc agttggtatg 4111
 gtttctgtga tcggggtaaa ctcccgctc cactattca aaagcagccc aactcatgct 4171
 ttggaatcca ctgaaataaa aatagttaca tgaagtttaa ctttgcttta atatcacttg 4231
 ttctcattg aatatacact ttgatcagac tttctattaa catttctagc taagagtttg 4291
 actcttagtg gtcactttac tgactttcca acataaaaca agtatctcag aagatacagc 4351
 tttcatcata gaaatggcca aaagaccata gctatatttc cttcagggtc tgggaggtgg 4411
 agtttttcaa ggaacactgg ccgttgtatt gttggcaggg gcccacaggc agctcgcaca 4471
 atcaaaggca ggaagcctca cccctgggtc tgtgaccccc cccacccac acacacacat 4531
 acttcaggct tggattctag gctccaagt gccagcatag aagcagcagc ctctctccaa 4591
 accctggctc tgtgagccat aggaaccagc actaggctcat cttctgacat agccctgggtg 4651
 aagggtgtgtg tgtgttggtg gccacacttg ctaaggcttt tgtgtctaag aattgagtat 4711
 ttgtacctag gtgtgagggg accagggtca gccagccttt ttcagatggc gccaggcaca 4771
 cacactacat caatggcttg ctgggtggctt caccactatc cagggtgactt aaaagagtgt 4831
 ttggaaaatg tccctgggtat acttcaattc ctactagaca ttgtaatgac aatgggtgtg 4891
 gtaaggaaga gagagttaaa actaccagtt gtggaataga aatagttgca tgtccaaaga 4951
 aggcttagaa tgattgtgca tatgcagttg gctcacataa ccagcatgaa cagtctctcc 5011
 ccaaatccat tagtgattca ctacccccg ccaagcacag ccctaaaaca attctcgtcc 5071
 actttcctgt taagaaacac agcagcaata tactttggca gcaaaccaga gcatatgatg 5131
 taacttgctc aaccttatct tcctttccaa attctatact aagcatctga tgttttttag 5191
 aataatttcc tttggaaagc caatgagaaa acaaattagg aagagagaga agtgagaaat 5251
 tgttgcatgg ctgaggaaca agatgcttaa aatctgaatg gaagtatttt gagagcagta 5311
 tttcatgtgc taagggttat aagaattctt ttagaaaggg attagaattt tactctgcta 5371
 gttacaagtt ttaaagtcac gctacggcat tatcacctg gcaggtaggt tttgttattg 5431

ttttacattt tgtgaaaaaa agttttgtag aagttacagc tagtgggtcctt ttccctccag 5491
 agccagtgat gagggtggga gcacttcagc tctgtaaggg gccagcgctc tgacctttaa 5551
 ccacatgaac taacctgcgt cagcagttgc agaaagtagc ctgttaggac agcagctgct 5611
 aagcgttgcc tgggtatttta gtggggagaa ggctgggact cttcatggca tcaacacttg 5671
 catgctctga atctttgatc agagatgagg tgccattttt ggcatttoca ccccgctctcg 5731
 tggtagcctt taaaagtggg agaagatgct gccctaattc cccgaggatg attgtcattc 5791
 catgcagcat aatgtgccgt gaggagtttt ctcatccag ttctttggac ttcgtaacat 5851
 tggaattgtt ttcccataat ttccggcatt ccataaatat ttgtcaagga caaagaaaag 5911
 gaatgtggat gtttattctt ttcatatgaa tgactttgta cacatgactt cctgctttca 5971
 ttatgaagga ggggaaacta gttcccttgt atggtaactc caaagttaaa aaattgtgca 6031
 tgtctgaggg gttgaatata ttttgtaaaa ctctaaatac atttgtattt ctgtgctgtt 6091
 ctaaagttta cctttttact tatatgaaag ataactatat atttaaatca tgtaagtgga 6151
 acacagtgta ggggggtttt ccaatcttat tttcatcag gttctcacac ccacgtagta 6211
 tgctgctcaa attttttctg gtgtgcaaat gtgaacattt gaacatttca gttaggtact 6271
 gagccagaaa aggttaattga agttttcaga aagcttctgt gcttagaaaa tattttgttg 6331
 ttttcttaaa atattagtat tttgtagctg gaagaataag atcaaggctt acatgtttca 6391
 ggccacttgg tcaactggctc ctgaatttag aaaacattgg attaatgagt tgggtgaaggc 6451
 atttagtggg tacaaaaaca gtttaaatat ttatgattaa aggcttttca caaacctttt 6511
 taaagaaaat ttagctgaga aaacttaaaa agttttctaa ggaagttaa ctgtggcaca 6571
 tgttttgatc agaaaggtag ttctctttgc tctggtagtt ttaaagtttg tactagttct 6631
 ttatttctgt tgttttttta aattgttaaa attataaatc acgtctaac atactgaatt 6691
 gtaaaacttg aattgtatct ttattttaag cataaatgag aataaaatga tcctgttcac 6751
 cctgcc 6757

<210> 320
 <211> 1840
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (182)..(1600)

<400> 320

ccggaacccc	gggtcgaccc	acgcgtccgg	tcagctgaag	ggaaacaaac	aaaaaggaac	60
cagaggccac	ttgtatatat	aggtctcttc	agcatttatt	gggggcagaa	gaggaagatt	120
tctgaagagt	gcagctgcct	gaaccgagcc	ctgccgaaca	gctgagaatt	gcactgcaac	180
c	atg agt gag aac aat aag aat tcc ttg gag agc agc cta cgg caa	226				
	Met Ser Glu Asn Asn Lys Asn Ser Leu Glu Ser Ser Leu Arg Gln					
	1 5 10					
cta aaa tgc cat ttc acc tgg aac ttg atg gag gga gaa aac tcc ttg	274					
Leu Lys Cys His Phe Thr Trp Asn Leu Met Glu Gly Glu Asn Ser Leu						
16 21 26 31						
gat gat ttt gaa gac aaa gta ttt tac cgg act gag ttt cag aat cgt	322					
Asp Asp Phe Glu Asp Lys Val Phe Tyr Arg Thr Glu Phe Gln Asn Arg						
32 37 42 47						
gaa ttc aaa gcc aca atg tgc aac cta ctg gcc tat cta aag cac ctc	370					
Glu Phe Lys Ala Thr Met Cys Asn Leu Leu Ala Tyr Leu Lys His Leu						
48 53 58 63						
aaa ggg caa aac gag gca gcc ctg gaa tgc tta cgt aaa gct gaa gag	418					
Lys Gly Gln Asn Glu Ala Ala Leu Glu Cys Leu Arg Lys Ala Glu Glu						
64 69 74 79						
tta atc cag caa gag cat gct gac cag gca gaa atc aga agt ctg gtc	466					
Leu Ile Gln Gln Glu His Ala Asp Gln Ala Glu Ile Arg Ser Leu Val						
80 85 90 95						
acc tgg gga aac tat gcc tgg gtc tac tat cac atg ggc cga ctc tca	514					
Thr Trp Gly Asn Tyr Ala Trp Val Tyr Tyr His Met Gly Arg Leu Ser						
96 101 106 111						
gac gtt cag att tat gta gac aag gtg aaa cat gtc tgt gag aag ttt	562					
Asp Val Gln Ile Tyr Val Asp Lys Val Lys His Val Cys Glu Lys Phe						
112 117 122 127						
tcc agt ccc tat aga att gag agt cca gag ctt gac tgt gag gaa ggg	610					
Ser Ser Pro Tyr Arg Ile Glu Ser Pro Glu Leu Asp Cys Glu Glu Gly						
128 133 138 143						
tgg aca cgg tta aag tgt gga gga aac caa aat gaa aga gcg aag gtg	658					
Trp Thr Arg Leu Lys Cys Gly Gly Asn Gln Asn Glu Arg Ala Lys Val						
144 149 154 159						
tgc ttt gag aag gct ctg gaa aag aag cca aag aac cca gaa ttc acc	706					
Cys Phe Glu Lys Ala Leu Glu Lys Lys Pro Lys Asn Pro Glu Phe Thr						
160 165 170 175						
tct gga ctg gca ata gca agc tac cgt ctg gac aac tgg cca cca tct	754					
Ser Gly Leu Ala Ile Ala Ser Tyr Arg Leu Asp Asn Trp Pro Pro Ser						
176 181 186 191						

cag aac gcc att gac cct ctg agg caa gcc att cgg ctg aat cct gac	802
Gln Asn Ala Ile Asp Pro Leu Arg Gln Ala Ile Arg Leu Asn Pro Asp	
192 197 202 207	
aac cag tac ctt aaa gtc ctc ctg gct ctg aag ctt cat aag atg cgt	850
Asn Gln Tyr Leu Lys Val Leu Leu Ala Leu Lys Leu His Lys Met Arg	
208 213 218 223	
gaa gaa ggt gaa gag gaa ggt gaa gga gag aag tta gtt gaa gaa gcc	898
Glu Glu Gly Glu Glu Glu Gly Glu Gly Glu Lys Leu Val Glu Glu Ala	
224 229 234 239	
ttg gag aaa gcc cca ggt gta aca gat gtt ctt cgc agt gca gcc aag	946
Leu Glu Lys Ala Pro Gly Val Thr Asp Val Leu Arg Ser Ala Ala Lys	
240 245 250 255	
ttt tat cga aga aaa gat gag cca gac aaa gcg att gaa ctg ctt aaa	994
Phe Tyr Arg Arg Lys Asp Glu Pro Asp Lys Ala Ile Glu Leu Leu Lys	
256 261 266 271	
aag gct tta gaa tac ata cca aac aat gcc tac ctg cat tgc caa att	1042
Lys Ala Leu Glu Tyr Ile Pro Asn Asn Ala Tyr Leu His Cys Gln Ile	
272 277 282 287	
ggg tgc tgc tat agg gca aaa gtc ttc caa gta atg aat cta aga gag	1090
Gly Cys Cys Tyr Arg Ala Lys Val Phe Gln Val Met Asn Leu Arg Glu	
288 293 298 303	
aat gga atg tat ggg aaa aga aag tta ctg gaa cta ata gga cac gct	1138
Asn Gly Met Tyr Gly Lys Arg Lys Leu Leu Glu Leu Ile Gly His Ala	
304 309 314 319	
gtg gct cat ctg aag aaa gct gat gag gcc aat gat aat ctc ttc cgt	1186
Val Ala His Leu Lys Lys Ala Asp Glu Ala Asn Asp Asn Leu Phe Arg	
320 325 330 335	
gtc tgt tcc att ctt gcc agc ctc cat gct cta gca gat cag tat gaa	1234
Val Cys Ser Ile Leu Ala Ser Leu His Ala Leu Ala Asp Gln Tyr Glu	
336 341 346 351	
gac gca gag tat tac ttc caa aag gaa ttc agt aaa gag ctt act cct	1282
Asp Ala Glu Tyr Tyr Phe Gln Lys Glu Phe Ser Lys Glu Leu Thr Pro	
352 357 362 367	
gta gcg aaa caa ctg ctc cat ctg cgg tat ggc aac tgt cag ctg tac	1330
Val Ala Lys Gln Leu Leu His Leu Arg Tyr Gly Asn Cys Gln Leu Tyr	
368 373 378 383	
caa atg aag tgt gaa gac aag gcc atc cac cac ttt ata gag ggt gta	1378
Gln Met Lys Cys Glu Asp Lys Ala Ile His His Phe Ile Glu Gly Val	
384 389 394 399	
aaa ata aac cag aaa tca agg gag aaa gaa aag atg aaa gac aaa ctg	1426
Lys Ile Asn Gln Lys Ser Arg Glu Lys Glu Lys Met Lys Asp Lys Leu	
400 405 410 415	
caa aaa att gcc aaa atg cga ctt tct aaa aat gga gca gat tct gag	1474

Gln Lys Ile Ala Lys Met Arg Leu Ser Lys Asn Gly Ala Asp Ser Glu
416 421 426 431

gct ttg cat gtc ttg gca ttc ctt cag gag ctg aat gaa aaa atg caa 1522
Ala Leu His Val Leu Ala Phe Leu Gln Glu Leu Asn Glu Lys Met Gln
432 437 442 447

caa gca gat gaa gac tct gag agg ggt ttg gag tct gga agc ctc atc 1570
Gln Ala Asp Glu Asp Ser Glu Arg Gly Leu Glu Ser Gly Ser Leu Ile
448 453 458 463

cct tca gca tca agc tgg aat ggg gaa tga a gaatagagat gtggtgcccc 1621
Pro Ser Ala Ser Ser Trp Asn Gly Glu *
464 469

ctaggctact gctgaaaggg agctgaaatt cctccaccaa gttggtattc aaaatatgta 1681

atgactggta tggcaaaaga ttggactaag acactggcca taccactgga cagggttatg 1741

ttaacacctg aattgctggg tcttgagaga gcccaaggag ttctgggaga gggaccagat 1801

tggggggtag gtccacgggc ttggtgatag acatatttc 1840

<210> 321
<211> 2539
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (178)..(963)

<400> 321
cggaactctg gaggaacgct gagctgagca gcaccgagga cagcgcccgg cagcgcccgc 60
gcccaggctc ccctccgcag ccctgactcg cgcacacgct gagcttttgc tcaactccct 120

tcgcgcggac acagacacac gcatattcac acaccagac acacaccccg ctgtaca 177
atg gca gaa tcc cac ctg cag tca tcc ctc atc aca gcc tca cag ttt 225
Met Ala Glu Ser His Leu Gln Ser Ser Leu Ile Thr Ala Ser Gln Phe
1 5 10 15

ttc gag atc tgg ctc cat ttc gac gct gac gga agt ggt tac ctg gaa 273
Phe Glu Ile Trp Leu His Phe Asp Ala Asp Gly Ser Gly Tyr Leu Glu
17 22 27 32

gga aag gag ctg cag aac ttg atc cag gag ctc cag cag gcg cga aag 321
Gly Lys Glu Leu Gln Asn Leu Ile Gln Glu Leu Gln Gln Ala Arg Lys
33 38 43 48

aag gct gga ttg gag tta tca cct gaa atg aaa act ttt gtg gat cag 369
Lys Ala Gly Leu Glu Leu Ser Pro Glu Met Lys Thr Phe Val Asp Gln
49 54 59 64

tat ggg caa aga gat gat gga aaa ata gga att gta gag ttg gct cac	417
Tyr Gly Gln Arg Asp Asp Gly Lys Ile Gly Ile Val Glu Leu Ala His	
65 70 75 80	
gta tta ccc aca gaa gag aat ttc ctg ctg ctc ttc cga tgc cag cag	465
Val Leu Pro Thr Glu Glu Asn Phe Leu Leu Leu Phe Arg Cys Gln Gln	
81 86 91 96	
ctg aag tcc tgt gag gaa ttc atg aag aca tgg aga aaa tat gat act	513
Leu Lys Ser Cys Glu Glu Phe Met Lys Thr Trp Arg Lys Tyr Asp Thr	
97 102 107 112	
gac cac agt ggc ttc ata gaa act gag gag ctt aag aac ttt cta aag	561
Asp His Ser Gly Phe Ile Glu Thr Glu Glu Leu Lys Asn Phe Leu Lys	
113 118 123 128	
gac ctg cta gaa aaa gca aac aag act gtt gat gac aca aaa tta gcc	609
Asp Leu Leu Glu Lys Ala Asn Lys Thr Val Asp Asp Thr Lys Leu Ala	
129 134 139 144	
gag tat aca gac cta atg ctg aaa cta ttt gat tca aat aat gat ggg	657
Glu Tyr Thr Asp Leu Met Leu Lys Leu Phe Asp Ser Asn Asn Asp Gly	
145 150 155 160	
aag ctg gaa tta act gag atg gcc agg tta cta cca gtg cag gag aat	705
Lys Leu Glu Leu Thr Glu Met Ala Arg Leu Leu Pro Val Gln Glu Asn	
161 166 171 176	
ttt ctt ctt aaa ttc cag gga atc aaa atg tgt ggg aaa gag ttc aat	753
Phe Leu Leu Lys Phe Gln Gly Ile Lys Met Cys Gly Lys Glu Phe Asn	
177 182 187 192	
aag gct ttt gag ctg tat gat cag gac ggc aat gga tac ata gat gaa	801
Lys Ala Phe Glu Leu Tyr Asp Gln Asp Gly Asn Gly Tyr Ile Asp Glu	
193 198 203 208	
aat gaa ctg gat gct tta ctg aag gat ctg tgc gag aag aat aaa cag	849
Asn Glu Leu Asp Ala Leu Leu Lys Asp Leu Cys Glu Lys Asn Lys Gln	
209 214 219 224	
gat ctg gat att aat aat att aca aca tac aag aag aac ata atg gct	897
Asp Leu Asp Ile Asn Asn Ile Thr Thr Tyr Lys Lys Asn Ile Met Ala	
225 230 235 240	
ttg tgc gat gga ggg aag ctg tac cga acg gat ctt gct ctt att ctc	945
Leu Ser Asp Gly Gly Lys Leu Tyr Arg Thr Asp Leu Ala Leu Ile Leu	
241 246 251 256	
tgt gct ggg gat aac tag agttgg tggcgcgaac cacttgctag tgatacactg	999
Cys Ala Gly Asp Asn *	
257 262	
tatctaaaaa ataactgtgc actataaggg agtaggctgt attttctttt atatctgtaa	1059
atttaactgc atatagataa ttatccagga tgtgtggctc attcttttca gcttgtttct	1119
atactgtttg taatatacag tttttgtaac catatgattg aaaagaagaa agtctatgct	1179

taggccagtc agtacaccca attttaaaaa ataacatatt cttgctttca caaatatagt	1239
tgaacaagat ttccctaaaa attccaccag gattaatctc taaaattcta gtctctgatt	1299
tgcaaatgca catttgtcac tgaataatgg aattatgtat aacaagccaa acattcttat	1359
tttagacaac catagaactg tcccacaaaa tattttctaag cttattttcta actattagga	1419
ggaatgtgct tttccatcta aaatactcac caaaatatag ttaattgtgg ctttatgaag	1479
ttaacagtct cattacagat ttagtttacc aatcaacagc atgtctactg cttggatcca	1539
tacaaaacta tcggttcaag ttgatgtgac aaggggaagg agcaccagat gacacataaa	1599
tctgtctgat tctatgectg tattttccaac aaacttactg tcagagaata tgacctaaat	1659
ccattttcta aactgttttc atgtgttgca aattattcta gtcaactgct gttttatgtc	1719
atactctgtg taatctctga ttaaatttaa tatactgcat atcctgggtg ctagtttgca	1779
tacttctgg attttctttc tatgtagaac tgttcatttc caccaagggc atctgctgcc	1839
tctgaaaata tttttttcta gctataacaa ctctattttt tactacataa ttaaatttta	1899
atgtaaaatt catagcatcc tgattattga atgttatatc atcaatactt ttgtgtattc	1959
tgtggattct atatttcata ttgagatcag cattcaaaat agttctatct ctatctgcaa	2019
atagtttcaa atgagtttaa aaaaataaca tctgaaaaga aatgctaattg taatcattta	2079
tcttatctag caagaagatt ctaaaacatt ctttaacata catctaagtc agtttcacat	2139
atttgtagct agaatatcct atactgggta tagttgatat gtaacagttg gtgattttag	2199
atttctttga ttgtgaaaca gggagctatg agagatgtgt ccatgtgaaa tttacagtta	2259
ctgcctagga gttaatgatc gttctgggtc agcttgaatg tccccattct ataaattcaa	2319
cacttatttt ctgaattcat aaaaataacc aaaaaatgtg agctataatg tttccctcaa	2379
gaacaaacag aaacgagatt tgccaaaaac taaaattcaa caaatgatgt tgagtgggag	2439
attggctttg ccttttagcgt gtaaattggaa gcactgccat tagactgaat ttaactacta	2499
agaataaata aagaagaaaa taaccttaaa aaaaaaaaaa	2539

<210> 322
 <211> 1311
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (241)..(795)

<400> 322

ctgcagggtac	cggtccggaa	ttcccgggtc	gacccacgcg	tccggaagtg	gcagggcagg	60
gtgtgtacca	ggaagaagat	gctggcgcac	cctgggctgg	ctggggaggt	gaggccagag	120
ggaggatgga	gcccagagag	ggaatgtggg	tgatgaggtt	gggccaggcc	cctaaacccc	180
aagccccaga	ggccactcc	agtgcccccc	acaggatctg	gagagctgct	ggagaacacc	240
atg gag gcc	atg gag aac	tcc atg gcc	cag cgc	tcg gac	ctc ctg gag	288
Met Glu Ala	Met Glu Asn	Ser Met Ala	Gln Arg	Ser Asp	Leu Leu Glu	
1	5	10		15		
ctc gac tgt	cag ctg aca	cgg gac aga	gtg gtg	gtg gtg	tca cat gat	336
Leu Asp Cys	Gln Leu Thr	Arg Asp Arg	Val Val	Val Val	Ser His Asp	
17	22	27		32		
gag aac ctg	tgc cgc cag	tcg ggc cta	aac agg	gat gtg	ggc agc ctg	384
Glu Asn Leu	Cys Arg Gln	Ser Gly Leu	Asn Arg	Asp Val	Gly Ser Leu	
33	38	43		48		
gac ttc gag	gac ctg ccc	ctc tac aag	gag aag	ctg gag	gtt tac ttc	432
Asp Phe Glu	Asp Leu Pro	Leu Tyr Lys	Glu Lys	Leu Glu	Val Tyr Phe	
49	54	59		64		
tct cca ggc	cac ttt gct	cac ggg tca	gac cgg	cgc atg	gtt cgt ctg	480
Ser Pro Gly	His Phe Ala	His Gly Ser	Asp Arg	Arg Met	Val Arg Leu	
65	70	75		80		
gag gac ctg	ttc cag agg	ttt cca agg	aca ccc	atg agc	gta gag atc	528
Glu Asp Leu	Phe Gln Arg	Phe Pro Arg	Thr Pro	Met Ser	Val Glu Ile	
81	86	91		96		
aaa ggg aag	aac gaa gag	ctc atc cgt	gag ata	gca ggc	ttg gtg aga	576
Lys Gly Lys	Asn Glu Glu	Leu Ile Arg	Glu Ile	Ala Gly	Leu Val Arg	
97	102	107		112		
cgc tat gac	cgt aat gaa	atc acc atc	tgg gcc	tcg gag	aag agc tcg	624
Arg Tyr Asp	Arg Asn Glu	Ile Thr Ile	Trp Ala	Ser Glu	Lys Ser Ser	
113	118	123		128		
gtc atg aag	aaa tgc aag	gct gcc tct	ctc tct	gtc gcc	cag gct gga	672
Val Met Lys	Lys Cys Lys	Ala Ala Ser	Leu Ser	Val Ala	Gln Ala Gly	
129	134	139		144		
gtg cgg tgg	tgc gac ctc	ggc tca ctg	caa cct	ctg cct	cct ggg ttc	720
Val Arg Trp	Cys Asp Leu	Gly Ser Leu	Gln Pro	Leu Pro	Pro Gly Phe	
145	150	155		160		
aag cga ttc	tca tgc ttc	agc ctc ccg	agt agc	tgg gat	tac aga acc	768
Lys Arg Phe	Ser Cys Phe	Ser Leu Pro	Ser Ser	Trp Asp	Tyr Arg Thr	
161	166	171		176		
ccg aga tgc	ccc tgt cct	tca caa taa	gccga	ggattctggg	tgctgctttc	820
Pro Arg Cys	Pro Cys Pro	Ser Gln *				

177

182

ctactacctg gggctgctgc ccttcatccc aatccctgag aagttcttct tctgcttctt 880
 gccaacatc atcaacagga cctatttccc attttctctgc tcttgctga accagttaat 940
 tggctgtggt ttcgaaatgg ctgatcatga ggaagagtct gatccgacac ttggaggagc 1000
 gaggggtgca ggtgaggccg tgaccaccac ttccaccgca cacagacctg gcagcagggt 1060
 tccggtccca ctctgctgcc aactagctgc atcactcggg cagggtggtct tttggtgcct 1120
 taatgaagag tcggattttg aagcagcctt cagcgtggga gccactggcg tcataacgga 1180
 ttatcccaca gccctgcggc actacctgga caaccatgga ccagctgccc ggacctccta 1240
 agtccagaag cctcgaggtc tctgttttct cttcctgaaa aataaatatt tgcctttcaa 1300
 aaaaaaaaaa a 1311

<210> 323

<211> 6487

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (164)..(4093)

<400> 323

ctgcaggaat tcggcacgag ccggcacaaa cctcagtggg ggttctgtgg ttgtttctgt 60
 ctttttttga tagaatcttt gattagtatc gaatttactg tatttggcca tgtgaactat 120
 tgggagcctc ctaggggtgag ggaaattaag agctttcaga gga atg agg cga ctg 175
 Met Arg Arg Leu
 1

att tgc aaa cgg atc tgt gat tat aaa agc ttc gat gat gaa gaa tca 223
 Ile Cys Lys Arg Ile Cys Asp Tyr Lys Ser Phe Asp Asp Glu Glu Ser
 5 10 15 20

gtg gat gga aat agg cca tca tca gct gca tca gcc ttc aag gtt cct 271
 Val Asp Gly Asn Arg Pro Ser Ser Ala Ala Ser Ala Phe Lys Val Pro
 21 26 31 36

gca cct aaa aca tcc gga aat cct gcc aac agt gca agg aag cct ggt 319
 Ala Pro Lys Thr Ser Gly Asn Pro Ala Asn Ser Ala Arg Lys Pro Gly
 37 42 47 52

tca gca ggt ggc cct aag gtt gga gca ggt gct tct aag gaa gga ggt 367
 Ser Ala Gly Gly Pro Lys Val Gly Ala Gly Ala Ser Lys Glu Gly Gly
 53 58 63 68

gct gga gca gtt gat gaa gat gat ttt ata aaa gct ttt aca gat gtc Ala Gly Ala Val Asp Glu Asp Asp Phe Ile Lys Ala Phe Thr Asp Val 69 74 79 84	415
cct tct att cag att tat tct agt cga gaa ctc gaa gaa aca tta aat Pro Ser Ile Gln Ile Tyr Ser Ser Arg Glu Leu Glu Glu Thr Leu Asn 85 90 95 100	463
aaa atc agg gaa att ttg tca gat gat aaa cat gac tgg gat cag cgt Lys Ile Arg Glu Ile Leu Ser Asp Asp Lys His Asp Trp Asp Gln Arg 101 106 111 116	511
gcc aat gca ctg aag aaa att cga tca ctg ctt gtt gct gga gct gca Ala Asn Ala Leu Lys Lys Ile Arg Ser Leu Leu Val ³ Ala Gly Ala Ala 117 122 127 132	559
cag tat gat tgc ttt ttt caa cat tta cga ttg ttg gat gga gca ctt Gln Tyr Asp Cys Phe Phe Gln His Leu Arg Leu Leu Asp Gly Ala Leu 133 138 143 148	607
aaa ctt tca gct aag gat ctt aga tcc cag gtg gtt aga gaa gct tgt Lys Leu Ser Ala Lys Asp Leu Arg Ser Gln Val Val Arg Glu Ala Cys 149 154 159 164	655
att act gta gcc cac ctt tca aca gtt ttg gga aac aag ttt gat cat Ile Thr Val Ala His Leu Ser Thr Val Leu Gly Asn Lys Phe Asp His 165 170 175 180	703
ggc gct gaa gcc att gta cct aca ctt ttt aat ctc gtc ccc aat agt Gly Ala Glu Ala Ile Val Pro Thr Leu Phe Asn Leu Val Pro Asn Ser 181 186 191 196	751
gca aaa gtc atg gca act tct gga tgt gca gca atc aga ttt atc att Ala Lys Val Met Ala Thr Ser Gly Cys Ala Ala Ile Arg Phe Ile Ile 197 202 207 212	799
cgg cat act cat gta ccc aga ctt ata cct tta ata aca agc aat tgc Arg His Thr His Val Pro Arg Leu Ile Pro Leu Ile Thr Ser Asn Cys 213 218 223 228	847
aca tca aaa tca gtt ccc gtg agg aga cgt tca ttt gaa ttt tta gat Thr Ser Lys Ser Val Pro Val Arg Arg Arg Ser Phe Glu Phe Leu Asp 229 234 239 244	895
tta ttg ttg caa gag tgg cag act cat tca ttg gaa aga cat gca gcc Leu Leu Leu Gln Glu Trp Gln Thr His Ser Leu Glu Arg His Ala Ala 245 250 255 260	943
gtc ttg gtt gaa act att aaa aag gga att cat gat gct gac gct gag Val Leu Val Glu Thr Ile Lys Lys Gly Ile His Asp Ala Asp Ala Glu 261 266 271 276	991
gcc aga gtg gag gca aga aag aca tac atg ggt ctt aga aac cac ttt Ala Arg Val Glu Ala Arg Lys Thr Tyr Met Gly Leu Arg Asn His Phe 277 282 287 292	1039
cct ggt gaa gct gaa aca tta tat aat tcc ctt gag cca tct tat cag	1087

Pro Gly Glu Ala Glu Thr Leu Tyr Asn Ser Leu Glu Pro Ser Tyr Gln	
293 298 303 308	
aag agt ctt caa act tac tta aag agt tct ggc agt gta gca tct ctt	1135
Lys Ser Leu Gln Thr Tyr Leu Lys Ser Ser Gly Ser Val Ala Ser Leu	
309 314 319 324	
cca caa tca gac agg tcc tca tcc agc tca cag gaa agt ctc aat cgc	1183
Pro Gln Ser Asp Arg Ser Ser Ser Ser Ser Gln Glu Ser Leu Asn Arg	
325 330 335 340	
cct ttt tct tcc aaa tgg tct aca gca aat cca tca act gtg gct gga	1231
Pro Phe Ser Ser Lys Trp Ser Thr Ala Asn Pro Ser Thr Val Ala Gly	
341 346 351 356	
aga gta tca gca ggc agc agc aaa gcc agt tcc ctt cca gga agc ctg	1279
Arg Val Ser Ala Gly Ser Ser Lys Ala Ser Ser Leu Pro Gly Ser Leu	
357 362 367 372	
cag cgt tca cga agt gac att gat gtg aat gct gct gca ggt gcc aag	1327
Gln Arg Ser Arg Ser Asp Ile Asp Val Asn Ala Ala Ala Gly Ala Lys	
373 378 383 388	
gca cat cat gct gct gga cag tct gtg cga agc ggg cgc tta ggt gca	1375
Ala His His Ala Ala Gly Gln Ser Val Arg Ser Gly Arg Leu Gly Ala	
389 394 399 404	
ggg gcc ctg aat gca ggt tcc tat gcg tca cta gag gat act tct gac	1423
Gly Ala Leu Asn Ala Gly Ser Tyr Ala Ser Leu Glu Asp Thr Ser Asp	
405 410 415 420	
aag ctg gat gga aca gca tct gaa gat ggc cgg gtg aga gca aaa ctt	1471
Lys Leu Asp Gly Thr Ala Ser Glu Asp Gly Arg Val Arg Ala Lys Leu	
421 426 431 436	
tca gca cca ctt gct ggc atg gga aat gcc aag gca gat tct aga gga	1519
Ser Ala Pro Leu Ala Gly Met Gly Asn Ala Lys Ala Asp Ser Arg Gly	
437 442 447 452	
aga agt cga aca aaa atg gtg tct caa tca cag cct ggt agc cgg tct	1567
Arg Ser Arg Thr Lys Met Val Ser Gln Ser Gln Pro Gly Ser Arg Ser	
453 458 463 468	
ggg tct cca gga aga gtt ctg acc aca aca gcc ctg tcc act gtg agc	1615
Gly Ser Pro Gly Arg Val Leu Thr Thr Thr Ala Leu Ser Thr Val Ser	
469 474 479 484	
tct ggt gtt caa aga gtc ctg gtc aat tca gcc tca gca caa aaa aga	1663
Ser Gly Val Gln Arg Val Leu Val Asn Ser Ala Ser Ala Gln Lys Arg	
485 490 495 500	
agc aag ata cca cgg agc cag ggc tgt agc aga gag gct agt cca tct	1711
Ser Lys Ile Pro Arg Ser Gln Gly Cys Ser Arg Glu Ala Ser Pro Ser	
501 506 511 516	
agg ctt tca gtg gcc cga agc agt cgt att cct cga cca agt gtg agt	1759
Arg Leu Ser Val Ala Arg Ser Ser Arg Ile Pro Arg Pro Ser Val Ser	

517	522	527	532	
caa gga tgc agc cgg gaa gct agt cgg gag agc agc aga gac aca agt				1807
Gln Gly Cys Ser Arg Glu Ala Ser Arg Glu Ser Ser Arg Asp Thr Ser				
533	538	543	548	
cct gtt cgc tct ttt cag ccc ctc gcc tcc aga cac cat tcc aga tca				1855
Pro Val Arg Ser Phe Gln Pro Leu Ala Ser Arg His His Ser Arg Ser				
549	554	559	564	
act ggt gcc ctc tac gcc ccc gaa gtg tat ggg gcc tca ggt cca ggt				1903
Thr Gly Ala Leu Tyr Ala Pro Glu Val Tyr Gly Ala Ser Gly Pro Gly				
565	570	575	580	
tat ggg atc agc caa tca agt cga ctg tcg tct tct gtt agt gcc atg				1951
Tyr Gly Ile Ser Gln Ser Ser Arg Leu Ser Ser Ser Val Ser Ala Met				
581	586	591	596	
cga gtc ctg aac aca ggt tct gat gtg gag gag gcg gtg gca gat gcc				1999
Arg Val Leu Asn Thr Gly Ser Asp Val Glu Glu Ala Val Ala Asp Ala				
597	602	607	612	
ttg ctc tta gga gac ata cgg act aag aaa aaa cca gct cga aga aga				2047
Leu Leu Leu Gly Asp Ile Arg Thr Lys Lys Lys Pro Ala Arg Arg Arg				
613	618	623	628	
tat gaa tca tat gga atg cat tca gat gat gac gcc aac agc gat gca				2095
Tyr Glu Ser Tyr Gly Met His Ser Asp Asp Asp Ala Asn Ser Asp Ala				
629	634	639	644	
tct agt got tgt tca gaa cgc tcc tat agt tct cga aat ggt agt att				2143
Ser Ser Ala Cys Ser Glu Arg Ser Tyr Ser Ser Arg Asn Gly Ser Ile				
645	650	655	660	
cct aca tat atg agg cag acg gaa gat gtg gca gaa gtc ctc aat aga				2191
Pro Thr Tyr Met Arg Gln Thr Glu Asp Val Ala Glu Val Leu Asn Arg				
661	666	671	676	
tgt gct agt tcc aat tgg tca gaa agg aaa gaa ggc ctc cta ggt ctg				2239
Cys Ala Ser Ser Asn Trp Ser Glu Arg Lys Glu Gly Leu Leu Gly Leu				
677	682	687	692	
cag aac tta tta aaa aat cag aga aca cta agt cga gtt gaa ctg aaa				2287
Gln Asn Leu Leu Lys Asn Gln Arg Thr Leu Ser Arg Val Glu Leu Lys				
693	698	703	708	
aga tta tgt gaa att ttc aca aga atg ttt gct gac cct cat ggc aag				2335
Arg Leu Cys Glu Ile Phe Thr Arg Met Phe Ala Asp Pro His Gly Lys				
709	714	719	724	
aga gta ttc agc atg ttt ttg gag act cta gtg gat ttc ata caa gtc				2383
Arg Val Phe Ser Met Phe Leu Glu Thr Leu Val Asp Phe Ile Gln Val				
725	730	735	740	
cac aaa gat gat ctt caa gat tgg ttg ttt gta ctg ctg aca caa cta				2431
His Lys Asp Asp Leu Gln Asp Trp Leu Phe Val Leu Leu Thr Gln Leu				
741	746	751	756	

cta aaa aaa atg ggt gct gat ttg ctt gga tct gtt cag gca aaa gtt	2479
Leu Lys Lys Met Gly Ala Asp Leu Leu Gly Ser Val Gln Ala Lys Val	
757 762 767 772	
cag aaa gcc ctt gat gtt aca aga gag tct ttt cca aat gat ctt cag	2527
Gln Lys Ala Leu Asp Val Thr Arg Glu Ser Phe Pro Asn Asp Leu Gln	
773 778 783 788	
ttc aat att cta atg aga ttt aca gtt gat cag acc cag aca cca agc	2575
Phe Asn Ile Leu Met Arg Phe Thr Val Asp Gln Thr Gln Thr Pro Ser	
789 794 799 804	
tta aag gtg aag gtt gct atc ctt aaa tac ata gaa act ctg gcc aaa	2623
Leu Lys Val Lys Val Ala Ile Leu Lys Tyr Ile Glu Thr Leu Ala Lys	
805 810 815 820	
cag atg gat cca gga gat ttt ata aat tcc agt gaa act cgc cta gca	2671
Gln Met Asp Pro Gly Asp Phe Ile Asn Ser Ser Glu Thr Arg Leu Ala	
821 826 831 836	
gtg tct cgg gtc atc act tgg aca aca gaa ccc aaa agt tct gat gtt	2719
Val Ser Arg Val Ile Thr Trp Thr Thr Glu Pro Lys Ser Ser Asp Val	
837 842 847 852	
cgg aag gca gca cag tca gtg ctg att tca tta ttt gaa ctc aat acc	2767
Arg Lys Ala Ala Gln Ser Val Leu Ile Ser Leu Phe Glu Leu Asn Thr	
853 858 863 868	
cca gag ttt aca atg tta tta gga gct tta cca aaa act ttt cag gat	2815
Pro Glu Phe Thr Met Leu Leu Gly Ala Leu Pro Lys Thr Phe Gln Asp	
869 874 879 884	
ggg gct acc aag ctt ctt cat aat cac ctt cga aac act ggc aat gga	2863
Gly Ala Thr Lys Leu Leu His Asn His Leu Arg Asn Thr Gly Asn Gly	
885 890 895 900	
acc cag agt tcc atg ggg agt cct ttg aca aga cca aca cca cga tca	2911
Thr Gln Ser Ser Met Gly Ser Pro Leu Thr Arg Pro Thr Pro Arg Ser	
901 906 911 916	
cca gct aac tgg tcc agt cct ctt act tct cct acc aat aca tca cag	2959
Pro Ala Asn Trp Ser Ser Pro Leu Thr Ser Pro Thr Asn Thr Ser Gln	
917 922 927 932	
aat act tta tct cca agt gca ttt gat tat gac aca gaa aat atg aac	3007
Asn Thr Leu Ser Pro Ser Ala Phe Asp Tyr Asp Thr Glu Asn Met Asn	
933 938 943 948	
tct gaa gat att tat agc tct ctt aga ggt gtc act gaa gca atc cag	3055
Ser Glu Asp Ile Tyr Ser Ser Leu Arg Gly Val Thr Glu Ala Ile Gln	
949 954 959 964	
aat ttc agc ttc cgt agc caa gaa gat atg aat gag cca ttg aaa agg	3103
Asn Phe Ser Phe Arg Ser Gln Glu Asp Met Asn Glu Pro Leu Lys Arg	
965 970 975 980	

gat tct aaa aaa gat gat ggc gat tca atg tgt ggt ggt cct ggg atg	3151
Asp Ser Lys Lys Asp Asp Gly Asp Ser Met Cys Gly Gly Pro Gly Met	
981 986 991 996	
tct gac cca aga gca gga ggt gat gct act gac tca agt caa aca gct	3199
Ser Asp Pro Arg Ala Gly Gly Asp Ala Thr Asp Ser Ser Gln Thr Ala	
997 1002 1007 1012	
ctt gat aat aaa gct tca ttg ctc cat tca atg cct act cac tcc tct	3247
Leu Asp Asn Lys Ala Ser Leu Leu His Ser Met Pro Thr His Ser Ser	
1013 1018 1023 1028	
cca cgc tct cga gac tat aat cca tat aac tat tca gat agc atc agt	3295
Pro Arg Ser Arg Asp Tyr Asn Pro Tyr Asn Tyr Ser Asp Ser Ile Ser	
1029 1034 1039 1044	
ccc ttc aac aag tct gcc ctc aag gaa gcc atg ttt gat gat gat gct	3343
Pro Phe Asn Lys Ser Ala Leu Lys Glu Ala Met Phe Asp Asp Asp Ala	
1045 1050 1055 1060	
gac cag ttt cct gac gat ctt tcc cta gat cat tct gac cta gtt gca	3391
Asp Gln Phe Pro Asp Asp Leu Ser Leu Asp His Ser Asp Leu Val Ala	
1061 1066 1071 1076	
gag ttg ttg aag gag ctg tct aac cat aat gag cgt gta gaa gaa aga	3439
Glu Leu Leu Lys Glu Leu Ser Asn His Asn Glu Arg Val Glu Glu Arg	
1077 1082 1087 1092	
aaa att gcc ctc tat gaa ctt atg aaa ctg aca cag gaa gaa tct ttt	3487
Lys Ile Ala Leu Tyr Glu Leu Met Lys Leu Thr Gln Glu Glu Ser Phe	
1093 1098 1103 1108	
agt gtt tgg gat gaa cac ttc aaa aca ata ttg ctt tta ttg ctt gaa	3535
Ser Val Trp Asp Glu His Phe Lys Thr Ile Leu Leu Leu Leu Glu	
1109 1114 1119 1124	
acg ctt gga gat aaa gag cct aca atc agg gct ttg gca tta aag gtt	3583
Thr Leu Gly Asp Lys Glu Pro Thr Ile Arg Ala Leu Ala Leu Lys Val	
1125 1130 1135 1140	
tta aga gaa atc cta agg cat caa cca gca aga ttt aaa aac tat gca	3631
Leu Arg Glu Ile Leu Arg His Gln Pro Ala Arg Phe Lys Asn Tyr Ala	
1141 1146 1151 1156	
gaa ttg act gtc atg aaa aca ttg gaa gca cat aaa gat cct cat aag	3679
Glu Leu Thr Val Met Lys Thr Leu Glu Ala His Lys Asp Pro His Lys	
1157 1162 1167 1172	
gag gtg gtg aga tct gct gag gaa gcg gca tca gtg ttg gcc act tca	3727
Glu Val Val Arg Ser Ala Glu Glu Ala Ala Ser Val Leu Ala Thr Ser	
1173 1178 1183 1188	
att agt cca gag cag tgc atc aaa gtg ctt tgt cct atc att caa act	3775
Ile Ser Pro Glu Gln Cys Ile Lys Val Leu Cys Pro Ile Ile Gln Thr	
1189 1194 1199 1204	
gca gac tac cca att aat ctg gct gca atc aaa atg caa aca aaa gtg	3823

aaacaaatta tcgagacatg ggagtgacca gcaccttttc tttaaatggg ggaacctggg	5074
ttcctttttac catgaaattg tcttacttga aaatattgat cctgatgaga gagaagatgg	5134
tgccaaggct gtctttgtat aatgggctca aattctctac ctcttcaggg ctaatacttt	5194
taactgagct gctgcctata gtgtcttttg gaaaactact taaaggggta ttttctgtta	5254
cttttttagca aattttttta atcacctctt gctacaccca ttcttttcat gtgcagccga	5314
ctcaaaaatt accagttttg gtgaaaggct aaattagata atttggaacc aggatactaa	5374
tgattttctca tctttacttt tttttaatcc taatataaag tgaatttgat tgaaaaggca	5434
aatagctatt agggaagcag tttgccattg ttgcagagtt atctgtactt tgtttaactg	5494
aaaaaaatgt agaaatatat gtaaagaatt taagacaaga gtactgaatg gatgatttgt	5554
cataggcttt cccctttctt tctgttctag cagcaggaaa agtttctcta tctctctcc	5614
ctctacctgt aacaattttg ttttctactg ttaattacat tgtgtattta tagttctatg	5674
cttactgttg tgcataact ggcaataaaa ctgtacataa cattacttga aaaagttaat	5734
aatgtatatc agtttttctg tctcactgtg taacaagtca ctcagtttta ttttaacttt	5794
agacggctct gtatcagtgg tggctctctg aattttgtaa gttcatctga ggagaaaaga	5854
tttttcaggt gtagctacca caatcaaagg tatatagcta catacgcatg tatatattac	5914
agcttatctg taagaagaaa atgcatttta aacacaactc ttctcagtag cattttatga	5974
cctttggata tgtttgtaat catttcgaat caaaatattg atttaatttt gacctctggg	6034
ttaagatact gctttaacta ctgttgacaa ccaagtagag tgacttaagc tgaacagtaa	6094
ctaactggaa aattagataa gcacctggca tctaattggca ggcaggcact caagaaatga	6154
attaactaca taatggaaaa gtatggttta atgtgtccaa atgaaagcta gtagatgtaa	6214
acatggaaaa attgtgttta caattttata atctcagttg ataagactat aagaaagctg	6274
attattttaa tcaactatata caatacacc ttaatttggt cattccagaa acatactgag	6334
atgtcagcta cttaaaaatg gtcacaaaaa gctactgttt atatttttcc tcttgctatt	6394
ctctcccaaa ttaattatta ataagtgttg ttcatttact gcactgctga gaactaatta	6454
aaattatata ttccagattg taaaaaaaaa aaa	6487

<210> 324

<211> 6445

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> (164)..(4051)

<400> 324

ctgcaggaat tcggcagcag cccgcacaaa cctcagtggt ggttctgtgg ttgtttctgt	60
ctttttttga tagaatcttt gattagtatc gaatttactg tatttgccca tgtgaactat	120
tgggagcctc ctaggggtgag ggaaattaag agctttcaga gga atg agg cga ctg	175
Met Arg Arg Leu	
1	
att tgc aaa cgg atc tgt gat tat aaa agc ttc gat gat gaa gaa tca	223
Ile Cys Lys Arg Ile Cys Asp Tyr Lys Ser Phe Asp Asp Glu Glu Ser	
5 10 15 20	
gtg gat gga aat agg cca tca tca gct gca tca gcc ttc aag gtt cct	271
Val Asp Gly Asn Arg Pro Ser Ser Ala Ala Ser Ala Phe Lys Val Pro	
21 26 31 36	
gca cct aaa aca tcc gga aat cct gcc aac agt gca agg aag cct ggt	319
Ala Pro Lys Thr Ser Gly Asn Pro Ala Asn Ser Ala Arg Lys Pro Gly	
37 42 47 52	
tca gca ggt ggc cct aag gtt gga gca ggt gct tct aag gaa gga ggt	367
Ser Ala Gly Gly Pro Lys Val Gly Ala Gly Ala Ser Lys Glu Gly Gly	
53 58 63 68	
gct gga gca gtt gat gaa gat gat ttt ata aaa gct ttt aca gat gtc	415
Ala Gly Ala Val Asp Glu Asp Asp Phe Ile Lys Ala Phe Thr Asp Val	
69 74 79 84	
cct tct att cag att tat tct agt cga gaa ctc gaa gaa aca tta aat	463
Pro Ser Ile Gln Ile Tyr Ser Ser Arg Glu Leu Glu Glu Thr Leu Asn	
85 90 95 100	
aaa atc agg gaa att ttg tca gat gat aaa cat gac tgg gat cag cgt	511
Lys Ile Arg Glu Ile Leu Ser Asp Asp Lys His Asp Trp Asp Gln Arg	
101 106 111 116	
gcc aat gca ctg aag aaa att cga tca ctg ctt gtt gct gga gct gca	559
Ala Asn Ala Leu Lys Lys Ile Arg Ser Leu Leu Val Ala Gly Ala Ala	
117 122 127 132	
cag tat gat tgc ttt ttt caa cat tta cga ttg ttg gat gga gca ctt	607
Gln Tyr Asp Cys Phe Phe Gln His Leu Arg Leu Leu Asp Gly Ala Leu	
133 138 143 148	
aaa ctt tca gct aag gat ctt aga tcc cag gtg gtt aga gaa gct tgt	655
Lys Leu Ser Ala Lys Asp Leu Arg Ser Gln Val Val Arg Glu Ala Cys	
149 154 159 164	
att act gta gcc cac ctt tca aca gtt ttg gga aac aag ttt gat cat	703
Ile Thr Val Ala His Leu Ser Thr Val Leu Gly Asn Lys Phe Asp His	
165 170 175 180	

ggc gct gaa gcc att gta cct aca ctt ttt aat ctc gtc ccc aat agt	751
Gly Ala Glu Ala Ile Val Pro Thr Leu Phe Asn Leu Val Pro Asn Ser	
181 186 191 196	
gca aaa gtc atg gca act tct gga tgt gca gca atc aga ttt atc att	799
Ala Lys Val Met Ala Thr Ser Gly Cys Ala Ala Ile Arg Phe Ile Ile	
197 202 207 212	
cgg cat act cat gta ccc aga ctt ata cct tta ata aca agc aat tgc	847
Arg His Thr His Val Pro Arg Leu Ile Pro Leu Ile Thr Ser Asn Cys	
213 218 223 228	
aca tca aaa tca gtt ccc gtg agg aga cgt tca ttt gaa ttt tta gat	895
Thr Ser Lys Ser Val Pro Val Arg Arg Arg Ser Phe Glu Phe Leu Asp	
229 234 239 244	
tta ttg ttg caa gag tgg cag act cat tca ttg gaa aga cat gca gcc	943
Leu Leu Leu Gln Glu Trp Gln Thr His Ser Leu Glu Arg His Ala Ala	
245 250 255 260	
gtc ttg gtt gaa act att aaa aag gga att cat gat gct gac gct gag	991
Val Leu Val Glu Thr Ile Lys Lys Gly Ile His Asp Ala Asp Ala Glu	
261 266 271 276	
gcc aga gtg gag gca aga aag aca tac atg ggt ctt aga aac cac ttt	1039
Ala Arg Val Glu Ala Arg Lys Thr Tyr Met Gly Leu Arg Asn His Phe	
277 282 287 292	
cct ggt gaa gct gaa aca tta tat aat tcc ctt gag cca tct tat cag	1087
Pro Gly Glu Ala Glu Thr Leu Tyr Asn Ser Leu Glu Pro Ser Tyr Gln	
293 298 303 308	
aag agt ctt caa act tac tta aag agt tct ggc agt gta gca tct ctt	1135
Lys Ser Leu Gln Thr Tyr Leu Lys Ser Ser Gly Ser Val Ala Ser Leu	
309 314 319 324	
cca caa tca gac agg tcc tca tcc agc tca cag gaa agt ctc aat cgc	1183
Pro Gln Ser Asp Arg Ser Ser Ser Ser Ser Gln Glu Ser Leu Asn Arg	
325 330 335 340	
cct ttt tct tcc aaa tgg tct aca gca aat cca tca act gtg gct gga	1231
Pro Phe Ser Ser Lys Trp Ser Thr Ala Asn Pro Ser Thr Val Ala Gly	
341 346 351 356	
aga gta tca gca ggc agc agc aaa gcc agt tcc ctt cca gga agc ctg	1279
Arg Val Ser Ala Gly Ser Ser Lys Ala Ser Ser Leu Pro Gly Ser Leu	
357 362 367 372	
cag cgt tca cga agt gac att gat gtg aat gct gct gca ggt gcc aag	1327
Gln Arg Ser Arg Ser Asp Ile Asp Val Asn Ala Ala Ala Gly Ala Lys	
373 378 383 388	
gca cat cat gct gct gga cag tct gtg cga agc ggg cgc tta ggt gca	1375
Ala His His Ala Ala Gly Gln Ser Val Arg Ser Gly Arg Leu Gly Ala	
389 394 399 404	

ggt gcc ctg aat gca ggt tcc tat gcg tca cta ggc cgg gtg aga gca	1423
Gly Ala Leu Asn Ala Gly Ser Tyr Ala Ser Leu Gly Arg Val Arg Ala	
405 410 415 420	
aaa ctt tca gca cca ctt gct ggc atg gga aat gcc aag gca gat tct	1471
Lys Leu Ser Ala Pro Leu Ala Gly Met Gly Asn Ala Lys Ala Asp Ser	
421 426 431 436	
aga gga aga agt cga aca aaa atg gtg tct caa tca cag cct ggt agc	1519
Arg Gly Arg Ser Arg Thr Lys Met Val Ser Gln Ser Gln Pro Gly Ser	
437 442 447 452	
cgg tct ggg tct cca gga aga gtt ctg acc aca aca gcc ctg tcc act	1567
Arg Ser Gly Ser Pro Gly Arg Val Leu Thr Thr Thr Ala Leu Ser Thr	
453 458 463 468	
gtg agc tct ggt gtt caa aga gtc ctg gtc aat tca gcc tca gca caa	1615
Val Ser Ser Gly Val Gln Arg Val Leu Val Asn Ser Ala Ser Ala Gln	
469 474 479 484	
aaa aga agc aag ata cca cgg agc cag ggc tgt agc aga gag gct agt	1663
Lys Arg Ser Lys Ile Pro Arg Ser Gln Gly Cys Ser Arg Glu Ala Ser	
485 490 495 500	
cca tct agg ctt tca gtg gcc cga agc agt cgt att cct cga cca agt	1711
Pro Ser Arg Leu Ser Val Ala Arg Ser Ser Arg Ile Pro Arg Pro Ser	
501 506 511 516	
gtg agt caa gga tgc agc cgg gaa gct agt cgg gag agc agc aga gac	1759
Val Ser Gln Gly Cys Ser Arg Glu Ala Ser Arg Glu Ser Ser Arg Asp	
517 522 527 532	
aca agt cct gtt cgc tct ttt cag ccc ctc gcc tcc aga cac cat tcc	1807
Thr Ser Pro Val Arg Ser Phe Gln Pro Leu Ala Ser Arg His His Ser	
533 538 543 548	
aga tca act ggt gcc ctc tac gcc ccc gaa gtg tat ggg gcc tca ggt	1855
Arg Ser Thr Gly Ala Leu Tyr Ala Pro Glu Val Tyr Gly Ala Ser Gly	
549 554 559 564	
cca ggt tat ggg atc agc caa tca agt cga ctg tcg tct tct gtt agt	1903
Pro Gly Tyr Gly Ile Ser Gln Ser Ser Arg Leu Ser Ser Ser Val Ser	
565 570 575 580	
gcc atg cga gtc ctg aac aca ggt tct gat gtg gag gag gcg gtg gca	1951
Ala Met Arg Val Leu Asn Thr Gly Ser Asp Val Glu Glu Ala Val Ala	
581 586 591 596	
gat gcc ttg ctc tta gga gac ata cgg act aag aaa aaa cca gct cga	1999
Asp Ala Leu Leu Leu Gly Asp Ile Arg Thr Lys Lys Lys Pro Ala Arg	
597 602 607 612	
aga aga tat gaa tca tat gga atg cat tca gat gat gac gcc aac agc	2047
Arg Arg Tyr Glu Ser Tyr Gly Met His Ser Asp Asp Asp Ala Asn Ser	
613 618 623 628	
gat gca tct agt gct tgt tca gaa cgc tcc tat agt tct cga aat ggt	2095

853	858	863	868	
cag gat ggt gct acc aag ctt ctt cat aat cac ctt cga aac act ggc				2815
Gln Asp Gly Ala Thr Lys Leu Leu His Asn His Leu Arg Asn Thr Gly				
869	874	879	884	
aat gga acc cag agt tcc atg ggg agt cct ttg aca aga cca aca cca				2863
Asn Gly Thr Gln Ser Ser Met Gly Ser Pro Leu Thr Arg Pro Thr Pro				
885	890	895	900	
cga tca cca gct aac tgg tcc agt cct ctt act tct oct acc aat aca				2911
Arg Ser Pro Ala Asn Trp Ser Ser Pro Leu Thr Ser Pro Thr Asn Thr				
901	906	911	916	
tca cag aat act tta tct cca agt gca ttt gat tat gac aca gaa aat				2959
Ser Gln Asn Thr Leu Ser Pro Ser Ala Phe Asp Tyr Asp Thr Glu Asn				
917	922	927	932	
atg aac tct gaa gat att tat agc tct ctt aga ggt gtc act gaa gca				3007
Met Asn Ser Glu Asp Ile Tyr Ser Ser Leu Arg Gly Val Thr Glu Ala				
933	938	943	948	
atc cag aat ttc agc ttc cgt agc caa gaa gat atg aat gag cca ttg				3055
Ile Gln Asn Phe Ser Phe Arg Ser Gln Glu Asp Met Asn Glu Pro Leu				
949	954	959	964	
aaa agg gat tct aaa aaa gat gat ggc gat tca atg tgt ggt ggt cct				3103
Lys Arg Asp Ser Lys Lys Asp Asp Gly Asp Ser Met Cys Gly Gly Pro				
965	970	975	980	
ggg atg tct gac cca aga gca gga ggt gat gct act gac tca agt caa				3151
Gly Met Ser Asp Pro Arg Ala Gly Gly Asp Ala Thr Asp Ser Ser Gln				
981	986	991	996	
aca gct ctt gat aat aaa gct tca ttg ctc cat tca atg cct act cac				3199
Thr Ala Leu Asp Asn Lys Ala Ser Leu Leu His Ser Met Pro Thr His				
997	1002	1007	1012	
tcc tct cca cgc tct cga gac tat aat cca tat aac tat tca gat agc				3247
Ser Ser Pro Arg Ser Arg Asp Tyr Asn Pro Tyr Asn Tyr Ser Asp Ser				
1013	1018	1023	1028	
atc agt ccc ttc aac aag tct gcc ctc aag gaa gcc atg ttt gat gat				3295
Ile Ser Pro Phe Asn Lys Ser Ala Leu Lys Glu Ala Met Phe Asp Asp				
1029	1034	1039	1044	
gat gct gac cag ttt cct gac gat ctt tcc cta gat cat tct gac cta				3343
Asp Ala Asp Gln Phe Pro Asp Asp Leu Ser Leu Asp His Ser Asp Leu				
1045	1050	1055	1060	
gtt gca gag ttg ttg aag gag ctg tct aac cat aat gag cgt gta gaa				3391
Val Ala Glu Leu Leu Lys Glu Leu Ser Asn His Asn Glu Arg Val Glu				
1061	1066	1071	1076	
gaa aga aaa att gcc ctc tat gaa ctt atg aaa ctg aca cag gaa gaa				3439
Glu Arg Lys Ile Ala Leu Tyr Glu Leu Met Lys Leu Thr Gln Glu Glu				
1077	1082	1087	1092	

tct ttt agt gtt tgg gat gaa cac ttc aaa aca ata ttg ctt tta ttg	3487
Ser Phe Ser Val Trp Asp Glu His Phe Lys Thr Ile Leu Leu Leu Leu	
1093 1098 1103 1108	
ctt gaa acg ctt gga gat aaa gag cct aca atc agg gct ttg gca tta	3535
Leu Glu Thr Leu Gly Asp Lys Glu Pro Thr Ile Arg Ala Leu Ala Leu	
1109 1114 1119 1124	
aag gtt tta aga gaa atc cta agg cat caa cca gca aga ttt aaa aac	3583
Lys Val Leu Arg Glu Ile Leu Arg His Gln Pro Ala Arg Phe Lys Asn	
1125 1130 1135 1140	
tat gca gaa ttg act gtc atg aaa aca ttg gaa gca cat aaa gat cct	3631
Tyr Ala Glu Leu Thr Val Met Lys Thr Leu Glu Ala His Lys Asp Pro	
1141 1146 1151 1156	
cat aag gag gtg gtg aga tct gct gag gaa gcg gca tca gtg ttg gcc	3679
His Lys Glu Val Val Arg Ser Ala Glu Glu Ala Ala Ser Val Leu Ala	
1157 1162 1167 1172	
act tca att agt cca gag cag tgc atc aaa gtg ctt tgt cct atc att	3727
Thr Ser Ile Ser Pro Glu Gln Cys Ile Lys Val Leu Cys Pro Ile Ile	
1173 1178 1183 1188	
caa act gca gac tac cca att aat ctg gct gca atc aaa atg caa aca	3775
Gln Thr Ala Asp Tyr Pro Ile Asn Leu Ala Ala Ile Lys Met Gln Thr	
1189 1194 1199 1204	
aaa gtg ata gag aga gtg tcc aag gaa acc cta aac ctg ctt ttg cca	3823
Lys Val Ile Glu Arg Val Ser Lys Glu Thr Leu Asn Leu Leu Leu Pro	
1205 1210 1215 1220	
gag att atg cca ggt cta ata cag ggt tat gat aat tca gag agc agt	3871
Glu Ile Met Pro Gly Leu Ile Gln Gly Tyr Asp Asn Ser Glu Ser Ser	
1221 1226 1231 1236	
gtt cgg aaa gct tgt gtc ttc tgc ctg gtg gct gtt cat gcg gta att	3919
Val Arg Lys Ala Cys Val Phe Cys Leu Val Ala Val His Ala Val Ile	
1237 1242 1247 1252	
ggt gat gaa cta aaa cca cat ctc agt caa ctt act ggc agt aaa atg	3967
Gly Asp Glu Leu Lys Pro His Leu Ser Gln Leu Thr Gly Ser Lys Met	
1253 1258 1263 1268	
aag cta ctg aat ctt tac atc aaa cgt gca caa aca ggt tct gga gga	4015
Lys Leu Leu Asn Leu Tyr Ile Lys Arg Ala Gln Thr Gly Ser Gly Gly	
1269 1274 1279 1284	
gct gat ccc act act gat gtt tct gga caa agt tag tgaa gctcatcaca	4065
Ala Asp Pro Thr Thr Asp Val Ser Gly Gln Ser *	
1285 1290 1295	
gcgaaccagg tctctcaaaa gaaaggacag atagaccacc ctcacaaatg aaaggaagtt	4125
ctcaaacaca tcctttggaa cttactattg tttccagtt ttagtttttt gtttcgtttc	4185

gttttgatt	ttctgtaaca	gaggactatc	ctcagtctgc	atgtaacttt	tatgatagtt	4245
attccaaatt	aaagaagaag	cagtattaac	atcaactgat	cgacacaaag	taatttttaa	4305
tttaattcat	catttcacat	gtttgtactt	tgtcttccca	ttaacctttg	ccagtgttat	4365
gattgtataa	atttttttaa	atgctgggta	aacaggaatg	cttaaagctt	taaaagttaa	4425
acagtctaaa	acattttttg	ttttattcaa	ctgcagaata	atatttttat	tgctactttg	4485
agttttgttt	cgtatcatgt	cctatgctag	aaatatttaa	atgatgtgaa	acaaagcagg	4545
actaatttga	actacagctg	gactccgttt	gtgtgatggg	gatacatgtc	attagttgca	4605
acttctttgg	ggatgatctat	agtttgaaaa	ctaaaacctc	aaagacagat	gttacagaat	4665
cagccagttc	tgtaaaactg	atattgtcta	ttgggtattg	atcttgccat	ctttatttaa	4725
aaccatgtcc	cttctatgat	cccttaagaa	agctgcacca	aatcatctgc	ctgttttttc	4785
ttgatactta	ctgaaataga	aggttttatt	gcagggttta	ttttggtttg	tttatatctt	4845
tgttgtgaat	gatgcttttt	tgtattttatt	aatatcaa	tcacttatga	ataaacttga	4905
taatggaaac	ggacaaaaaa	aatcaagtgc	gtgtgtgtcc	ttgacctctt	tctgtttctc	4965
acgtaataaa	caaattatcg	agacatggga	gtgaccagca	ccttttcttt	aaatgggtgga	5025
acctgggttc	cttttaccat	gaaattgtct	tacttgaaaa	tattgatcct	gatgagagag	5085
aagatgggtgc	caaggctgtc	tttgtataat	gggctcaa	tctctacctc	ttcagggcta	5145
atacttttaa	ctgagctgct	gcctatagt	tcttttgga	aactacttaa	agggtgattt	5205
tctgttactt	tttagcaa	ttttttaatc	acctcttgct	acaccttctc	ttttcatgtg	5265
cagccgactc	aaaaattacc	agttttgggtg	aaaggctaaa	ttagataatt	tggaaccagg	5325
atactaata	gttctcatct	ttactttttt	ttaatcctaa	tataaagtga	atttgattga	5385
aaaggcaa	atagctattag	gaagcagttt	gccattgttg	cagagttatc	tgtactttgt	5445
ttactgaaa	aaaatgtaga	aatatatgta	aagaatttaa	gacaagagta	ctgaatggat	5505
gatttgtcat	aggctttccc	ctttctttct	gttctagcag	caggaaaagt	ttctctatat	5565
cctctccctc	tacctgtaac	aattttgttt	tctactgtta	attacattgt	gtatttatag	5625
ttctatgctt	actgttgtgc	atatactggc	aataaaactg	tacataacat	tacttgaaaa	5685
agttaataat	gtatatcagt	ttttctgtct	cactgtgtaa	caagtcactc	agttttattt	5745
taactttaga	cggctttgta	tcagtgggtg	tctcttgaat	tttgtaagtt	catctgagga	5805
gaaaagattt	ttcaggtgta	gtaccacaa	tcaaagggtat	atagctacat	acgcatgtat	5865
atattacagc	ttatctgtaa	gaagaaaatg	catttttaac	acaactcttc	tcagtagcat	5925

tttatgacct ttggatatgt ttgtaatcat ttogaatcaa aatattgatt taattttgac 5985
 ctctgggttta agatactgct ttaactactg ttgacaacca agtagagtga ctttaagctga 6045
 acagtaacta actggaaaat tagataagca cctggcatct aatggcaggc aggcactcaa 6105
 gaaatgaatt aactacataa tggaaaagta tggtttaatg tgtccaaatg aaagctagta 6165
 gatgtaaaca tggaaaaaatt gtgtttacaa ttttataatc tcagttgata agactataag 6225
 aaagctgatt atttaaataca ctatatacaa tacaccctta atttgttcat tccagaaaca 6285
 tactgagatg tcagctactt aaaaatgggc acaaaaagct actgtttata tttttcctcc 6345
 tgctattctc tcccaaatta attattaata agtggtgttc atttactgca ctgctgagaa 6405
 ctaattaaaa ttatatattc cagattgtaa aaaaaaaaaa 6445

<210> 325
 <211> 6475
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (219) .. (5957)

<400> 325
 gcacagcccc gccggtgttt caggcccttt aagaggcgag ctggagccgg agccattttc 60
 ccccttcgg ccgcgggcgag gaggagccgg agcgggagtg acaccgagcc ggaccagcg 120
 cgacctgagg cggtccggg tgactcgggc cagtgtagag gtctcaggc cgccggcagg 180
 agcagctggg ccaattccct ggccgggagc ggaagggg atg gcg tcg ggc ctg 233
 Met Ala Ser Gly Leu
 1
 ggc tcc ccg tcc ccc tgc tcg gcg ggc agt gag gag gag gat atg gat 281
 Gly Ser Pro Ser Pro Cys Ser Ala Gly Ser Glu Glu Glu Asp Met Asp
 6 11 16 21
 gca ctt ttg aac aac agc ctg ccc cca ccc cac cca gaa aat gaa gag 329
 Ala Leu Leu Asn Asn Ser Leu Pro Pro Pro His Pro Glu Asn Glu Glu
 22 27 32 37
 gac cca gaa gag gat ttg tca gaa aca gag act cca aag ctc aag aag 377
 Asp Pro Glu Glu Asp Leu Ser Glu Thr Glu Thr Pro Lys Leu Lys Lys
 38 43 48 53
 aag aaa aag cct aag aaa cct cgg gac cct aaa atc cct aag agc aag 425
 Lys Lys Lys Pro Lys Lys Pro Arg Asp Pro Lys Ile Pro Lys Ser Lys
 54 59 64 69

cgc caa aaa aag gag cgt atg ctc tta tgc cgg cag ctg ggg gac agc	473
Arg Gln Lys Lys Glu Arg Met Leu Leu Cys Arg Gln Leu Gly Asp Ser	
70 75 80 85	
tct ggg gag ggg cca gag ttt gtg gag gag gag gaa gag gtg gct ctg	521
Ser Gly Glu Gly Pro Glu Phe Val Glu Glu Glu Glu Glu Val Ala Leu	
86 91 96 101	
cgc tca gac agt gag ggc agc gac tat act cct ggc aag aag aag aag	569
Arg Ser Asp Ser Glu Gly Ser Asp Tyr Thr Pro Gly Lys Lys Lys Lys	
102 107 112 117	
aag aag ctt gga cct aag aaa gag aag aag agc aaa tcc aag cgg aag	617
Lys Lys Leu Gly Pro Lys Lys Glu Lys Lys Ser Lys Ser Lys Arg Lys	
118 123 128 133	
gag gag gag gag gag gat gat gat gat gat gat tca aag gag cct aaa	665
Glu Glu Glu Glu Glu Asp Asp Asp Asp Asp Asp Ser Lys Glu Pro Lys	
134 139 144 149	
tca tct gct cag ctc ctg gaa gac tgg ggc atg gaa gac att gac cac	713
Ser Ser Ala Gln Leu Leu Glu Asp Trp Gly Met Glu Asp Ile Asp His	
150 155 160 165	
gtg ttc tca gag gag gat tat cga acc ctc acc aac tac aag gcc ttc	761
Val Phe Ser Glu Glu Asp Tyr Arg Thr Leu Thr Asn Tyr Lys Ala Phe	
166 171 176 181	
agc cag ttt gtc aga ccc ctc att gct gcc aaa aat ccc aag att gct	809
Ser Gln Phe Val Arg Pro Leu Ile Ala Ala Lys Asn Pro Lys Ile Ala	
182 187 192 197	
gtc tcc aag atg atg atg gtt ttg ggt gca aaa tgg cgg gag ttc agt	857
Val Ser Lys Met Met Met Val Leu Gly Ala Lys Trp Arg Glu Phe Ser	
198 203 208 213	
acc aat aac ccc ttc aaa ggc agt tct ggg gca tca gtg gca gct gcg	905
Thr Asn Asn Pro Phe Lys Gly Ser Ser Gly Ala Ser Val Ala Ala Ala	
214 219 224 229	
gca gca gca gcg gta gct gtg gtg gag agc atg gtg aca gcc act gag	953
Ala Ala Ala Ala Val Ala Val Val Glu Ser Met Val Thr Ala Thr Glu	
230 235 240 245	
gtt gca cca cca cct ccc cct gtg gag gtg cct atc cgc aag gcc aag	1001
Val Ala Pro Pro Pro Pro Pro Val Glu Val Pro Ile Arg Lys Ala Lys	
246 251 256 261	
acc aag gag ggc aaa ggt ccc aat gct cgg agg aag ccc aag ggc agc	1049
Thr Lys Glu Gly Lys Gly Pro Asn Ala Arg Arg Lys Pro Lys Gly Ser	
262 267 272 277	
cct cgt gta cct gat gcc aag aag cct aaa ccc aag aaa gta gct ccc	1097
Pro Arg Val Pro Asp Ala Lys Lys Pro Lys Pro Lys Lys Val Ala Pro	
278 283 288 293	

ctg aaa atc aag ctg gga ggt ttt ggt tcc aag cgt aag aga tcc tcg	1145
Leu Lys Ile Lys Leu Gly Gly Phe Gly Ser Lys Arg Lys Arg Ser Ser	
294 299 304 309	
agt gag gat gat gac tta gat gtg gaa tct gac ttc gat gat gcc agt	1193
Ser Glu Asp Asp Asp Leu Asp Val Glu Ser Asp Phe Asp Asp Ala Ser	
310 315 320 325	
atc aat agc tat tct gtt tct gat ggt tcc acc agc cgt agt agc cgc	1241
Ile Asn Ser Tyr Ser Val Ser Asp Gly Ser Thr Ser Arg Ser Ser Arg	
326 331 336 341	
agc cgc aag aaa ctc cga acc act aaa aag aaa aaa ggc gag gag	1289
Ser Arg Lys Lys Leu Arg Thr Thr Lys Lys Lys Lys Lys Gly Glu Glu	
342 347 352 357	
gag gtg act gct gtg gat ggt tat gag aca gac cac cag gac tat tgc	1337
Glu Val Thr Ala Val Asp Gly Tyr Glu Thr Asp His Gln Asp Tyr Cys	
358 363 368 373	
gag gtg tgc cag caa ggc ggt gag atc atc ctg tgt gat acc tgt ccc	1385
Glu Val Cys Gln Gln Gly Gly Glu Ile Ile Leu Cys Asp Thr Cys Pro	
374 379 384 389	
cgt gct tac cac atg gtc tgc ctg gat ccc gac atg gag aag gct ccc	1433
Arg Ala Tyr His Met Val Cys Leu Asp Pro Asp Met Glu Lys Ala Pro	
390 395 400 405	
gag ggc aag tgg agc tgc cca cac tgc gag aag gaa ggc atc cag tgg	1481
Glu Gly Lys Trp Ser Cys Pro His Cys Glu Lys Glu Gly Ile Gln Trp	
406 411 416 421	
gaa gct aaa gag gac aat tcg gag ggt gag gag atc ctg gaa gag gtt	1529
Glu Ala Lys Glu Asp Asn Ser Glu Gly Glu Glu Ile Leu Glu Glu Val	
422 427 432 437	
ggg gga gac ctc gaa gag gag gat gac cac cat atg gaa ttc tgt cgg	1577
Gly Gly Asp Leu Glu Glu Glu Asp Asp His His Met Glu Phe Cys Arg	
438 443 448 453	
gtc tgc aag gat ggt ggg gaa ctg ctc tgc tgt gat acc tgt cct tct	1625
Val Cys Lys Asp Gly Gly Glu Leu Leu Cys Cys Asp Thr Cys Pro Ser	
454 459 464 469	
tcc tac cac atc cac tgc ctg aat ccc cca ctt cca gag atc ccc aac	1673
Ser Tyr His Ile His Cys Leu Asn Pro Pro Leu Pro Glu Ile Pro Asn	
470 475 480 485	
ggg gaa tgg ctc tgt ccc cgt tgt acg tgt cca gct ctg aag ggc aaa	1721
Gly Glu Trp Leu Cys Pro Arg Cys Thr Cys Pro Ala Leu Lys Gly Lys	
486 491 496 501	
gtg cag aag atc cta atc tgg aag tgg ggt cag cca cca tct ccc aca	1769
Val Gln Lys Ile Leu Ile Trp Lys Trp Gly Gln Pro Pro Ser Pro Thr	
502 507 512 517	
cca gtg cct cgg cct cca gat gct gat ccc aac acg ccc tcc cca aag	1817

Pro Val Pro Arg Pro Pro Asp Ala Asp Pro Asn Thr Pro Ser Pro Lys	
518 523 528 533	
ccc ttg gag ggg cgg cca gag cgg cag ttc ttt gtg aaa tgg caa ggc	1865
Pro Leu Glu Gly Arg Pro Glu Arg Gln Phe Phe Val Lys Trp Gln Gly	
534 539 544 549	
atg tct tac tgg cac tgc tcc tgg gtt tct gaa ctg cag ctg gag ctg	1913
Met Ser Tyr Trp His Cys Ser Trp Val Ser Glu Leu Gln Leu Glu Leu	
550 555 560 565	
cac tgt cag gtg atg ttc cga aac tat cag cgg aag aat gat atg gat	1961
His Cys Gln Val Met Phe Arg Asn Tyr Gln Arg Lys Asn Asp Met Asp	
566 571 576 581	
gag cca cct tct ggg gac ttt ggt ggt gat gaa gag aaa agc cga aag	2009
Glu Pro Pro Ser Gly Asp Phe Gly Gly Asp Glu Glu Lys Ser Arg Lys	
582 587 592 597	
cga aag aac aag gac cct aaa ttt gca gag atg gag gaa cgc ttc tat	2057
Arg Lys Asn Lys Asp Pro Lys Phe Ala Glu Met Glu Glu Arg Phe Tyr	
598 603 608 613	
cgc tat ggg ata aaa ccc gag tgg atg atg atc cac cga atc ctc aac	2105
Arg Tyr Gly Ile Lys Pro Glu Trp Met Met Ile His Arg Ile Leu Asn	
614 619 624 629	
cac agt gtg gac aag aag ggc cac gtc cac tac ttg atc aag tgg cgg	2153
His Ser Val Asp Lys Lys Gly His Val His Tyr Leu Ile Lys Trp Arg	
630 635 640 645	
gac tta cct tac gat cag gct tct tgg gag agt gag gat gtg gag atc	2201
Asp Leu Pro Tyr Asp Gln Ala Ser Trp Glu Ser Glu Asp Val Glu Ile	
646 651 656 661	
cag gat tac gac ctg ttc aag cag agc tat tgg aat cac agg gag tta	2249
Gln Asp Tyr Asp Leu Phe Lys Gln Ser Tyr Trp Asn His Arg Glu Leu	
662 667 672 677	
atg agg ggt gag gaa ggc cga cca ggc aag aag ctc aag aag gtg aag	2297
Met Arg Gly Glu Glu Gly Arg Pro Gly Lys Lys Leu Lys Lys Val Lys	
678 683 688 693	
ctt cgg aag ttg gag agg cct cca gaa acg cca aca gtt gat cca aca	2345
Leu Arg Lys Leu Glu Arg Pro Pro Glu Thr Pro Thr Val Asp Pro Thr	
694 699 704 709	
gtg aag tat gag cga cac gca gag tac ctg gat gct aca ggt gga acc	2393
Val Lys Tyr Glu Arg His Ala Glu Tyr Leu Asp Ala Thr Gly Gly Thr	
710 715 720 725	
ctg cac ccc tat caa atg gag ggc ctg aat tgg ttg cgc ttc tcc tgg	2441
Leu His Pro Tyr Gln Met Glu Gly Leu Asn Trp Leu Arg Phe Ser Trp	
726 731 736 741	
gct cag ggc act gac acc atc ttg gct gat gag atg ggc ctt ggg aaa	2489
Ala Gln Gly Thr Asp Thr Ile Leu Ala Asp Glu Met Gly Leu Gly Lys	

742	747	752	757	
act gta cag aca gca gtc ttc ctg tat tcc ctt tac aag gag ggt cat				2537
Thr Val Gln Thr Ala Val Phe Leu Tyr Ser Leu Tyr Lys Glu Gly His				
758	763	768	773	
tcc aaa ggc ccc ttc cta gtg agc gcc cct ctt tct acc atc atc aac				2585
Ser Lys Gly Pro Phe Leu Val Ser Ala Pro Leu Ser Thr Ile Ile Asn				
774	779	784	789	
tgg gag cgg gag ttt gaa atg tgg gct cca gac atg tat gtc gta acc				2633
Trp Glu Arg Glu Phe Glu Met Trp Ala Pro Asp Met Tyr Val Val Thr				
790	795	800	805	
tat gtg ggt gac aag gac agc cgt gcc atc atc cga gag aat gag ttc				2681
Tyr Val Gly Asp Lys Asp Ser Arg Ala Ile Ile Arg Glu Asn Glu Phe				
806	811	816	821	
tcc ttt gaa gac aat gcc att cgt ggt ggc aag aag gcc tcc cgc atg				2729
Ser Phe Glu Asp Asn Ala Ile Arg Gly Gly Lys Lys Ala Ser Arg Met				
822	827	832	837	
aag aaa gag gca tct gtg aaa ttc cat gtg ctg ctg aca tcc tat gaa				2777
Lys Lys Glu Ala Ser Val Lys Phe His Val Leu Leu Thr Ser Tyr Glu				
838	843	848	853	
ttg atc acc att gac atg gct att ttg ggc tct att gat tgg gcc tgc				2825
Leu Ile Thr Ile Asp Met Ala Ile Leu Gly Ser Ile Asp Trp Ala Cys				
854	859	864	869	
ctc atc gtg gat gaa gcc cat cgg ctg aag aac aat cag tct aag ttc				2873
Leu Ile Val Asp Glu Ala His Arg Leu Lys Asn Asn Gln Ser Lys Phe				
870	875	880	885	
ttc cgg gta ttg aat ggt tac tca ctc cag cac aag ctg ttg ctg act				2921
Phe Arg Val Leu Asn Gly Tyr Ser Leu Gln His Lys Leu Leu Leu Thr				
886	891	896	901	
ggg aca cca tta caa aac aat ctg gaa gag ttg ttt cat ctg ctc aac				2969
Gly Thr Pro Leu Gln Asn Asn Leu Glu Glu Leu Phe His Leu Leu Asn				
902	907	912	917	
ttt ctc acc ccc gag agg ttc cac aat ttg gaa ggt ttt ttg gag gag				3017
Phe Leu Thr Pro Glu Arg Phe His Asn Leu Glu Gly Phe Leu Glu Glu				
918	923	928	933	
ttt gct gac att gcc aag gag gac cag ata aaa aaa ctg cat gac atg				3065
Phe Ala Asp Ile Ala Lys Glu Asp Gln Ile Lys Lys Leu His Asp Met				
934	939	944	949	
ctg ggg ccg cac atg ttg cgg cgg ctc aaa gcc gat gtg ttc aag aac				3113
Leu Gly Pro His Met Leu Arg Arg Leu Lys Ala Asp Val Phe Lys Asn				
950	955	960	965	
atg ccc tcc aag aca gaa cta att gtg cgt gtg gag ctg agc cct atg				3161
Met Pro Ser Lys Thr Glu Leu Ile Val Arg Val Glu Leu Ser Pro Met				
966	971	976	981	

cag aag aaa tac tac aag tac atc ctc act cga aat ttt gaa gca ctc	3209
Gln Lys Lys Tyr Tyr Lys Tyr Ile Leu Thr Arg Asn Phe Glu Ala Leu	
982 987 992 997	
aat gcc cga ggt ggt ggc aac cag gtg tct ctg ctg aat gtg gtg atg	3257
Asn Ala Arg Gly Gly Gly Asn Gln Val Ser Leu Leu Asn Val Val Met	
998 1003 1008 1013	
gat ctt aag aag tgc tgc aac cat cca tac ctc ttc cct gtg gct gca	3305
Asp Leu Lys Lys Cys Cys Asn His Pro Tyr Leu Phe Pro Val Ala Ala	
1014 1019 1024 1029	
atg gaa gct cct aag atg cct aat ggc atg tat gat ggc agt gcc cta	3353
Met Glu Ala Pro Lys Met Pro Asn Gly Met Tyr Asp Gly Ser Ala Leu	
1030 1035 1040 1045	
atc aga gca tct ggg aaa tta ttg ctg ctg cag aaa atg ctc aag aac	3401
Ile Arg Ala Ser Gly Lys Leu Leu Leu Leu Gln Lys Met Leu Lys Asn	
1046 1051 1056 1061	
ctt aag gag ggt ggg cat cgt gta ctc atc ttt tcc cag atg acc aag	3449
Leu Lys Glu Gly Gly His Arg Val Leu Ile Phe Ser Gln Met Thr Lys	
1062 1067 1072 1077	
atg cta gac ctg cta gag gat ttc ttg gaa cat gaa ggt tat aaa tac	3497
Met Leu Asp Leu Leu Glu Asp Phe Leu Glu His Glu Gly Tyr Lys Tyr	
1078 1083 1088 1093	
gaa cgc atc gat ggt gga atc act ggg aac atg cgg caa gag gcc att	3545
Glu Arg Ile Asp Gly Gly Ile Thr Gly Asn Met Arg Gln Glu Ala Ile	
1094 1099 1104 1109	
gac cgc ttc aat gca ccg ggt gct cag cag ttc tgc ttc ttg ctt tcc	3593
Asp Arg Phe Asn Ala Pro Gly Ala Gln Gln Phe Cys Phe Leu Leu Ser	
1110 1115 1120 1125	
act cga gct ggg ggc ctt gga atc aat ctg gcc act gct gac aca gtt	3641
Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Thr Ala Asp Thr Val	
1126 1131 1136 1141	
att atc tat gac tct gac tgg aac ccc cat aat gac att cag gcc ttt	3689
Ile Ile Tyr Asp Ser Asp Trp Asn Pro His Asn Asp Ile Gln Ala Phe	
1142 1147 1152 1157	
agc aga gct cac cgg att ggg caa aat aaa aag gta atg atc tac cgg	3737
Ser Arg Ala His Arg Ile Gly Gln Asn Lys Lys Val Met Ile Tyr Arg	
1158 1163 1168 1173	
ttt gtg acc cgt gcg tca gtg gag gag cgc atc acg cag gtg gca aag	3785
Phe Val Thr Arg Ala Ser Val Glu Glu Arg Ile Thr Gln Val Ala Lys	
1174 1179 1184 1189	
aag aaa atg atg ctg acg cat cta gtg gtg cgg cct ggg ctg ggc tcc	3833
Lys Lys Met Met Leu Thr His Leu Val Val Arg Pro Gly Leu Gly Ser	
1190 1195 1200 1205	

aag act gga tct atg tcc aaa cag gag ctt gat gat atc ctc aaa ttt	3881
Lys Thr Gly Ser Met Ser Lys Gln Glu Leu Asp Asp Ile Leu Lys Phe	
1206 1211 1216 1221	
ggc act gag gaa cta ttc aag gat gaa gcc act gat gga gga gga gac	3929
Gly Thr Glu Glu Leu Phe Lys Asp Glu Ala Thr Asp Gly Gly Gly Asp	
1222 1227 1232 1237	
aac aaa gag gga gaa gat agc agt gtt atc cac tac gat gat aag gcc	3977
Asn Lys Glu Gly Glu Asp Ser Ser Val Ile His Tyr Asp Asp Lys Ala	
1238 1243 1248 1253	
att gaa cgg ctg cta gac cgt aac cag gat gag act gaa gac aca gaa	4025
Ile Glu Arg Leu Leu Asp Arg Asn Gln Asp Glu Thr Glu Asp Thr Glu	
1254 1259 1264 1269	
ttg cag ggc atg aat gaa tat ttg agc tca ttc aaa gtg gcc cag tat	4073
Leu Gln Gly Met Asn Glu Tyr Leu Ser Ser Phe Lys Val Ala Gln Tyr	
1270 1275 1280 1285	
gtg gta cgg gaa gaa gaa atg ggg gag gaa gag gag gta gaa cgg gaa	4121
Val Val Arg Glu Glu Glu Met Gly Glu Glu Glu Glu Val Glu Arg Glu	
1286 1291 1296 1301	
atc att aaa cag gaa gaa agt gtg gat cct gac tac tgg gag aaa ttg	4169
Ile Ile Lys Gln Glu Glu Ser Val Asp Pro Asp Tyr Trp Glu Lys Leu	
1302 1307 1312 1317	
ctg cgg cac cat tat gag cag cag caa gaa gat cta gcc cga aat ctg	4217
Leu Arg His His Tyr Glu Gln Gln Gln Glu Asp Leu Ala Arg Asn Leu	
1318 1323 1328 1333	
ggc aaa gga aaa aga atc cgt aaa cag gtc aac tac aat gat ggc tcc	4265
Gly Lys Gly Lys Arg Ile Arg Lys Gln Val Asn Tyr Asn Asp Gly Ser	
1334 1339 1344 1349	
cag gag gac cga gat tgg cag gac gac cag tcc gac aac cag tcc gat	4313
Gln Glu Asp Arg Asp Trp Gln Asp Asp Gln Ser Asp Asn Gln Ser Asp	
1350 1355 1360 1365	
tac tca gtg gct tca gag gaa ggt gat gaa gac ttt gat gaa cgt tca	4361
Tyr Ser Val Ala Ser Glu Glu Gly Asp Glu Asp Phe Asp Glu Arg Ser	
1366 1371 1376 1381	
gaa gct ccc cgt agg ccc agt cgt aag ggc ctg cgg aat gat aaa gat	4409
Glu Ala Pro Arg Arg Pro Ser Arg Lys Gly Leu Arg Asn Asp Lys Asp	
1382 1387 1392 1397	
aag cca ttg cct cct ctg ttg gcc cgt gtt ggt ggg aat att gaa gta	4457
Lys Pro Leu Pro Pro Leu Leu Ala Arg Val Gly Gly Asn Ile Glu Val	
1398 1403 1408 1413	
ctt ggt ttt aat gct cgt cag cga aaa gcc ttt ctt aat gca att atg	4505
Leu Gly Phe Asn Ala Arg Gln Arg Lys Ala Phe Leu Asn Ala Ile Met	
1414 1419 1424 1429	
cga tat ggt atg cca cct cag gat gct ttt act acc cag tgg ctt gta	4553

Arg Tyr Gly Met Pro Pro Gln Asp Ala Phe Thr Thr Gln Trp Leu Val	
1430 1435 1440 1445	
aga gac ctg cga ggc aaa tca gag aaa gag ttc aag gca tat gtc tct	4601
Arg Asp Leu Arg Gly Lys Ser Glu Lys Glu Phe Lys Ala Tyr Val Ser	
1446 1451 1456 1461	
ctt ttc atg cgg cat tta tgt gag ccg ggg gca gat ggg gct gag acc	4649
Leu Phe Met Arg His Leu Cys Glu Pro Gly Ala Asp Gly Ala Glu Thr	
1462 1467 1472 1477	
ttt gct gat ggt gtc ccc cga gaa ggc ctg tct cgc cag cat gtc ctt	4697
Phe Ala Asp Gly Val Pro Arg Glu Gly Leu Ser Arg Gln His Val Leu	
1478 1483 1488 1493	
act aga att ggt gtt atg tct ttg att cgc aag aag gtt cag gag ttt	4745
Thr Arg Ile Gly Val Met Ser Leu Ile Arg Lys Lys Val Gln Glu Phe	
1494 1499 1504 1509	
gaa cat gtt aat ggg cgc tgg agc atg cct gaa ctg gct gag gtg gag	4793
Glu His Val Asn Gly Arg Trp Ser Met Pro Glu Leu Ala Glu Val Glu	
1510 1515 1520 1525	
gaa aac aag aag atg tcc cag cca ggg tca ccc tcc cca aaa act cct	4841
Glu Asn Lys Lys Met Ser Gln Pro Gly Ser Pro Ser Pro Lys Thr Pro	
1526 1531 1536 1541	
aca ccc tcc act cca ggg gac acg cag ccc aac act cct gca cct gtc	4889
Thr Pro Ser Thr Pro Gly Asp Thr Gln Pro Asn Thr Pro Ala Pro Val	
1542 1547 1552 1557	
cca cct gct gaa gat ggg ata aaa ata gag gaa aat agc ctc aaa gaa	4937
Pro Pro Ala Glu Asp Gly Ile Lys Ile Glu Glu Asn Ser Leu Lys Glu	
1558 1563 1568 1573	
gaa gag agc ata gaa gga gaa aag gag gtt aaa tct aca gcc cct gag	4985
Glu Glu Ser Ile Glu Gly Glu Lys Glu Val Lys Ser Thr Ala Pro Glu	
1574 1579 1584 1589	
act gcc att gag tgt aca cag gcc cct gcc cct gcc tca gag gat gaa	5033
Thr Ala Ile Glu Cys Thr Gln Ala Pro Ala Pro Ala Ser Glu Asp Glu	
1590 1595 1600 1605	
aag gtc gtt gtt gaa ccc cct gag gga gag gag aaa gtg gaa aag gca	5081
Lys Val Val Val Glu Pro Pro Glu Gly Glu Glu Lys Val Glu Lys Ala	
1606 1611 1616 1621	
gag gtg aag gag aga aca gag gaa cct atg gag aca gag ccc aaa ggt	5129
Glu Val Lys Glu Arg Thr Glu Glu Pro Met Glu Thr Glu Pro Lys Gly	
1622 1627 1632 1637	
gct gct gat gta gag aag gtg gag gaa aag tca gca ata gat ctg acc	5177
Ala Ala Asp Val Glu Lys Val Glu Glu Lys Ser Ala Ile Asp Leu Thr	
1638 1643 1648 1653	
cct att gtg gta gaa gac aaa gaa gag aag aaa gaa gaa gaa gag aaa	5225
Pro Ile Val Val Glu Asp Lys Glu Glu Lys Lys Glu Glu Glu Glu Lys	

1654	1659	1664	1669	
aaa gag gtg atg ctt cag aat gga gag acc ccc aag gac ctg aat gat				5273
Lys Glu Val Met Leu Gln Asn Gly Glu Thr Pro Lys Asp Leu Asn Asp				
1670	1675	1680	1685	
gag aaa cag aag aaa aat att aaa caa cgt ttc atg ttt aac att gca				5321
Glu Lys Gln Lys Lys Asn Ile Lys Gln Arg Phe Met Phe Asn Ile Ala				
1686	1691	1696	1701	
gat ggt ggt ttt act gag ttg cac tcc ctt tgg cag aat gaa gag cgg				5369
Asp Gly Gly Phe Thr Glu Leu His Ser Leu Trp Gln Asn Glu Glu Arg				
1702	1707	1712	1717	
gca gcc aca gtt acc aag aag act tat gag atc tgg cat cga cgg cat				5417
Ala Ala Thr Val Thr Lys Lys Thr Tyr Glu Ile Trp His Arg Arg His				
1718	1723	1728	1733	
gac tac tgg ctg cta gcc ggc att ata aac cat ggc tat gcc cgg tgg				5465
Asp Tyr Trp Leu Leu Ala Gly Ile Ile Asn His Gly Tyr Ala Arg Trp				
1734	1739	1744	1749	
caa gac atc cag aat gac cca cgc tat gcc atc ctc aat gag cct ttc				5513
Gln Asp Ile Gln Asn Asp Pro Arg Tyr Ala Ile Leu Asn Glu Pro Phe				
1750	1755	1760	1765	
aag ggt gaa atg aac cgt ggc aat ttc tta gag atc aag aat aaa ttt				5561
Lys Gly Glu Met Asn Arg Gly Asn Phe Leu Glu Ile Lys Asn Lys Phe				
1766	1771	1776	1781	
cta gct cga agg ttt aag ctc tta gaa caa gct ctg gtg att gag gaa				5609
Leu Ala Arg Arg Phe Lys Leu Leu Glu Gln Ala Leu Val Ile Glu Glu				
1782	1787	1792	1797	
cag ctg cgc cgg gct gct tac ttg aac atg tca gaa gac cct tct cac				5657
Gln Leu Arg Arg Ala Ala Tyr Leu Asn Met Ser Glu Asp Pro Ser His				
1798	1803	1808	1813	
cct tcc atg gcc ctc aac acc cgc ttt gct gag gtg gag tgt ttg gcg				5705
Pro Ser Met Ala Leu Asn Thr Arg Phe Ala Glu Val Glu Cys Leu Ala				
1814	1819	1824	1829	
gaa agt cat cag cac ctg tcc aag gag tca atg gca gga aac aag cca				5753
Glu Ser His Gln His Leu Ser Lys Glu Ser Met Ala Gly Asn Lys Pro				
1830	1835	1840	1845	
gcc aat gca gtc ctg cac aaa gtt ctg aaa cag ctg gaa gaa ctg ctg				5801
Ala Asn Ala Val Leu His Lys Val Leu Lys Gln Leu Glu Glu Leu Leu				
1846	1851	1856	1861	
agt gac atg aaa gct gat gtg act cga ctc cca gct acc att gcc cga				5849
Ser Asp Met Lys Ala Asp Val Thr Arg Leu Pro Ala Thr Ile Ala Arg				
1862	1867	1872	1877	
att ccc cca gtt gct gtg agg tta cag atg tca gag cgt aac att ctc				5897
Ile Pro Pro Val Ala Val Arg Leu Gln Met Ser Glu Arg Asn Ile Leu				
1878	1883	1888	1893	

agc cgc ctg gca aac cgg gca ccc gaa cct acc cca cag cag gta gcc 5945
 Ser Arg Leu Ala Asn Arg Ala Pro Glu Pro Thr Pro Gln Gln Val Ala
 1894 1899 1904 1909

cag cag cag tga aga tgcagactga taccacctcc accgctgagc agtgaccttc 6000
 Gln Gln Gln *
 1910

ctcactttct cttgtcccag cttctcccct gggggcctga gagaccctca ccttccttct 6060
 gcccatcttc catgttgtaa aggaacagcc ccagtgcact gggggagggg agggagtgag 6120
 gggcagtggg gcccttcttg cagaagagac atgcagcagt agcgtctggcg ccattctgcag 6180
 gagctggcgg gctggccttc tggaccctgg cttctcccca ctgtaacgcc tggtacacac 6240
 aaactgttgt gggttcctgc caggcttgaa gaaaatgatc tgaatttttt cctccttttg 6300
 gttttatttt gttggtttat tttgtgtttt cttttctcct ttttggggg tattcagagt 6360
 gggctggggc cctgggcgag acacagctac ctctgttggc atctttttaa taccaggaac 6420
 ccagcggctc tagccactga gcggctaaat gaaataaagt ggaaaaaaaa aaaaa 6475

<210> 326
 <211> 2064
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (85)..(1620)

<400> 326
 gatggctcag gggtcttgga cattggcgct acgaccttag ggcgccctag ctttaccagg 60

acttgagtg gcgataaggg ccca atg gca gaa aca gtg tct acc cag gtt 111
 Met Ala Glu Thr Val Ser Thr Gln Val
 1 5

ggg aca gag ggc ggg ctg agg gct tgc cat cag caa aac ggt gac gct 159
 Gly Thr Glu Gly Gly Leu Arg Ala Ser His Gln Gln Asn Gly Asp Ala
 10 15 20 25

ggg ggc gac gcg aag gtt gag ctg tcc ccc ggg ccc ccg aag ccg gct 207
 Gly Gly Asp Ala Lys Val Glu Leu Ser Pro Gly Pro Pro Lys Pro Ala
 26 31 36 41

ggc cgg gaa gtg gag ccg gcc cca gta ggc ggg gag cat ccc tgc gct 255
 Gly Arg Glu Val Glu Pro Ala Pro Val Gly Gly Glu His Pro Ser Ala
 42 47 52 57

gca gcc cca ggc ccg ggc aag cat aag aag cgg cgg ggc gca acc agg 303

Ala	Ala	Pro	Gly	Pro	Gly	Lys	His	Lys	Lys	Arg	Arg	Gly	Ala	Thr	Arg		
58					63					68					73		
gag	cgt	gtc	gtg	ccg	ccc	ccg	aag	aag	cgg	cgg	acc	ggg	gtg	agc	ttc	351	
Glu	Arg	Val	Val	Pro	Pro	Pro	Lys	Lys	Arg	Arg	Thr	Gly	Val	Ser	Phe		
74					79					84					89		
gga	gat	gag	cac	ttt	gca	gaa	acc	agt	tat	tac	ttc	gag	ggc	ggc	ctg	399	
Gly	Asp	Glu	His	Phe	Ala	Glu	Thr	Ser	Tyr	Tyr	Phe	Glu	Gly	Gly	Leu		
90					95					100					105		
cgt	aag	gtg	cgg	ccc	tat	tac	ttt	gac	ttc	cgg	acc	tac	tgc	aaa	ggg	447	
Arg	Lys	Val	Arg	Pro	Tyr	Tyr	Phe	Asp	Phe	Arg	Thr	Tyr	Cys	Lys	Gly		
106					111					116					121		
cgc	tgg	gtg	ggc	cac	agc	ttg	ctg	cac	gtc	ttc	agt	acc	gag	ttc	cga	495	
Arg	Trp	Val	Gly	His	Ser	Leu	Leu	His	Val	Phe	Ser	Thr	Glu	Phe	Arg		
122					127					132					137		
gct	cag	ccc	ctg	gct	tac	tat	gag	gcc	gcg	gtc	cgg	gcg	ggc	cgc	ctg	543	
Ala	Gln	Pro	Leu	Ala	Tyr	Tyr	Glu	Ala	Ala	Val	Arg	Ala	Gly	Arg	Leu		
138					143					148					153		
caa	ctc	aac	gag	aag	ccg	gtg	cag	gac	ctc	aac	atc	gtg	ctc	aag	gac	591	
Gln	Leu	Asn	Glu	Lys	Pro	Val	Gln	Asp	Leu	Asn	Ile	Val	Leu	Lys	Asp		
154					159					164					169		
aat	gat	ttc	ttg	cgg	aac	aca	gtg	cac	agg	cat	gag	cca	cca	gtc	aca	639	
Asn	Asp	Phe	Leu	Arg	Asn	Thr	Val	His	Arg	His	Glu	Pro	Pro	Val	Thr		
170					175					180					185		
gca	gag	ccc	att	cgc	ctg	cta	gct	gag	aac	gaa	gat	gtg	gtg	gtt	gta	687	
Ala	Glu	Pro	Ile	Arg	Leu	Leu	Ala	Glu	Asn	Glu	Asp	Val	Val	Val	Val		
186					191					196					201		
gac	aag	cct	tcc	tcc	att	ccc	gtt	cac	ccc	tgt	ggc	cgc	ttc	cga	cac	735	
Asp	Lys	Pro	Ser	Ser	Ile	Pro	Val	His	Pro	Cys	Gly	Arg	Phe	Arg	His		
202					207					212					217		
aac	aca	gtt	atc	ttc	atc	cta	ggc	aag	gag	cac	caa	ctc	aag	gag	cta	783	
Asn	Thr	Val	Ile	Phe	Ile	Leu	Gly	Lys	Glu	His	Gln	Leu	Lys	Glu	Leu		
218					223					228					233		
cac	ccc	ttg	cat	cgg	ctt	gac	cgc	ott	acc	tca	ggg	gtg	ctt	atg	ttt	831	
His	Pro	Leu	His	Arg	Leu	Asp	Arg	Leu	Thr	Ser	Gly	Val	Leu	Met	Phe		
234					239					244					249		
gcc	aag	aca	gct	gca	gtc	tct	gag	aga	att	cac	gag	cag	gtt	cgg	gac	879	
Ala	Lys	Thr	Ala	Ala	Val	Ser	Glu	Arg	Ile	His	Glu	Gln	Val	Arg	Asp		
250					255					260					265		
cgg	cag	ctg	gag	aag	gag	tac	gtg	tgc	cgg	gtg	gaa	ggg	gag	ttc	ccc	927	
Arg	Gln	Leu	Glu	Lys	Glu	Tyr	Val	Cys	Arg	Val	Glu	Gly	Glu	Phe	Pro		
266					271					276					281		
act	gag	gaa	gtg	acc	tgt	aaa	gaa	ccc	atc	tta	gtg	gtg	tct	tac	aaa	975	
Thr	Glu	Glu	Val	Thr	Cys	Lys	Glu	Pro	Ile	Leu	Val	Val	Ser	Tyr	Lys		

282	287	292	297	
gta ggg gtg tgc cgt gta gat ccc cgg ggc aag ccc tgt gag aca gtg Val Gly Val Cys Arg Val Asp Pro Arg Gly Lys Pro Cys Glu Thr Val 298 303 308 313				1023
ttc cag agg cta agc tac aat ggc cag tcc agt gtg gta cgg tgc cgg Phe Gln Arg Leu Ser Tyr Asn Gly Gln Ser Ser Val Val Arg Cys Arg 314 319 324 329				1071
cca ctc aca ggc cgc aca cac cag att cga gtc cac ctt cag ttc ttg Pro Leu Thr Gly Arg Thr His Gln Ile Arg Val His Leu Gln Phe Leu 330 335 340 345				1119
ggc cat ccc att ctc aac gac ccc atc tac aac tca gtt gcc tgg ggt Gly His Pro Ile Leu Asn Asp Pro Ile Tyr Asn Ser Val Ala Trp Gly 346 351 356 361				1167
cct tct cga ggc cgg ggc ggc tac att ccc aag aca aac gag gag ttg Pro Ser Arg Gly Arg Gly Gly Tyr Ile Pro Lys Thr Asn Glu Glu Leu 362 367 372 377				1215
cta cgg gac ctg gta gca gag cac cag gcc aaa cag agc ctg gat gtg Leu Arg Asp Leu Val Ala Glu His Gln Ala Lys Gln Ser Leu Asp Val 378 383 388 393				1263
cta gat ctc tgt gag ggt gac ctg tcc cca gga ctc aca gac tct acg Leu Asp Leu Cys Glu Gly Asp Leu Ser Pro Gly Leu Thr Asp Ser Thr 394 399 404 409				1311
gcc ccc tcc tca gag ttg ggc aag gac gac ctg gaa gag ttg gct gca Ala Pro Ser Ser Glu Leu Gly Lys Asp Asp Leu Glu Glu Leu Ala Ala 410 415 420 425				1359
gct gcc cag aag atg gag gaa gta gct gag gca gcc cct cag gag ttg Ala Ala Gln Lys Met Glu Glu Val Ala Glu Ala Ala Pro Gln Glu Leu 426 431 436 441				1407
gac aca ata gcc ttg gca tca gag aag gca gtt gaa aca gat gtc atg Asp Thr Ile Ala Leu Ala Ser Glu Lys Ala Val Glu Thr Asp Val Met 442 447 452 457				1455
aat caa gag aca gac cca ctc tgt gca gag tgc cgg ctg gtg cga cag Asn Gln Glu Thr Asp Pro Leu Cys Ala Glu Cys Arg Leu Val Arg Gln 458 463 468 473				1503
gat ccc ttg ccc caa gac ctt gtg atg ttc cta cat gcc cta cgc tat Asp Pro Leu Pro Gln Asp Leu Val Met Phe Leu His Ala Leu Arg Tyr 474 479 484 489				1551
aaa ggg cca ggc ttt gag tac ttt tca cca atg cct gcc tgg gca cag Lys Gly Pro Gly Phe Glu Tyr Phe Ser Pro Met Pro Ala Trp Ala Gln 490 495 500 505				1599
gat gac tgg caa aag gac tga gg gtgtggccaa tggagggatt gcttcttggg Asp Asp Trp Gln Lys Asp * 506 511				1652

ttgtgacaag gatgggctat agggcaaggg ctgaccccat gggctagtag ttgggggtttc 1712
 tataggaatg aggacgggct tctaaagaga cctgctcata cttgctacct ccttccagtg 1772
 ggaatttggga gacttttttg tttgtaaata tatccctttt tctaaccatct ttgatgtctg 1832
 gttttctttcc ggcttctttt ttattactga tgtaaaattc acataacata aaattaacca 1892
 ctttaactag ccaggcacag tggctcatgg ctataatcct agtactttgg gaggtagaag 1952
 tgaaaggatc actggaggcc aagagttcaa ggttaaagtg aactgtgatt gtgctgctgc 2012
 actccagagc ctaggtgaca gagtaagacc ctgtctctta aaaaaaaaaa aa 2064

<210> 327
 <211> 6080
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (96)..(2543)

<400> 327
 gtaccgtccg aattccaggt cgacttcgct gtcgacgatt tcgtttgggt ctctacaatt 60
 tcattcattcc aatttcatta tatgtgacag tcgaa atg cag aaa ttt ctt gga 113
 Met Gln Lys Phe Leu Gly
 1
 tca ttt ttt att ggc tgg gat ctt gat ctg tat cat gaa gaa tca gat 161
 Ser Phe Phe Ile Gly Trp Asp Leu Asp Leu Tyr His Glu Glu Ser Asp
 7 12 17 22
 cag aaa gct caa gtc aat act tcc gat ctg aat gaa gag ctt gga cag 209
 Gln Lys Ala Gln Val Asn Thr Ser Asp Leu Asn Glu Glu Leu Gly Gln
 23 28 33 38
 gta gag tac gtg ttt aca gat aaa act ggt aca ctg aca gaa aat gag 257
 Val Glu Tyr Val Phe Thr Asp Lys Thr Gly Thr Leu Thr Glu Asn Glu
 39 44 49 54
 atg cag ttt cgg gaa tgt tca att aat ggc atg aaa tac caa gaa att 305
 Met Gln Phe Arg Glu Cys Ser Ile Asn Gly Met Lys Tyr Gln Glu Ile
 55 60 65 70
 aat ggt aga ctt gta ccc gaa gga cca aca cca gac tct tca gaa gga 353
 Asn Gly Arg Leu Val Pro Glu Gly Pro Thr Pro Asp Ser Ser Glu Gly
 71 76 81 86
 aac tta tct tat ctt agt agt tta tcc cat ctt aac aac tta tcc cat 401
 Asn Leu Ser Tyr Leu Ser Ser Leu Ser His Leu Asn Asn Leu Ser His
 87 92 97 102

ctt	aca	acc	agt	tcc	tct	ttc	aga	acc	agt	cct	gaa	aat	gaa	act	gaa	449
Leu	Thr	Thr	Ser	Ser	Ser	Phe	Arg	Thr	Ser	Pro	Glu	Asn	Glu	Thr	Glu	
103					108					113					118	
cta	att	aaa	gaa	cat	gat	ctc	ttc	ttt	aaa	gca	gtc	agt	ctc	tgt	cac	497
Leu	Ile	Lys	Glu	His	Asp	Leu	Phe	Phe	Lys	Ala	Val	Ser	Leu	Cys	His	
119					124					129					134	
act	gta	cag	att	aac	aat	gtt	caa	act	gac	tgc	act	ggt	gat	ggt	ccc	545
Thr	Val	Gln	Ile	Asn	Asn	Val	Gln	Thr	Asp	Cys	Thr	Gly	Asp	Gly	Pro	
135					140					145					150	
tgg	caa	tcc	aac	ctg	gca	cca	tgc	cag	ttg	gag	tac	tat	gca	tct	tca	593
Trp	Gln	Ser	Asn	Leu	Ala	Pro	Ser	Gln	Leu	Glu	Tyr	Tyr	Ala	Ser	Ser	
151					156					161					166	
cca	gat	gaa	aag	gct	cta	gta	gaa	gct	gct	gca	agg	att	ggt	att	gtg	641
Pro	Asp	Glu	Lys	Ala	Leu	Val	Glu	Ala	Ala	Ala	Arg	Ile	Gly	Ile	Val	
167					172					177					182	
ctt	att	ggc	aat	tct	gaa	gaa	act	atg	gag	gtt	aaa	act	ctt	gga	aaa	689
Leu	Ile	Gly	Asn	Ser	Glu	Glu	Thr	Met	Glu	Val	Lys	Thr	Leu	Gly	Lys	
183					188					193					198	
ctg	gaa	cgg	tac	aaa	ctg	ctt	cat	att	ctg	gaa	ttt	gat	tca	gat	cgt	737
Leu	Glu	Arg	Tyr	Lys	Leu	Leu	His	Ile	Leu	Glu	Phe	Asp	Ser	Asp	Arg	
199					204					209					214	
agg	aga	atg	agt	gta	att	gtt	cag	gca	cct	tca	ggt	gag	aag	tta	tta	785
Arg	Arg	Met	Ser	Val	Ile	Val	Gln	Ala	Pro	Ser	Gly	Glu	Lys	Leu	Leu	
215					220					225					230	
ttt	gct	aaa	gga	gct	gag	tca	tca	att	ctc	cct	aaa	tgt	ata	ggt	gga	833
Phe	Ala	Lys	Gly	Ala	Glu	Ser	Ser	Ile	Leu	Pro	Lys	Cys	Ile	Gly	Gly	
231					236					241					246	
gaa	ata	gaa	aaa	acc	aga	att	cat	gta	gat	gaa	ttt	gct	ttg	aaa	ggg	881
Glu	Ile	Glu	Lys	Thr	Arg	Ile	His	Val	Asp	Glu	Phe	Ala	Leu	Lys	Gly	
247					252					257					262	
cta	aga	act	ctg	tgt	ata	gca	tat	aga	aaa	ttt	aca	tca	aaa	gag	tat	929
Leu	Arg	Thr	Leu	Cys	Ile	Ala	Tyr	Arg	Lys	Phe	Thr	Ser	Lys	Glu	Tyr	
263					268					273					278	
gag	gaa	ata	gat	aaa	cgc	ata	ttt	gaa	gcc	agg	act	gcc	ttg	cag	cag	977
Glu	Glu	Ile	Asp	Lys	Arg	Ile	Phe	Glu	Ala	Arg	Thr	Ala	Leu	Gln	Gln	
279					284					289					294	
cgg	gaa	gag	aaa	ttg	gca	gct	gtt	ttc	cag	ttc	ata	gag	aaa	gac	ctg	1025
Arg	Glu	Glu	Lys	Leu	Ala	Ala	Val	Phe	Gln	Phe	Ile	Glu	Lys	Asp	Leu	
295					300					305					310	
ata	tta	ctt	gga	gcc	aca	gca	gta	gaa	gac	aga	cta	caa	gat	aaa	gtt	1073
Ile	Leu	Leu	Gly	Ala	Thr	Ala	Val	Glu	Asp	Arg	Leu	Gln	Asp	Lys	Val	
311					316					321					326	

cga gaa act att gaa gca ttg aga atg gct ggt atc aaa gta tgg gta	1121
Arg Glu Thr Ile Glu Ala Leu Arg Met Ala Gly Ile Lys Val Trp Val	
327 332 337 342	
ctt act ggg gat aaa cat gaa aca gct gtt agt gtg agt tta tca tgt	1169
Leu Thr Gly Asp Lys His Glu Thr Ala Val Ser Val Ser Leu Ser Cys	
343 348 353 358	
ggc cat ttt cat aga acc atg aac atc ctt gaa ctt ata aac cag aaa	1217
Gly His Phe His Arg Thr Met Asn Ile Leu Glu Leu Ile Asn Gln Lys	
359 364 369 374	
tca gac agc gag tgt gct gaa caa ttg agg cag ctt gcc aga aga att	1265
Ser Asp Ser Glu Cys Ala Glu Gln Leu Arg Gln Leu Ala Arg Arg Ile	
375 380 385 390	
aca gag gat cat gtg att cag cat ggg ctg gta gtg gat ggg acc agc	1313
Thr Glu Asp His Val Ile Gln His Gly Leu Val Val Asp Gly Thr Ser	
391 396 401 406	
cta tct ctt gca ctc agg gag cat gaa aaa cta ttt atg gaa gtt tgc	1361
Leu Ser Leu Ala Leu Arg Glu His Glu Lys Leu Phe Met Glu Val Cys	
407 412 417 422	
aga aat tgt tca gct gta tta tgc tgt cgt atg gct cca ctg cag aaa	1409
Arg Asn Cys Ser Ala Val Leu Cys Cys Arg Met Ala Pro Leu Gln Lys	
423 428 433 438	
gca aaa gta ata aga cta ata aaa ata tca cct gag aaa cct ata aca	1457
Ala Lys Val Ile Arg Leu Ile Lys Ile Ser Pro Glu Lys Pro Ile Thr	
439 444 449 454	
ttg gct gtt ggt gat ggt gct aat gac gta agc atg ata caa gaa gcc	1505
Leu Ala Val Gly Asp Gly Ala Asn Asp Val Ser Met Ile Gln Glu Ala	
455 460 465 470	
cat gtt ggc ata gga atc atg ggt aaa gaa gga aga cag gct gca aga	1553
His Val Gly Ile Gly Ile Met Gly Lys Glu Gly Arg Gln Ala Ala Arg	
471 476 481 486	
aac agt gac tat gca ata gcc aga ttt aag ttc ctc tcc aaa ttg ctt	1601
Asn Ser Asp Tyr Ala Ile Ala Arg Phe Lys Phe Leu Ser Lys Leu Leu	
487 492 497 502	
ttt gtt cat ggt cat ttt tat tat att aga ata gct acc ctt gta cag	1649
Phe Val His Gly His Phe Tyr Tyr Ile Arg Ile Ala Thr Leu Val Gln	
503 508 513 518	
tat ttt ttt tat aag aat gtg tgc ttt atc aca ccc cag ttt tta tat	1697
Tyr Phe Phe Tyr Lys Asn Val Cys Phe Ile Thr Pro Gln Phe Leu Tyr	
519 524 529 534	
cag ttc tac tgt ttg ttt tct cag caa aca ttg tat gac agc gtg tac	1745
Gln Phe Tyr Cys Leu Phe Ser Gln Gln Thr Leu Tyr Asp Ser Val Tyr	
535 540 545 550	
ctg act tta tac aat att tgt ttt act tcc cta cct att ctg ata tat	1793

Leu Thr Leu Tyr Asn Ile Cys Phe Thr Ser Leu Pro Ile Leu Ile Tyr	
551 556 561 566	
agt ctt ttg gaa cag cat gta gac cct cat gtg tta caa aat aag ccc	1841
Ser Leu Leu Glu Gln His Val Asp Pro His Val Leu Gln Asn Lys Pro	
567 572 577 582	
acc ctt tat cga gac att agt aaa aac cgc ctc tta agt att aaa aca	1889
Thr Leu Tyr Arg Asp Ile Ser Lys Asn Arg Leu Leu Ser Ile Lys Thr	
583 588 593 598	
ttt ctt tat tgg acc atc ctg ggc ttc agt cat gcc ttt att ttc ttt	1937
Phe Leu Tyr Trp Thr Ile Leu Gly Phe Ser His Ala Phe Ile Phe Phe	
599 604 609 614	
ttt gga tcc tat tta cta ata ggg aaa gat aca tct ctg ctt gga aat	1985
Phe Gly Ser Tyr Leu Leu Ile Gly Lys Asp Thr Ser Leu Leu Gly Asn	
615 620 625 630	
ggc cag atg ttt gga aac tgg aca ttt ggc act ttg gtc ttc aca gtc	2033
Gly Gln Met Phe Gly Asn Trp Thr Phe Gly Thr Leu Val Phe Thr Val	
631 636 641 646	
atg gtt att aca gtc aca gta aag atg gct ctg gaa act cat ttt tgg	2081
Met Val Ile Thr Val Thr Val Lys Met Ala Leu Glu Thr His Phe Trp	
647 652 657 662	
act tgg atc aac cat ctc gtt acc tgg gga tct att ata ttt tat ttt	2129
Thr Trp Ile Asn His Leu Val Thr Trp Gly Ser Ile Ile Phe Tyr Phe	
663 668 673 678	
gta ttt tcc ttg ttt tat gga ggg att ctc tgg cca ttt ttg ggc tcc	2177
Val Phe Ser Leu Phe Tyr Gly Gly Ile Leu Trp Pro Phe Leu Gly Ser	
679 684 689 694	
cag aat atg tat ttt gtg ttt att cag ctc ctg tca agt ggt tct gct	2225
Gln Asn Met Tyr Phe Val Phe Ile Gln Leu Leu Ser Ser Gly Ser Ala	
695 700 705 710	
tgg ttt gcc ata atc ctc atg gtt gtt aca tgt cta ttt ctt gat atc	2273
Trp Phe Ala Ile Ile Leu Met Val Val Thr Cys Leu Phe Leu Asp Ile	
711 716 721 726	
ata aag aag gtc ttt gac cga cac ctc cac cct aca agt act gaa aag	2321
Ile Lys Lys Val Phe Asp Arg His Leu His Pro Thr Ser Thr Glu Lys	
727 732 737 742	
gca cag ctt act gaa aca aat gca ggt atc aag tgc ttg gac tcc atg	2369
Ala Gln Leu Thr Glu Thr Asn Ala Gly Ile Lys Cys Leu Asp Ser Met	
743 748 753 758	
tgc tgt ttc ccg gaa gga gaa gca gcg tgt gca tct gtt gga aga atg	2417
Cys Cys Phe Pro Glu Gly Glu Ala Ala Cys Ala Ser Val Gly Arg Met	
759 764 769 774	
ctg gaa cga gtt ata gga aga tgt agt cca acc cac atc agc aga tca	2465
Leu Glu Arg Val Ile Gly Arg Cys Ser Pro Thr His Ile Ser Arg Ser	

775	780	785	790	
tggt agt gca tgc gat cct ttc tat acc aac gac agg agc atc ttg act				2513
Trp Ser Ala Ser Asp Pro Phe Tyr Thr Asn Asp Arg Ser Ile Leu Thr				
791	796	801	806	
ctc tcc aca atg gac tca tct act tgt taa a ggggcagtag tactttgtgg				2564
Leu Ser Thr Met Asp Ser Ser Thr Cys *				
807	812			
gagccagttc acctcctttc ctaaaattca gtgtgatcac cctgttaatg gccacactag				2624
ctctgaaatt aatttcctaaa atctttgttag tagttcatat ccaactcagag ttataatggc				2684
aaacaaacag aaagcattag tacaagcccc tcccaacacc cttaatttga atctgaacat				2744
gttaaaattht gagaataaag agacattttt catctctttg tctggtttgt cctttgtgct				2804
tatgggactc ctaatggcat ttcagtcctgt tgctgaggcc attatatttt aatataaatg				2864
tagaaaaaag agagaaatct tagtaaagag tatthtttttag tattagcttg attattgact				2924
cttctattta aatctgcttc tgtaaattat gctgaaagtt tgcccttgaga actctatttt				2984
tttatttagag ttatatthta agctthttcat gggaaaagtt aatgtgaata ctgaggaatt				3044
ttggtccctc agtgacctgt gttgttaatt cattaatgca ttctgagttc acagagcaaa				3104
ttaggagaat catttccaac cattattttac tgcagtatgg ggagtaaatt tataccaatt				3164
cctctaactg tactgtaaca cagcctgtaa agttagccat ataaatgcaa gggatatatca				3224
tatatacaaa tcaggaatca ggtccgttca ccgaacttca aattgatgtt tactaatatt				3284
tttgtgacag agtataaaga ccttatagtg ggtaaattag atactattag catattatta				3344
atttaatgtc tttatcattg gatctthttgc atgctthtaatt ctgggttaaca tathhhaatt				3404
tgctthtttt ctctthtacct gaaggctctg tgtatagtat ttcatgacat cgttgtacag				3464
thhaactatc aataaaaaagt ttggacagta thhaaatatt gcaaatatgt thhaattatac				3524
aaatcagaat agtatgggta attaaatgaa taaaaaaaga agagcctctt tctgcagccg				3584
acttagacat gctcttccct thctataagc tagattthtag aataaagggt thcagthhaat				3644
aatctthattt tcaggthtatg tcacttaact tatagcaaac taccacaata cagtgagthc				3704
tgccagtgth ccagtacaag gcatattthca ggtgtggctg tggaatgtaa aaatgctcaa				3764
cttgtatcag gtaatgthtag caataaatta aatgctaaga atgattaatc ggggtacatgt				3824
tactgthhaatt aactcattgc actthcaaac ctaactthca thctgaaatt atcaagtagt				3884
tcagtattgt catttgthttt tgtthttattg aaaagthaat ttgtcthaag atthtagaagt				3944
gattattagc thgagaacta thaccagct ctaagcaaat aatgattgta tacatathha				4004

gataatgggtt	aaatgcgggtt	ttaccaagtt	ttcccttgaa	aatgtaattc	ctttatggag	4064		
atattattgtg	cagocctaag	cttccttccc	atttcatgaa	tataaggctt	ctagaattgg	4124		
actggcaggg	gaaagaatgg	tagagacaga	aattaagact	ttatccttgt	ttgcttgtaa	4184		
actattat	tottgcta	at	gtaacattt	g	tctgttccag	tgatgtaagg	atattaagtt	4244
attaagctaa	atattaat	tt	tcaaaaatag	tccttcttta	acttagatat	ttcatagctg	4304	
gatttaggaa	gatctgttat	tctggaagta	ctaaaaagaa	taatacaacg	tacaatgtct	4364		
gcattcacta	attcatgttc	cagaagagga	aataatgaag	atatactcag	tagagtacta	4424		
ggtagggagga	tatggaaatt	tgctcataaa	atctcttata	aaacgtgcat	ataacaaaat	4484		
gacacccagt	aggcctgcat	tacatttaca	tgaccgtgtt	tatttgccat	caaataaact	4544		
gagtactgac	accagacaaa	gactccaaag	tcataaaata	gcctatgacc	aactgcagca	4604		
agacaggagg	tcagctcgcc	tataatgggtg	cttaaagtgt	gattgatgta	atcttctgta	4664		
ctcaccat	tt	gaagttagtt	aaggagaact	ttat	tttttttt	aaaaaaaagta	aatggcaacc	4724
actagtgtgc	tcacotgaa	ctgttactcc	aaatccactc	cg	tttttttaa	gcaaaattat	4784	
cttgtgatt	tt	taagaaaaga	gttttctatt	tatttaagaa	agtaacaatg	cagtctgcaa	4844	
gctttcagta	gttttctagt	gctatattca	tcctgtaaaa	ctcttactac	gtaaccagta	4904		
atcacaagga	aagtgtcccc	tttgcata	tt	ttttaa	at	ttttctttg	gaaagtatga	4964
tggtgataat	taacttaacc	ttatctgcca	aaaccagagc	aaaatgctaa	atacgttatt	5024		
gctaatacagt	ggtctcaaat	cgatttgcct	ccctttgcct	cg	ctctgaggg	ctgtaagcct	5084	
gaagatagt	g	caagcacca	agtcagtttc	caaaattgcc	cctcagctgc	tttaagt	gac	5144
tcagcacccct	gcctcagctt	cagcaggcgt	aggctcacc	tg	ggcgaggagc	aaagtatggg	5204	
ccaggggagaa	ctacagctac	gaagacctgc	tg	tcgagttg	agaaaagggg	agaatttatg	5264	
gtctgaatt	tt	tctaactgtc	ctctttcttg	ggtctaaagc	tcataataca	caaaggcttc	5324	
cggacctgag	ccacacccag	gccctatcct	gaacaggaga	ctaaacagag	gcaaatcaac	5384		
cctaggaaat	acttgcattc	tgccctacgg	ttagtaccag	gactgaggtc	atttctactg	5444		
gaaaagattg	tgagattgaa	cttatctgat	cgcttgagac	tcctaatagg	caggagtcaa	5504		
ggccactaga	aaattgacag	ttaagagcca	aaagttttta	aaatatgcta	ctctgaaaaa	5564		
tctcgtgaag	gctgtaggaa	aaggggagaat	cttccatgtt	ggtgtttttc	ctgtaaagat	5624		
cagtttgggg	tatgatataa	gcaggtatta	ataaaaataa	cacaccaaag	agttacgtaa	5684		

aacatgtttt attaatTTTtg gtccccacgt acagacattt tatttctatt ttgaaatgag 5744
 ttatctattt tcataaaagt aaaacactat taaagtgctg ttttatgtga aataacttga 5804
 atgttggtcc tataaaaaat agatcataac tcatgatatg tttgtaatca tggtaattta 5864
 gatTTTTatg aggaatgagt atctggaaat attgtagcaa tacttggttt aaaatTTTtg 5924
 acctgagaca ctgtggctgt ctaatgtaat cctttaaaaa ttctctgcat tgtcagtaaa 5984
 tgtagtatat tattgtacag ctactcataa ttttttaaag tttatgaagt tatatTTtC 6044
 aaataaaaaac tttcctatat aattaaaaaa aaaaaa 6080

<210> 328
 <211> 4663
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (292)..(3600)

<400> 328
 attataccga aaagaagttc tagagaaatt aatagaaaaa tgtgtttcta aaggctacgt 60
 cttccagatg gagatgattg ttcgggcaag acagttgaat tatactattg gcgagcaccc 120
 gcggccgcgg cgcgagccgg agtccgccga gccggagcgc gacgaggccc cgggcgcgcc 180
 ctccccgctg ccgccaccgc cgtgcgcgcg ccatccgccc gccgccgcgc cgcgtgtccg 240
 gcccccgagc acgccggccc cgcgcgcgcg ccgaggccga gtcaagaaac t atg ttc 297
 Met Phe
 1

caa ctt cct gtc aac aat ctt ggc agt tta aga aaa gcc cgg aaa act 345
 Gln Leu Pro Val Asn Asn Leu Gly Ser Leu Arg Lys Ala Arg Lys Thr
 3 8 13 18

gtg aaa aaa ata ctt agt gac att ggg ttg gaa tac tgt aaa gaa cat 393
 Val Lys Lys Ile Leu Ser Asp Ile Gly Leu Glu Tyr Cys Lys Glu His
 19 24 29 34

ata gaa gat ttt aaa caa ttt gaa cct aat gac ttt tat ttg aaa aac 441
 Ile Glu Asp Phe Lys Gln Phe Glu Pro Asn Asp Phe Tyr Leu Lys Asn
 35 40 45 50

act aca tgg gag gat gta gga ctg tgg gac cca tca ctt acg aaa aac 489
 Thr Thr Trp Glu Asp Val Gly Leu Trp Asp Pro Ser Leu Thr Lys Asn
 51 56 61 66

cag gac tat cgg aca aaa cct ttc tgc tgc agc gct tgt cca ttt tcc 537
 Gln Asp Tyr Arg Thr Lys Pro Phe Cys Cys Ser Ala Cys Pro Phe Ser

67	72	77	82	
tca aaa ttc ttc tct gcc tac aaa agt cat ttc cgc aat gtc cat agt				585
Ser Lys Phe Phe Ser Ala Tyr Lys Ser His Phe Arg Asn Val His Ser				
83	88	93	98	
gaa gac ttt gaa aat agg att ctc ctt aat tgc ccc tac tgt acc ttc				633
Glu Asp Phe Glu Asn Arg Ile Leu Leu Asn Cys Pro Tyr Cys Thr Phe				
99	104	109	114	
aat gca gac aaa aag act ttg gaa aca cac att aaa ata ttt cat gct				681
Asn Ala Asp Lys Lys Thr Leu Glu Thr His Ile Lys Ile Phe His Ala				
115	120	125	130	
ccg aac gcc agc gca cca agt agc agc ctc agc act ttc aaa gat aaa				729
Pro Asn Ala Ser Ala Pro Ser Ser Ser Leu Ser Thr Phe Lys Asp Lys				
131	136	141	146	
aac aaa aat gat ggc ctt aaa cct aag cag gct gac agt gta gag caa				777
Asn Lys Asn Asp Gly Leu Lys Pro Lys Gln Ala Asp Ser Val Glu Gln				
147	152	157	162	
gct gtt tat tac tgt aag aag tgc act tac cga gat cct ctt tat gaa				825
Ala Val Tyr Tyr Cys Lys Lys Cys Thr Tyr Arg Asp Pro Leu Tyr Glu				
163	168	173	178	
ata gtt agg aag cac att tac agg gaa cat ttt cag cat gtg gca gca				873
Ile Val Arg Lys His Ile Tyr Arg Glu His Phe Gln His Val Ala Ala				
179	184	189	194	
cct tac ata gca aag gca gga gaa aaa tca ctc aat ggg gca gtc ccc				921
Pro Tyr Ile Ala Lys Ala Gly Glu Lys Ser Leu Asn Gly Ala Val Pro				
195	200	205	210	
tta ggc tcg aat gcc cga gaa gag agt agt att cac tgc aag cga tgc				969
Leu Gly Ser Asn Ala Arg Glu Glu Ser Ser Ile His Cys Lys Arg Cys				
211	216	221	226	
ctt ttc atg cca aag tcc tat gaa gct ttg gta cag cat gtc atc gaa				1017
Leu Phe Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val Ile Glu				
227	232	237	242	
gac cat gaa cgt ata ggc tat cag gtc act gcc atg att ggg cac aca				1065
Asp His Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly His Thr				
243	248	253	258	
aat gta gtg gtt ccc cga tcc aaa ccc ttg atg cta att gct ccc aaa				1113
Asn Val Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala Pro Lys				
259	264	269	274	
cct caa gac aag aag agc atg gga ctc cca cca agg atc ggt tcc ctt				1161
Pro Gln Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly Ser Leu				
275	280	285	290	
gct tct gga aat gtc cgg tct tta cca tca cag cag atg gtg aat cga				1209
Ala Ser Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val Asn Arg				
291	296	301	306	

ctc tca ata cca aag cct aac tta aat tct aca gga gtc aac atg atg	1257
Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn Met Met	
307 312 317 322	
tcc agt gtt cat ctg cag cag aac aac tat gga gtc aaa tct gta ggc	1305
Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser Val Gly	
323 328 333 338	
cag ggt tac agt gtt ggt cag tca atg aga ctg ggt cta ggt ggc aac	1353
Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly Gly Asn	
339 344 349 354	
gca cca gtt tcc att cct caa caa tct cag tct gta aag cag tta ctt	1401
Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln Leu Leu	
355 360 365 370	
cca agt gga aac gga agg tct tat ggg ctt ggg tca gag cag agg tcc	1449
Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg Ser	
371 376 381 386	
cag gca cca gca aga tac tcc ctg cag tct gct aat gcc tct tct ctc	1497
Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser Leu	
387 392 397 402	
tca tcg ggc cag tta aag tct cct tcc ctc tct cag tca cag gca tcc	1545
Ser Ser Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln Ala Ser	
403 408 413 418	
aga gtg tta ggt cag tcc agt tcc aaa cct gct gca gct gcc aca ggc	1593
Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala Thr Gly	
419 424 429 434	
cct ccc cca ggt aac act tcc tca act caa aag tgg aaa ata tgt aca	1641
Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys Thr	
435 440 445 450	
atc tgt aat gag ctt ttt cct gaa aat gtc tat agt gtg cac ttc gaa	1689
Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His Phe Glu	
451 456 461 466	
aaa gaa cat aaa gct gag aaa gtc cca gca gta gcc aac tac att atg	1737
Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr Ile Met	
467 472 477 482	
aaa ata cac aat ttt act agc aaa tgc ctc tac tgt aat cgc tat tta	1785
Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr Leu	
483 488 493 498	
ccc aca gat act ctg ctc aac cat atg tta att cat ggt ctg tct tgt	1833
Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu Ser Cys	
499 504 509 514	
cca tat tgc cgt tca act ttc aat gat gtg gaa aag atg gcc gca cac	1881
Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala Ala His	
515 520 525 530	

atg cgg atg gtt cac att gat gaa gag atg gga cct aaa aca gat tct	1929
Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr Asp Ser	
531 536 541 546	
act ttg agt ttt gat ttg aca ttg cag cag ggt agt cac act aac atc	1977
Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr Asn Ile	
547 552 557 562	
cat ctc ctg gta act aca tac aat ctg agg gat gcc cca gct gaa tct	2025
His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu Ser	
563 568 573 578	
gtt gct tac cat gcc caa aat aat cct cca gtt cct cca aag cca cag	2073
Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys Pro Gln	
579 584 589 594	
cca aag gtt cag gaa aag gca gat atc cct gta aaa agt tca cct caa	2121
Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser Pro Gln	
595 600 605 610	
gct gca gtg ccc tat aaa aaa gat gtt ggg aaa acc ctt tgt cct ctt	2169
Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys Pro Leu	
611 616 621 626	
tgc ttt tca atc cta aaa gga ccc ata tct gat gca ctt gca cat cac	2217
Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala His His	
627 632 637 642	
tta cga gag agg cac caa gtt att cag acg gtt cat cca gtt gag aaa	2265
Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val Glu Lys	
643 648 653 658	
aag ctc acc tac aaa tgt atc cat tgc ctt ggt gtg tat acc agc aac	2313
Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr Ser Asn	
659 664 669 674	
atg acc gcc tca act atc act ctg cat cta gtt cac tgc agg ggc gtt	2361
Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg Gly Val	
675 680 685 690	
gga aag acc caa aat ggc cag gat aag aca aat gca ccc tct cgg ctt	2409
Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg Leu	
691 696 701 706	
aat cag tct cca agt ctg gca cct gtg aag cgc act tac gag caa atg	2457
Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln Met	
707 712 717 722	
gaa ttt ccc tta ctg aaa aaa cga aag tta gat gat gat agt gat tca	2505
Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp Ser	
723 728 733 738	
ccc agc ttc ttt gaa gag aag cct gaa gag cct gtt gtt tta gct tta	2553
Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu Ala Leu	
739 744 749 754	
gac ccc aag ggt cat gaa gat gat tcc tat gaa gcc agg aaa agc ttt	2601

Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser Phe	
755 760 765 770	
cta aca aag tat ttc aac aaa cag ccc tat ccc acc agg aga gaa att	2649
Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu Ile	
771 776 781 786	
gag aag cta gca gcc agt tta tgg tta tgg aag agt gac atc gct tcc	2697
Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala Ser	
787 792 797 802	
cat ttt agt aac aaa agg aag aag tgt gtc cgt gat tgt gaa aag tac	2745
His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu Lys Tyr	
803 808 813 818	
aag cct ggc gtg ttg ctg ggg ttt aac atg aaa gaa tta aat aaa gtc	2793
Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn Lys Val	
819 824 829 834	
aag cat gag atg gat ttt gat gct gag tgg cta ttt gaa aat cat gat	2841
Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn His Asp	
835 840 845 850	
gag aag gat tcc aga gtc aat gct agt aag act gct gac aaa aag ctc	2889
Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys Lys Leu	
851 856 861 866	
aac ctt ggg aag gaa gat gac agt tcc tca gac agt ttt gaa aat ttg	2937
Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu Asn Leu	
867 872 877 882	
gaa gaa gaa tcc aat gaa agt ggt agc cct ttt gac cct gtt ttt gaa	2985
Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val Phe Glu	
883 888 893 898	
gtt gaa cct aaa atc tct aac gat aac cca gag gaa cat gta ctg aag	3033
Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val Leu Lys	
899 904 909 914	
gta att cct gag gat gct tca gaa tct gag gag aag cta gac caa aaa	3081
Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln Lys	
915 920 925 930	
gag gat ggt tca aaa tac gaa act att cat ttg act gag gaa cca acc	3129
Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu Pro Thr	
931 936 941 946	
aaa cta atg cac aat gca tct gat agt gag gtt gac caa gac gat gtt	3177
Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp Asp Val	
947 952 957 962	
gtt gag tgg aaa gac ggt gct tct cca tct gag agt ggg cct gga tcc	3225
Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly Ser	
963 968 973 978	
caa caa gtg tca gac ttt gag gac aat acc tgc gaa atg aaa cca gga	3273
Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys Pro Gly	

979	984	989	994	
acc tgg tct gac gag tct tcc caa agc gaa gat gca agg agc agt aag				3321
Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser Lys				
995	1000	1005	1010	
cca gct gcc aaa aaa aag gct acc atg caa ggt gac aga gag cag ttg				3369
Pro Ala Ala Lys Lys Lys Ala Thr Met Gln Gly Asp Arg Glu Gln Leu				
1011	1016	1021	1026	
aaa tgg aag aat agt tcc tat gga aaa gtt gaa ggg ttt tgg tct aag				3417
Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp Ser Lys				
1027	1032	1037	1042	
gac cag tca cag tgg aag aat gca tct gag aat gat gag cgc tta tct				3465
Asp Gln Ser Gln Trp Lys Asn Ala Ser Glu Asn Asp Glu Arg Leu Ser				
1043	1048	1053	1058	
aac ccc cag att gag tgg cag aat agc aca att gac agt gag gat ggg				3513
Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp Ser Glu Asp Gly				
1059	1064	1069	1074	
gaa cag ttt gac aac atg act gat gga gta gct gag ccc atg cat ggc				3561
Glu Gln Phe Asp Asn Met Thr Asp Gly Val Ala Glu Pro Met His Gly				
1075	1080	1085	1090	
agc tta gcc gga gtt aaa ctg agc agc caa cag gcc taa gtgccaggtt				3610
Ser Leu Ala Gly Val Lys Leu Ser Ser Gln Gln Ala *				
1091	1096	1101		
ccttggcggtt ggtgacatgc tgcagcctgg aactctgatc tccagtgtga ctgcaaagct				3670
gtttttctcac tgggtactgcc ttgtgagtac tgggttgact gtggggcatg tggccgctgc				3730
agttccagtg gttattttcta agtctatgac aggacaggct gttctttgctt cagaaccttc				3790
tctgacagac acggttaacta aatgtgaaaa accaataagc tgggtgactca tgaatacaca				3850
cgaggaaaag cagaggttta ttttatctgc cttttcaaca tttctttccc tctgtgaaat				3910
gattggtcag atgtctttga gaagtgttaa actaattcac atggtagtgt agggccaaca				3970
tacaagctac cagtctaattg tgtatagtag actttgggaa aagcgatttt ttttcatgta				4030
ttcattctga atagttgaaa tgtatatttg tacagtcttt tagacctatt caagtgatgc				4090
tcatgatcct gttactgtgt gcccatcata gatttctttt tttagtgttg cccttgctgt				4150
gtaataaacg ctctatctag tttacctagc aaaagctcaa aactgcgcta gtatggactt				4210
tttggacaga cttagttttt gcacataacc ttgtacaatc ttgcaacaga ggccagccac				4270
gtaagatata tatctggact ctcttgatt ataggatttt tcttgttctg aatatccttg				4330
acattacagc tgtcaaaaac aaaaactggg atttcagatc tgttttctga aatcttttaa				4390
gctaaaatca catgcaagaa ttgactttgc agtactaat tttgacacct tttagatctg				4450

tataaaagtg tgttgtgttg aagcagcaaa ccaatgagtg ctgcattttg gatatttagt 4510
 ttatcttta gttcaacacc atcatggtgg attcatttat accatctaata atatgacaca 4570
 ctgtttagt atgtataatt ttgtgatctt tattttccct ttgtattcat ttttaagcatc 4630
 taaataaatt gctgtattgt gaaaaaaaaaaa aaa 4663

<210> 329
 <211> 4928
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (241)..(3513)

<400> 329
 ccactttgta caagaaagct gggtagcgcgt aagcttgggc cctcgagggg atactctaga 60
 gcggccgcga cagggccagc gagagccccc cagcccgccg cagctgccgc ctgcgccgcg 120
 ccgggcccga gagcacggcg gcgggagcgc ggccttagga ggcggccgga gcggtgggca 180
 cagctcggcg cggagcgtcc tgtcaggcgg cggccgaggg cgtcgcggac tctccccgcg 240
 atg atg ccg atg ata tta act gtt ttc ttg agc aac aat gaa cag att 288
 Met Met Pro Met Ile Leu Thr Val Phe Leu Ser Asn Asn Glu Gln Ile
 1 5 10 15
 tta aca gaa gtt cct ata aca ccg gaa aca acc tgt cga gat gtt gta 336
 Leu Thr Glu Val Pro Ile Thr Pro Glu Thr Thr Cys Arg Asp Val Val
 17 22 27 32
 gaa ttt tgc aag gaa cct gga gaa ggc agc tgc cat tta gct gaa gtg 384
 Glu Phe Cys Lys Glu Pro Gly Glu Gly Ser Cys His Leu Ala Glu Val
 33 38 43 48
 tgg agg gga aat gaa cgt ccc ata ccc ttt gat cat atg atg tac gaa 432
 Trp Arg Gly Asn Glu Arg Pro Ile Pro Phe Asp His Met Met Tyr Glu
 49 54 59 64
 cat ctt cag aaa tgg ggt cca cgg agg gaa gaa gtg aaa ttt ttc ctt 480
 His Leu Gln Lys Trp Gly Pro Arg Arg Glu Glu Val Lys Phe Phe Leu
 65 70 75 80
 cga cac gag gac tcc cca act gag aac agt gaa caa ggt ggc cgt cag 528
 Arg His Glu Asp Ser Pro Thr Glu Asn Ser Glu Gln Gly Gly Arg Gln
 81 86 91 96
 acc caa gag caa cga act cag aga aat gta ata aat gta cct gga gaa 576
 Thr Gln Glu Gln Arg Thr Gln Arg Asn Val Ile Asn Val Pro Gly Glu
 97 102 107 112

aaa cgt act gaa aat ggg gtt ggg aat cca cgt gtt gaa ctt acc ctc	624
Lys Arg Thr Glu Asn Gly Val Gly Asn Pro Arg Val Glu Leu Thr Leu	
113 118 123 128	
tca gag ctc caa gat atg gca gct agg caa cag cag cag att gaa aat	672
Ser Glu Leu Gln Asp Met Ala Ala Arg Gln Gln Gln Gln Ile Glu Asn	
129 134 139 144	
cag cag cag atg ttg gtt gcc aag gaa cag cgt tta cat ttt cta aag	720
Gln Gln Gln Met Leu Val Ala Lys Glu Gln Arg Leu His Phe Leu Lys	
145 150 155 160	
caa cag gag cgc cgt cag cag cag tct att tct gaa aat gaa aag ctt	768
Gln Gln Glu Arg Arg Gln Gln Gln Ser Ile Ser Glu Asn Glu Lys Leu	
161 166 171 176	
cag aaa ttg aaa gaa cga gtt gaa gcc cag gag aac aag ctg aag aaa	816
Gln Lys Leu Lys Glu Arg Val Glu Ala Gln Glu Asn Lys Leu Lys Lys	
177 182 187 192	
att cgt gca atg aga gga caa gtc gac tac agc aaa atc atg aac ggc	864
Ile Arg Ala Met Arg Gly Gln Val Asp Tyr Ser Lys Ile Met Asn Gly	
193 198 203 208	
aat ctg tct gct gaa ata gaa agg ttc agt gcc atg ttc cag gaa aag	912
Asn Leu Ser Ala Glu Ile Glu Arg Phe Ser Ala Met Phe Gln Glu Lys	
209 214 219 224	
aag cag gaa gta cag act gca att tta agg gtt gat cag ctt agt cag	960
Lys Gln Glu Val Gln Thr Ala Ile Leu Arg Val Asp Gln Leu Ser Gln	
225 230 235 240	
caa ttg gaa gat tta aag aaa gga aaa ctg aat ggg ttc cag tct tac	1008
Gln Leu Glu Asp Leu Lys Lys Gly Lys Leu Asn Gly Phe Gln Ser Tyr	
241 246 251 256	
aat ggc aaa ttg acg gga cca gcg gcg gtg gag tta aaa aga ctg tac	1056
Asn Gly Lys Leu Thr Gly Pro Ala Ala Val Glu Leu Lys Arg Leu Tyr	
257 262 267 272	
caa gaa cta cag att cgt aac caa ctt aac cag gaa caa aat tca aaa	1104
Gln Glu Leu Gln Ile Arg Asn Gln Leu Asn Gln Glu Gln Asn Ser Lys	
273 278 283 288	
ctt cag cag cag aag gaa ctc tta aat aag cgc aac atg gag gtg gcc	1152
Leu Gln Gln Gln Lys Glu Leu Leu Asn Lys Arg Asn Met Glu Val Ala	
289 294 299 304	
atg atg gac aag cga atc agt gaa ctg cgt gaa cgt ctc tat ggg aaa	1200
Met Met Asp Lys Arg Ile Ser Glu Leu Arg Glu Arg Leu Tyr Gly Lys	
305 310 315 320	
aaa att cag ctg aac cgt gtg aat ggc acg tca tca cca cag tcc cct	1248
Lys Ile Gln Leu Asn Arg Val Asn Gly Thr Ser Ser Pro Gln Ser Pro	
321 326 331 336	

ctg agc aca tcg ggc agg gtc gct gct gtg ggg cct tat atc cag gtt	1296
Leu Ser Thr Ser Gly Arg Val Ala Ala Val Gly Pro Tyr Ile Gln Val	
337 342 347 352	
ccc agt gcc gga agc ttt cct gtg ctg ggg gac cct ata aag ccc cag	1344
Pro Ser Ala Gly Ser Phe Pro Val Leu Gly Asp Pro Ile Lys Pro Gln	
353 358 363 368	
tct ctc agt att gcc tca aat gct gct cat gga aga tcc aaa tcc gct	1392
Ser Leu Ser Ile Ala Ser Asn Ala Ala His Gly Arg Ser Lys Ser Ala	
369 374 379 384	
aat gat gga aac tgg cca aca tta aaa cag aat tct agc tct tcc gtg	1440
Asn Asp Gly Asn Trp Pro Thr Leu Lys Gln Asn Ser Ser Ser Val	
385 390 395 400	
aaa cca gtg cag gtg gcc ggt gca gac tgg aag gat ccg agc gtg gag	1488
Lys Pro Val Gln Val Ala Gly Ala Asp Trp Lys Asp Pro Ser Val Glu	
401 406 411 416	
ggg tct gtc aag cag ggc act gtc tcc agc cag cct gtg ccc ttc tca	1536
Gly Ser Val Lys Gln Gly Thr Val Ser Ser Gln Pro Val Pro Phe Ser	
417 422 427 432	
gca ctg gga ccc acg gag aag ccg ggc atc gag att ggt aaa gtg cca	1584
Ala Leu Gly Pro Thr Glu Lys Pro Gly Ile Glu Ile Gly Lys Val Pro	
433 438 443 448	
cct ccc atc ccg ggt gta ggc aag cag ctg cct cca agc tat ggg aca	1632
Pro Pro Ile Pro Gly Val Gly Lys Gln Leu Pro Pro Ser Tyr Gly Thr	
449 454 459 464	
tac cca agt cct aca cct ctg ggt cct ggg tcg aca agc tcc ctg gaa	1680
Tyr Pro Ser Pro Thr Pro Leu Gly Pro Gly Ser Thr Ser Ser Leu Glu	
465 470 475 480	
agg agg aag gaa ggc agc ttg ccc agg ccc agt gca ggc ctg cca agt	1728
Arg Arg Lys Glu Gly Ser Leu Pro Arg Pro Ser Ala Gly Leu Pro Ser	
481 486 491 496	
cga cag agg ccc acc ctg ctg ccc gcc aca ggc agc acc ccc cag cca	1776
Arg Gln Arg Pro Thr Leu Leu Pro Ala Thr Gly Ser Thr Pro Gln Pro	
497 502 507 512	
ggc tcc tca caa cag att cag cag agg att tcc gta ccg cca agt ccc	1824
Gly Ser Ser Gln Gln Ile Gln Gln Arg Ile Ser Val Pro Pro Ser Pro	
513 518 523 528	
acg tac ccg cca gcg gga cca cct gca ttt cca gct ggg gac agc aag	1872
Thr Tyr Pro Pro Ala Gly Pro Pro Ala Phe Pro Ala Gly Asp Ser Lys	
529 534 539 544	
cct gaa ctc cca ctg aca gtg gcc att agg cct ttc ctg gct gat aaa	1920
Pro Glu Leu Pro Leu Thr Val Ala Ile Arg Pro Phe Leu Ala Asp Lys	
545 550 555 560	
ggg tca agg cca cag tct ccc agg aaa gga ccc cag aca gtg aat tca	1968

Gly Ser Arg Pro Gln Ser Pro Arg Lys Gly Pro Gln Thr Val Asn Ser	
561 566 571 576	
agt tcc ata tac tcc atg tac ctc cag caa gcc aca cca cct aag aat	2016
Ser Ser Ile Tyr Ser Met Tyr Leu Gln Gln Ala Thr Pro Pro Lys Asn	
577 582 587 592	
tac cag ccg gca gca cac agc gcc tta aat aag tca gtt aaa gca gtg	2064
Tyr Gln Pro Ala Ala His Ser Ala Leu Asn Lys Ser Val Lys Ala Val	
593 598 603 608	
tat ggt aag ccc gtt tta cct tcg ggt tca acc tct cca tcg ccg ctg	2112
Tyr Gly Lys Pro Val Leu Pro Ser Gly Ser Thr Ser Pro Ser Pro Leu	
609 614 619 624	
ccg ttt ctt cac ggg tca ctg tcc acg gcc aca cca cag cct cag cca	2160
Pro Phe Leu His Gly Ser Leu Ser Thr Gly Thr Pro Gln Pro Gln Pro	
625 630 635 640	
cct tca gaa agt act gag aaa gag cct gag cag gat ggc ccc gcc gcc	2208
Pro Ser Glu Ser Thr Glu Lys Glu Pro Glu Gln Asp Gly Pro Ala Ala	
641 646 651 656	
ccc gca gat ggc agc acc gtg gag agc ctg cca cgg cca ctc agc ccc	2256
Pro Ala Asp Gly Ser Thr Val Glu Ser Leu Pro Arg Pro Leu Ser Pro	
657 662 667 672	
acc aag ctc acg ccc atc gtg cat tcg cca ctg cgc tac cag agt gat	2304
Thr Lys Leu Thr Pro Ile Val His Ser Pro Leu Arg Tyr Gln Ser Asp	
673 678 683 688	
gca gac ctg gag gcc ctc cgc agg aag ctg gcc aac gcg ccc cgg ccc	2352
Ala Asp Leu Glu Ala Leu Arg Arg Lys Leu Ala Asn Ala Pro Arg Pro	
689 694 699 704	
ctg aaa aag cgc agc tcc atc aca gag ccc gag ggc ccc ggc ggg ccc	2400
Leu Lys Lys Arg Ser Ser Ile Thr Glu Pro Glu Gly Pro Gly Gly Pro	
705 710 715 720	
aac atc cag aag ctg ctg tac cag cgc ttc aac acc ctg gcc ggt ggc	2448
Asn Ile Gln Lys Leu Leu Tyr Gln Arg Phe Asn Thr Leu Ala Gly Gly	
721 726 731 736	
atg gag ggc acc cct ttc tac cag ccc agc ccc tcc cag gac ttc atg	2496
Met Glu Gly Thr Pro Phe Tyr Gln Pro Ser Pro Ser Gln Asp Phe Met	
737 742 747 752	
ggc acc ttg gcc gat gtg gac aat gga aac acc aat gcc aat gga aac	2544
Gly Thr Leu Ala Asp Val Asp Asn Gly Asn Thr Asn Ala Asn Gly Asn	
753 758 763 768	
ctg gaa gag ctc ccc cct gcc cag ccc aca gcc cca ctc ccc gct gag	2592
Leu Glu Glu Leu Pro Pro Ala Gln Pro Thr Ala Pro Leu Pro Ala Glu	
769 774 779 784	
cct gcc ccg tca tca gat gcc aat gat aat gag tta cct tcc ccc gaa	2640
Pro Ala Pro Ser Ser Asp Ala Asn Asp Asn Glu Leu Pro Ser Pro Glu	

785	790	795	800	
cca gag gag ctc atc tgt	ccc caa acc acc	cac caa act gcc gag ccg		2688
Pro Glu Glu Leu Ile Cys	Pro Gln Thr Thr His	Gln Thr Ala Glu Pro		
801	806	811	816	
gca gag gac aat aac aac	aac gtg gcc acg gtc	ccc acc acg gag cag		2736
Ala Glu Asp Asn Asn Asn	Asn Val Ala Thr Val	Pro Thr Thr Glu Gln		
817	822	827	832	
atc ccg agt cct gtg gct	gag gcc cca tct cca	ggg gaa gag cag gtc		2784
Ile Pro Ser Pro Val Ala	Glu Ala Pro Ser Pro	Gly Glu Glu Gln Val		
833	838	843	848	
cct cca gca cct ctt ccc	cct gcc agc cac cct	cct gcc acc tcc acg		2832
Pro Pro Ala Pro Leu Pro	Pro Ala Ser His Pro	Pro Ala Thr Ser Thr		
849	854	859	864	
aac aag cgg acc aac ttg	aag aag ccc aac tcg	gag cgg acg ggg cac		2880
Asn Lys Arg Thr Asn Leu	Lys Lys Pro Asn Ser	Glu Arg Thr Gly His		
865	870	875	880	
ggg ctg aga gtc cgg ttt	aac ccc ctg gca ctg	ctc cta gac gcg tct		2928
Gly Leu Arg Val Arg Phe	Asn Pro Leu Ala Leu	Leu Leu Leu Asp Ala Ser		
881	886	891	896	
ctg gaa gga gag ttc gat	ctg gtg cag agg atc	atc atc tat gag gtg gaa		2976
Leu Glu Gly Glu Phe Asp	Leu Val Gln Arg Ile	Ile Ile Tyr Glu Val Glu		
897	902	907	912	
gat ccc agc aag ccc aac	gac gaa ggg atc acc	cca ctg cac aac gcc		3024
Asp Pro Ser Lys Pro Asn	Asp Glu Gly Ile Thr	Pro Leu His Asn Ala		
913	918	923	928	
gtc tgc gcc ggc cac cat	cac atc gtg aag ttc	ctg ctg gat ttt ggt		3072
Val Cys Ala Gly His His	His Ile Val Lys Phe	Leu Leu Asp Phe Gly		
929	934	939	944	
gtc aac gtg aat gct gct	gat agt gat gga tgg	acg ccg ctg cac tgc		3120
Val Asn Val Asn Ala Ala	Asp Ser Asp Gly Trp	Thr Pro Leu His Cys		
945	950	955	960	
gct gcc tct tgt aac agc	gtt cac ctc tgc aaa	cag ctg gtg gag agt		3168
Ala Ala Ser Cys Asn Ser	Val His Leu Cys Lys	Gln Leu Val Glu Ser		
961	966	971	976	
ggg gcc gcc att ttt gcc	tca acc ata agc gac	att gaa act gct gca		3216
Gly Ala Ala Ile Phe Ala	Ser Thr Ile Ser Asp	Ile Glu Thr Ala Ala		
977	982	987	992	
gac aag tgt gag gag atg	gag gaa ggc tac atc	cag tgc tcc cag ttt		3264
Asp Lys Cys Glu Glu Met	Glu Glu Gly Tyr Ile	Gln Cys Ser Gln Phe		
993	998	1003	1008	
cta tat ggg gtg cag gaa	aag ctg ggt gtg atg	aac aaa ggt gtg gcg		3312
Leu Tyr Gly Val Gln Glu	Lys Leu Gly Val Met	Asn Lys Gly Val Ala		
1009	1014	1019	1024	

tat gct ctg tgg gac tac gag gcc cag aac agt gac gag ctg tcc ttc	3360
Tyr Ala Leu Trp Asp Tyr Glu Ala Gln Asn Ser Asp Glu Leu Ser Phe	
1025 1030 1035 1040	
cac gaa ggg gac gcc ctc acc atc ctg agg cgc aag gac gaa agc gag	3408
His Glu Gly Asp Ala Leu Thr Ile Leu Arg Arg Lys Asp Glu Ser Glu	
1041 1046 1051 1056	
act gag tgg tgg tgg gct cgc ctt gga gac cgg gag ggc tat gtg ccc	3456
Thr Glu Trp Trp Trp Ala Arg Leu Gly Asp Arg Glu Gly Tyr Val Pro	
1057 1062 1067 1072	
aaa aac ctg ctg ggg ctg tat cca cgg atc aaa ccc cga cag cga aca	3504
Lys Asn Leu Leu Gly Leu Tyr Pro Arg Ile Lys Pro Arg Gln Arg Thr	
1073 1078 1083 1088	
ctc gcc tga acttcct tttaggagcac cgcatgggtct tgccagctac caggagccac	3560
Leu Ala *	
1089	
ttaagagatt attgtgctgt tttccaggaa agctgcagct agaaaatggg cttaatggtg	3620
ctcacttttag cagacagcgt ccacaatgtg aatcctacag tttccagggtg aggccctttc	3680
tccagtttgc ccattaactg ggagaggtac tttcgccctcc aaggactgaa ttttgccaat	3740
tactataaat ccaaataaat acccactttc aaacaccca cccctcttgc cattaagaag	3800
tcccataacc cccggttggt tgccagttaa gacagaagct cttactgact tggccccgag	3860
gccatcacc cctccagcag tgaacactgt ccgccgctgt gaggcctgct cccctgcgac	3920
cgccctgccc cccgtcaccg aatcggacac tcaccttttc tcacacttcc cacacatgat	3980
ccttcttccc ttcacacca aaggagcctc tgtatggaaa catgtccagt gttgctgccc	4040
agtgtgtatg cctcccagta cccactctgc tcggccgcct tgggggttcc gcttccctgtt	4100
ccagttcacc taaaggctga ttgtgcaggc ccagcactgt ggctggactg ccgcgccacg	4160
ggcaccagga ccctaagac caagtgacaa ctgggagagc ctcagcatat actcttctcc	4220
tccgatctca cagcctgtca tgctgctcag tgtggttctc acccctgcaa gctcaaattc	4280
agttccctga atggagtcag gtgctggagg ccgtggcagc ggaggggtgg tgggggtggg	4340
gctgggggtg gactggtgtg agggcagacc agggccaggt agacggggct gtttggtgcc	4400
tgaaggatgg cagacgcctg gtgtcaggag gggccgccac caaggagcag cagctggggc	4460
agaggagctg gggtcagggg ccacccctct ctgccgatct ccctgcctgg gctggctgtg	4520
aggccacctt tgtcccaggc ccagcctcaa ggcaaggagg gcgcttcact gaggtgtgaa	4580
ttgtacgtac aggccttttta tataccaaaa gtatttttttg actagaccat tcaaagctac	4640

```

ccgaactatg ttggaaatTT tttttttctc attaaaatac aggcccttag gctctatttt 4700
tcattgtatga gtcgtgtgta atttatgtaa aaatgtgtgt acagactcac tgatgcagca 4760
ctgttagccca tcaccttgga gcaactgactg tacatagtgt ggtgaagaaa agtgaacgcc 4820
cttgttagagc agcccgacca caggagcatg gccgctgcca gccagacgc tgctgacgct 4880
gtgtaaatgt gcacaataaa cccgtctcac cccggaaaaa aaaaaaaaa 4928

```

```

<210> 330
<211> 7615
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (153)..(3587)

```

```

<220>
<221> misc_feature
<222> (1)...(7615)
<223> n = a,t,c or g

```

```

<400> 330
aatcaactca tcaactctgtg taccacaan gtcggggcc agaaagagtg cgataatgcc 60
ctgcnnnnnn tccgagactg ttaaggggat gttggacaca tcctaataaa cctgttagtg 120
acctctctta ctttgactgc attgagagtg tg atg gaa aac tcc aag gtt ctg 173
Met Glu Asn Ser Lys Val Leu
1 5

ggt gaa tcg atg gca ggg att tca cag aat gcc aag acc gga gac ctc 221
Gly Glu Ser Met Ala Gly Ile Ser Gln Asn Ala Lys Thr Gly Asp Leu
8 13 18 23

cct gcc ttt ggg gaa tgt gtg ggg att gca tcc aag gct ctc tgt ggg 269
Pro Ala Phe Gly Glu Cys Val Gly Ile Ala Ser Lys Ala Leu Cys Gly
24 29 34 39

ctg aca gag gct gca gcc cag gct gca tac ttg gtt ggc atc ttt gat 317
Leu Thr Glu Ala Ala Ala Gln Ala Ala Tyr Leu Val Gly Ile Phe Asp
40 45 50 55

cca aac agc cag gca ggc cac cag ggc ctg gtg gac ccc atc cag ttt 365
Pro Asn Ser Gln Ala Gly His Gln Gly Leu Val Asp Pro Ile Gln Phe
56 61 66 71

gcc agg gct aac cag gcc atc cag atg gca tgc cag aac ttg gtg gac 413
Ala Arg Ala Asn Gln Ala Ile Gln Met Ala Cys Gln Asn Leu Val Asp
72 77 82 87

cct ggc agc agc cca tca cag gtc ctg tca gcc gcc aca att gtt gcc 461

```

Pro Gly Ser Ser Pro Ser Gln Val Leu Ser Ala Ala Thr Ile Val Ala	
88 93 98 103	
aag cac acg tca gcc ttg tgt aat gcc tgc cgc atc gcc tca tcc aag	509
Lys His Thr Ser Ala Leu Cys Asn Ala Cys Arg Ile Ala Ser Ser Lys	
104 109 114 119	
acg gcc aac cca gta gcc aag agg cac ttc gtc cag tcg gcc aag gaa	557
Thr Ala Asn Pro Val Ala Lys Arg His Phe Val Gln Ser Ala Lys Glu	
120 125 130 135	
gtc gcc aac agc act gcc aac ctg gtg aag acc atc aag gcc ctg gat	605
Val Ala Asn Ser Thr Ala Asn Leu Val Lys Thr Ile Lys Ala Leu Asp	
136 141 146 151	
ggg gat ttc tct gaa gac aac cgc aat aag tgt cgc atc gcc acc gca	653
Gly Asp Phe Ser Glu Asp Asn Arg Asn Lys Cys Arg Ile Ala Thr Ala	
152 157 162 167	
gcc ttg att gaa gct gtg gag aac ctg aca gcg ttc gcc tca aac cct	701
Pro Leu Ile Glu Ala Val Glu Asn Leu Thr Ala Phe Ala Ser Asn Pro	
168 173 178 183	
gag ttt gtc agc att cct gcc cag atc agc tcc gag ggt tcc cag gca	749
Glu Phe Val Ser Ile Pro Ala Gln Ile Ser Ser Glu Gly Ser Gln Ala	
184 189 194 199	
cag gaa cca atc ctg gtc tca gcc aag acc atg ctg gag agt tca tcg	797
Gln Glu Pro Ile Leu Val Ser Ala Lys Thr Met Leu Glu Ser Ser Ser	
200 205 210 215	
tac ctc att cgc act gca cgc tct ctg gcc atc aac ccc aaa gac cca	845
Tyr Leu Ile Arg Thr Ala Arg Ser Leu Ala Ile Asn Pro Lys Asp Pro	
216 221 226 231	
ccc acc tgg tct gta ctg gct gga cat tcc cat aca gtg tcc gac tcc	893
Pro Thr Trp Ser Val Leu Ala Gly His Ser His Thr Val Ser Asp Ser	
232 237 242 247	
atc aag agt ctc atc act tct atc agg gac aag gcc cct gga cag agg	941
Ile Lys Ser Leu Ile Thr Ser Ile Arg Asp Lys Ala Pro Gly Gln Arg	
248 253 258 263	
gag tgt gat tac tcc atc gat ggc atc aac cgg tgc atc cgg gac atc	989
Glu Cys Asp Tyr Ser Ile Asp Gly Ile Asn Arg Cys Ile Arg Asp Ile	
264 269 274 279	
gag cag gcc tcg ctg gcc gcc gtc agc cag agc ctg gcc acg agg gac	1037
Glu Gln Ala Ser Leu Ala Ala Val Ser Gln Ser Leu Ala Thr Arg Asp	
280 285 290 295	
gac atc tct gtg gag gcc ctg cag gag cag ctg act tcg gtg gtc cag	1085
Asp Ile Ser Val Glu Ala Leu Gln Glu Gln Leu Thr Ser Val Val Gln	
296 301 306 311	
gaa atc gga cac ctt atc gat ccc atc gcc aca gcg gct cgg gga gaa	1133
Glu Ile Gly His Leu Ile Asp Pro Ile Ala Thr Ala Ala Arg Gly Glu	

312	317	322	327	
gca gct cag ctg gga cat aag gtg aca caa ctg gca agc tat ttt gag				1181
Ala Ala Gln Leu Gly His Lys Val Thr Gln Leu Ala Ser Tyr Phe Glu				
328	333	338	343	
ccc ttg atc tta gcc gca gtt ggt gtg gcc tcc aag att ctt gat cat				1229
Pro Leu Ile Leu Ala Ala Val Gly Val Ala Ser Lys Ile Leu Asp His				
344	349	354	359	
cag cag cag atg acg gtg ctg gac cag acc aag act ctc gca gag tct				1277
Gln Gln Gln Met Thr Val Leu Asp Gln Thr Lys Thr Leu Ala Glu Ser				
360	365	370	375	
gcc ttg cag atg ttg tat gca gcc aaa gaa ggt ggc gga aac ccc aag				1325
Ala Leu Gln Met Leu Tyr Ala Ala Lys Glu Gly Gly Gly Asn Pro Lys				
376	381	386	391	
gca caa cac acc cat gac gcc atc aca gag gcc gcc cag ttg atg aag				1373
Ala Gln His Thr His Asp Ala Ile Thr Glu Ala Ala Gln Leu Met Lys				
392	397	402	407	
gaa gcc gtg gat gac atc atg gtg acg ctg aac gaa gct gcc agt gaa				1421
Glu Ala Val Asp Asp Ile Met Val Thr Leu Asn Glu Ala Ala Ser Glu				
408	413	418	423	
gtg ggg ctg gtt ggg ggc atg gtg gac gcc att gca gaa gcc atg agc				1469
Val Gly Leu Val Gly Gly Met Val Asp Ala Ile Ala Glu Ala Met Ser				
424	429	434	439	
aag ctg gat gaa ggc act cct cca gaa cca aag gga aca ttt gtc gac				1517
Lys Leu Asp Glu Gly Thr Pro Pro Glu Pro Lys Gly Thr Phe Val Asp				
440	445	450	455	
tat cag acg act gtg gtt aaa tac tcc aaa agc att gcg gtg aca gct				1565
Tyr Gln Thr Thr Val Val Lys Tyr Ser Lys Ser Ile Ala Val Thr Ala				
456	461	466	471	
cag gaa atg atg act aag tcg gtt act aac ccg gag gag ttg gga gga				1613
Gln Glu Met Met Thr Lys Ser Val Thr Asn Pro Glu Glu Leu Gly Gly				
472	477	482	487	
ctg gct tca caa atg acc agt gac tat ggg cac ctg gct ttc cag ggc				1661
Leu Ala Ser Gln Met Thr Ser Asp Tyr Gly His Leu Ala Phe Gln Gly				
488	493	498	503	
cag atg gca gca gcc acg gcg gaa cca gag gag atc gga ttc cag att				1709
Gln Met Ala Ala Ala Thr Ala Glu Pro Glu Glu Ile Gly Phe Gln Ile				
504	509	514	519	
cgc act cgt gtg cag gac ctg ggc cac ggc tgt atc ttc ctg gtg cag				1757
Arg Thr Arg Val Gln Asp Leu Gly His Gly Cys Ile Phe Leu Val Gln				
520	525	530	535	
aag gca ggg gcc ctc cag gtc tgc ccc aca gac agc tac acc aag agg				1805
Lys Ala Gly Ala Leu Gln Val Cys Pro Thr Asp Ser Tyr Thr Lys Arg				
536	541	546	551	

gag ctg atc gaa tgc gcc cgt gcc gtc acg gaa aag gtc tcc ttg gtg	1853
Glu Leu Ile Glu Cys Ala Arg Ala Val Thr Glu Lys Val Ser Leu Val	
552 557 562 567	
ctc tcg gct ctc cag gcc ggg aac aaa gga acc cag gca tgc att aca	1901
Leu Ser Ala Leu Gln Ala Gly Asn Lys Gly Thr Gln Ala Cys Ile Thr	
568 573 578 583	
gcc gcc acc gct gtg tct ggg atc att gcc gac ctg gac acc acc att	1949
Ala Ala Thr Ala Val Ser Gly Ile Ile Ala Asp Leu Asp Thr Thr Ile	
584 589 594 599	
atg ttt gca aca gcg ggg acg ctg aat gca gag aac agt gag acc ttc	1997
Met Phe Ala Thr Ala Gly Thr Leu Asn Ala Glu Asn Ser Glu Thr Phe	
600 605 610 615	
gca gac cac agg gag aac att ctc aag acg gcc aag gcc ttg gta gaa	2045
Ala Asp His Arg Glu Asn Ile Leu Lys Thr Ala Lys Ala Leu Val Glu	
616 621 626 631	
gac acg aaa cta ctt gtg tca gga gct gcg tcc act cct gac aag ctg	2093
Asp Thr Lys Leu Leu Val Ser Gly Ala Ala Ser Thr Pro Asp Lys Leu	
632 637 642 647	
gcc cag gcg gcc cag tcc tca gca gcc acc atc acc cag ctc gca gaa	2141
Ala Gln Ala Ala Gln Ser Ser Ala Ala Thr Ile Thr Gln Leu Ala Glu	
648 653 658 663	
gtg gtc aag ctg ggg gca gcc agc ctg ggc tcc gac gac ccc gag acc	2189
Val Val Lys Leu Gly Ala Ala Ser Leu Gly Ser Asp Asp Pro Glu Thr	
664 669 674 679	
cag gtg gtt ttg atc aat gcc atc aaa gat gtg gcc aag gcc ctt tct	2237
Gln Val Val Leu Ile Asn Ala Ile Lys Asp Val Ala Lys Ala Leu Ser	
680 685 690 695	
gat ctc atc agt gct acc aag gga gct gcc agc aag cca gtg gac gac	2285
Asp Leu Ile Ser Ala Thr Lys Gly Ala Ala Ser Lys Pro Val Asp Asp	
696 701 706 711	
cct tcc atg tac cag ctc aag ggg gct gcc aag gtg atg gtg acc aat	2333
Pro Ser Met Tyr Gln Leu Lys Gly Ala Ala Lys Val Met Val Thr Asn	
712 717 722 727	
gtc acc tcg ctc ctc aag act gta aag gca gtg gag gat gag gcc acc	2381
Val Thr Ser Leu Leu Lys Thr Val Lys Ala Val Glu Asp Glu Ala Thr	
728 733 738 743	
cgg ggc acc agg gcg ctt gag gcc aca att gaa tgc ata aag cag gag	2429
Arg Gly Thr Arg Ala Leu Glu Ala Thr Ile Glu Cys Ile Lys Gln Glu	
744 749 754 759	
ctt acg gtg ttc cag tca aaa gac gta cct gaa aag aca tca tca cct	2477
Leu Thr Val Phe Gln Ser Lys Asp Val Pro Glu Lys Thr Ser Ser Pro	
760 765 770 775	

gaa gaa tcc ata agg atg acg aaa ggc atc acc atg gca aca gcc aaa	2525
Glu Glu Ser Ile Arg Met Thr Lys Gly Ile Thr Met Ala Thr Ala Lys	
776 781 786 791	
gcc gtg gca gct ggg aac tca tgt aga cag gag gac gtg att gct act	2573
Ala Val Ala Ala Gly Asn Ser Cys Arg Gln Glu Asp Val Ile Ala Thr	
792 797 802 807	
gcc aac ctg agc cgg aaa gcc gtg tca gat atg ttg acg gct tgc aag	2621
Ala Asn Leu Ser Arg Lys Ala Val Ser Asp Met Leu Thr Ala Cys Lys	
808 813 818 823	
caa gca tcc ttc cac ccc gat gtc agt gac gag gtg aga acc aga gcc	2669
Gln Ala Ser Phe His Pro Asp Val Ser Asp Glu Val Arg Thr Arg Ala	
824 829 834 839	
ttg cgt ttc ggg acg gag tgc acc ctt ggc tac ttg gac ctc ctg gag	2717
Leu Arg Phe Gly Thr Glu Cys Thr Leu Gly Tyr Leu Asp Leu Leu Glu	
840 845 850 855	
cac gtc ttg gtg att ctt cag aaa cca acc cca gaa ttc aag cag cag	2765
His Val Leu Val Ile Leu Gln Lys Pro Thr Pro Glu Phe Lys Gln Gln	
856 861 866 871	
ctg gcc gct ttc tcc aag cga gtc gcc ggc gct gtg aca gag ctc atc	2813
Leu Ala Ala Phe Ser Lys Arg Val Ala Gly Ala Val Thr Glu Leu Ile	
872 877 882 887	
cag gcg gcg gaa gcc atg aaa gga aca gag tgg gtg gat cca gaa gac	2861
Gln Ala Ala Glu Ala Met Lys Gly Thr Glu Trp Val Asp Pro Glu Asp	
888 893 898 903	
cca act gtc att gca gaa aca gag tta ctg ggg gct gca gca tcc atc	2909
Pro Thr Val Ile Ala Glu Thr Glu Leu Leu Gly Ala Ala Ala Ser Ile	
904 909 914 919	
gaa gct gct gct aag aag tta gag caa ctg aag cca aga gca aaa cca	2957
Glu Ala Ala Ala Lys Lys Leu Glu Gln Leu Lys Pro Arg Ala Lys Pro	
920 925 930 935	
aaa caa gcg gat gag acc ctg gac ttt gag gaa cag atc ttg gaa gct	3005
Lys Gln Ala Asp Glu Thr Leu Asp Phe Glu Glu Gln Ile Leu Glu Ala	
936 941 946 951	
gct aaa tcc att gct gct gcc aca agc gcc ctg gtc aaa tcg gcc tca	3053
Ala Lys Ser Ile Ala Ala Ala Thr Ser Ala Leu Val Lys Ser Ala Ser	
952 957 962 967	
gca gcc cag agg gag ctg gtg gcc caa gga aag gtg ggc tcc atc cct	3101
Ala Ala Gln Arg Glu Leu Val Ala Gln Gly Lys Val Gly Ser Ile Pro	
968 973 978 983	
gcc aat gct gca gac gac gga cag tgg tca cag ggg ctg att tct gct	3149
Ala Asn Ala Ala Asp Asp Gly Gln Trp Ser Gln Gly Leu Ile Ser Ala	
984 989 / 994 999	
gcc cgg atg gtg gcg gct gcg acc agc agt ctc tgt gag gcg gcc aat	3197

gctccttgta caaccagac ccattctgta ttttgtggcc cagaaaactg aacgattatt	4237
ttgttcctcc gtagtccaaa gggcagagtt gcggaaggcc gtcggggctt ggtgagcagg	4297
ggctgtaata cagtctgtgg gctccttacc ctgcagaggc tgtttcagct cacacagagt	4357
catccacaca aaccacggc tcccagttga cagtcagtgg aatgctcgtc tccttagcgt	4417
ccagggtggg gattctgctg gaataaagag cttcctcagt gactcatctt taggtccac	4477
gctggtttct gtgccttcag aatggtcaca agcccggtt ggaaaggatc tgcttacaaa	4537
cctgtccctt gtctccaac ccaaacgcc ttttttctg tcttaatatc cagaaaatct	4597
aaatgcatcc taaaatcaat gtgaaccttt aacaagatag ttttacttat tatcacataa	4657
gacataagat gttttcattt tctggatgtc acacttcag aatttcatat ttttcccctc	4717
ttttctttcc ccttttcaga gccctcccat aggaaggga gggcttgaat ttacccttaa	4777
tctgcacctt tagccaaggc agtgcattga agatgaatgg ctctgggggc cagaatctaa	4837
tgccaggagg caggagtgtt tgaaagaatt catagtgggg aaggtaaaag ttaatggaag	4897
tacatgattt tcaaaaactgg taacagttaa aggcactcac cctccgcctc tctctctctc	4957
tctctctctg gtgtgctatc atgtcttggc ctcacccac actatagttt caaagttcca	5017
ctgacggggg aaagttgggtg ctttggctct ccgaagatgt cacctttcga ccttgcccga	5077
tcttgtttca ccagactcta gcccatgtca tgggttttaa atacataaac ttctgacagc	5137
ttcccatatt tataagttac ttataagtgc tgcacgtatt agaatttttt ttttcagac	5197
cagtaaagtt agagaaaaga cgctgtaaag gaaaagcaag tgagagtatg tgtaggacac	5257
tgacagtgtg tgggcaccag ttctgaagag gaggggagct gctggagccc tagcctgttg	5317
gggaaaagct ggcacactct tggctcggcc tctttgagtg gagctgatcc aacacctcat	5377
gcctgccttg gccggacact gagaggaggg gcacacgtgc ttccagagac actcaggagt	5437
cagaccccaa tgctcagagt cacaatgtgt tcatggcctc ctgtaacagg actctgggga	5497
tcccctctgt ggcccagccc accccaccct ctgctcttct atgctgtgcc cagggcagct	5557
gccctcttct gcctgtgccc catcccatcc tgaaaaccca ggaccaaggc aggggcaggc	5617
agccagttct tccaccttgc ctgagagtca tttaaaacct ttactgcatt tgataccaga	5677
aaagcctcca gagacaaacc aaatgcaaag gcctttcctt tataactcta aagaacaggc	5737
atcgaaagtt ttttttcta ggagctatat aaatactcac ctttctggag tcgtccagt	5797
ctgggagctt tggggagtgt ggttctcagt tatcacctgg tatgggtcca gtttctcatc	5857
tgctctttcc tcatccacc tgcacatgtg tatgtgaacg gcttcgtggc cggtgtggtg	5917

gtttctcatt tcataagata gttgaagggc catgccttgt ctggatgta tttaataggc 5977
 actactgagg tgcctcaga tggtagtgag ggggccttct ggtccttcaa aggaaaataa 6037
 cacaggcatg agttcatttg ggagtgtgaa ctttcagaac acctaataag agagtgggtg 6097
 cagagtaaaa acggccccag gtctggagca tagaagtgt tctctgtgaa gagagagccg 6157
 gtgtgttgac atgtggttct tctcacaccc ctctactcct cgagggtttt gaatccttgg 6217
 gctgattttt gtgccagaaa ttgctgttcc cgatggccaa aaggggaacc tgaactggat 6277
 ttcagaactg ccagtgatt tgaataatta gattttactt gggcctttca ggagtcttta 6337
 gatagggatg ctgaggtcat atttagttca atgaacagcc cttgtttaag ttttgccagt 6397
 gtccagccag ctgtggccct ggccatctgt gcaggcaggt tcctcaattc ctggttggcc 6457
 ctgcagtcgg tcaacacagt ccctccaggt cggtgcaga ggcagctgcc cagcctgcag 6517
 tctatgcacg ggccttaaga aatgagctgc ctgtagctc acggcatatg cttttatcag 6577
 ggaaaaccct tcgagcttct tctgattctc acctgcttgc tttctggctg tcttagtcag 6637
 tgtgtttaca ggcaactaaa gcctgttcct aatttatcaa aaaattataa ccaaaattca 6697
 ccatagccta agagagtaaa cccacctcc aaagtgatgc caaggccaaa acctcatcaa 6757
 ggaaccagac acaggtcaaa agtggtgagc aagccatggc ctctgctcct ggggaactca 6817
 cacgctgacc cccgaggagc cttggtttcc tccctggcag atagtcccca gaatcttctc 6877
 tcccagcttt gaggttctgg gctctggaaa ggcctctggg atgctggcct taagatctca 6937
 gcacagacta tcagcatggt ccattctcag attcctggag gaaaggtagc ctctgttgac 6997
 caaggggctg gctgcttctg agacttacca acccaagaaa tttggagaca tttccctcag 7057
 gctaaaaggc agcgggtccc agagttcaga aagcaaaaga tcttgacaac tgtgccagta 7117
 gtggctctgg tctatctct ccacagtgtt ggcctctgct ggggaaggca tctttcccaa 7177
 aggtatcccc aagtaocatg ttgaaaatgt cctcagtctg ttgctccatc tttctgagcc 7237
 tctgcttggg atgtcatggt tatggctact acggatgagt gtgtgcagag tttgggttga 7297
 ttcttttaaa tgctacaaac aagagctatt tcttttcaat aaaaaagggt tggattcggc 7357
 ctcttctct gagccacct ccagccctc caggagcat cagtgtacct gagtcacttt 7417
 gtctgcatct cttcatocca caaaacacga ggctgggtct cattcagcgg cctctacca 7477
 accttaaga tccagaagaa aacaggaacg ttcagctctg ccctgtgtcg tatctaata 7537
 catacattaa tttatctaac cacataagtt attttttttt atttgccaga aataaacctt 7597

taaaggaaaa aaaaaaaaa

7615

<210> 331
<211> 1987
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (460)..(1830)

<400> 331

tgcccgtagc agcgccgtgag ccaagcttgg cacgaagggt aaatttttct gcatttaaaa 60
aatgtgcgga ttggtctgga atccagaggc tggtaccacc ttcctttcta aaataaaatc 120
tctctggcat gaagtcaccg cctatttcac atccggtttg cctggggacg tattactact 180
gtcttggtaa agagaaatct tttgttgtat agctgcagat tggatattgg gaagcaaatt 240
tgggtgtgaa atcttcagca aaggagcacg cagagtccat gatggctcat accaagtgag 300
tgagaggcag agcgaggacg cccctttgct ctggcgcgcc cggactcgga ctgcgagact 360
cgcgctgggt ccagttctctc cacgattctc tctccagac ttttccccgg tcttaagaga 420
tcctgtgtcc agagggggcc ttagctgctc cagcccgcg atg agg aaa agt cca 474
Met Arg Lys Ser Pro
1
ggt ctg tct gac tgt ctt tgg gcc tgg atc ctc ctt ctg agc aca ctg 522
Gly Leu Ser Asp Cys Leu Trp Ala Trp Ile Leu Leu Leu Ser Thr Leu
6 11 16 21
act gga aga agc tat gga cag ccg tca tta caa gat gaa ctt aaa gac 570
Thr Gly Arg Ser Tyr Gly Gln Pro Ser Leu Gln Asp Glu Leu Lys Asp
22 27 32 37
aat acc act gtc ttc acc agg att ttg gac aga ctc cta gat ggt tat 618
Asn Thr Thr Val Phe Thr Arg Ile Leu Asp Arg Leu Leu Asp Gly Tyr
38 43 48 53
gac aat cgc ctg aga cca gga ttg gga gag cgt gta acc gaa gtg aag 666
Asp Asn Arg Leu Arg Pro Gly Leu Gly Glu Arg Val Thr Glu Val Lys
54 59 64 69
act gat atc ttc gtc acc agt ttc gga ccc gtt tca gac cat gat atg 714
Thr Asp Ile Phe Val Thr Ser Phe Gly Pro Val Ser Asp His Asp Met
70 75 80 85
gaa tat aca ata gat gta ttt ttc cgt caa agc tgg aag gat gaa agg 762
Glu Tyr Thr Ile Asp Val Phe Phe Arg Gln Ser Trp Lys Asp Glu Arg
86 91 96 101

tta aaa ttt aaa gga cct atg aca gtc ctc cgg tta aat aac cta atg	810
Leu Lys Phe Lys Gly Pro Met Thr Val Leu Arg Leu Asn Asn Leu Met	
102 107 112 117	
gca agt aaa atc tgg act ccg gac aca ttt ttc cac aat gga aag aag	858
Ala Ser Lys Ile Trp Thr Pro Asp Thr Phe Phe His Asn Gly Lys Lys	
118 123 128 133	
tca gtg gcc cac aac atg acc atg ccc aac aaa ctc ctg cgg atc aca	906
Ser Val Ala His Asn Met Thr Met Pro Asn Lys Leu Leu Arg Ile Thr	
134 139 144 149	
gag gat ggc acc ttg ctg tac acc atg agg ctg aca gtg aga gct gaa	954
Glu Asp Gly Thr Leu Leu Tyr Thr Met Arg Leu Thr Val Arg Ala Glu	
150 155 160 165	
tgt ccg atg cat ttg gag gac ttc cct atg gat gcc cat gct tgc cca	1002
Cys Pro Met His Leu Glu Asp Phe Pro Met Asp Ala His Ala Cys Pro	
166 171 176 181	
cta aaa ttt gga agt tat gct tat aca aga gca gaa gtt gtt tat gaa	1050
Leu Lys Phe Gly Ser Tyr Ala Tyr Thr Arg Ala Glu Val Val Tyr Glu	
182 187 192 197	
tgg acc aga gag cca gca cgc tca gtg gtt gta gca gaa gat gga tca	1098
Trp Thr Arg Glu Pro Ala Arg Ser Val Val Val Ala Glu Asp Gly Ser	
198 203 208 213	
cgt cta aac cag tat gac ctt ctt gga caa aca gta gac tct gga att	1146
Arg Leu Asn Gln Tyr Asp Leu Leu Gly Gln Thr Val Asp Ser Gly Ile	
214 219 224 229	
gtc cag tca agt aca gga gaa tat gtt gtt atg acc act cat ttc cac	1194
Val Gln Ser Ser Thr Gly Glu Tyr Val Val Met Thr Thr His Phe His	
230 235 240 245	
ttg aag aga aag att ggc tac ttt gtt att caa aca tac ctg cca tgc	1242
Leu Lys Arg Lys Ile Gly Tyr Phe Val Ile Gln Thr Tyr Leu Pro Cys	
246 251 256 261	
ata atg aca gtg att ctc tca caa gtc tcc ttc tgg ctc aac aga gag	1290
Ile Met Thr Val Ile Leu Ser Gln Val Ser Phe Trp Leu Asn Arg Glu	
262 267 272 277	
tct gta cca gca aga act gtc ttt gga gta aca act gtg ctc acc atg	1338
Ser Val Pro Ala Arg Thr Val Phe Gly Val Thr Thr Val Leu Thr Met	
278 283 288 293	
aca aca ttg agc atc agt gcc aga aac tcc ctc cct aag gtg gct tat	1386
Thr Thr Leu Ser Ile Ser Ala Arg Asn Ser Leu Pro Lys Val Ala Tyr	
294 299 304 309	
gca aca gct atg gat tgg ttt att gcc gtg tgc tat gcc ttt gtg ttc	1434
Ala Thr Ala Met Asp Trp Phe Ile Ala Val Cys Tyr Ala Phe Val Phe	
310 315 320 325	
tca gct ctg att gag ttt gcc aca gta aac tat ttc act aag aga ggt	1482

Ser	Ala	Leu	Ile	Glu	Phe	Ala	Thr	Val	Asn	Tyr	Phe	Thr	Lys	Arg	Gly	
326					331					336					341	
tat	gca	tg	gat	ggc	aaa	agt	gtg	ggt	cca	gaa	aag	cca	aag	aaa	gta	1530
Tyr	Ala	Trp	Asp	Gly	Lys	Ser	Val	Val	Pro	Glu	Lys	Pro	Lys	Lys	Val	
342					347					352					357	
aag	gat	cct	ctt	att	aag	aaa	aac	aac	act	tac	gct	cca	aca	gca	acc	1578
Lys	Asp	Pro	Leu	Ile	Lys	Lys	Asn	Asn	Thr	Tyr	Ala	Pro	Thr	Ala	Thr	
358					363					368					373	
agc	tac	acc	cct	aat	ttg	gcc	agg	ggc	gac	ccg	ggc	tta	gcc	acc	att	1626
Ser	Tyr	Thr	Pro	Asn	Leu	Ala	Arg	Gly	Asp	Pro	Gly	Leu	Ala	Thr	Ile	
374					379					384					389	
gct	aaa	agt	gca	acc	ata	gaa	cct	aaa	gag	gtc	aag	ccc	gaa	aca	aaa	1674
Ala	Lys	Ser	Ala	Thr	Ile	Glu	Pro	Lys	Glu	Val	Lys	Pro	Glu	Thr	Lys	
390					395					400					405	
cca	cca	gaa	ccc	aag	aaa	acc	ttt	aac	agt	gtc	agc	aaa	att	gac	cga	1722
Pro	Pro	Glu	Pro	Lys	Lys	Thr	Phe	Asn	Ser	Val	Ser	Lys	Ile	Asp	Arg	
406					411					416					421	
ctg	tca	aga	ata	gcc	ttc	ccg	ctg	cta	ttt	gga	atc	ttt	aac	tta	gtc	1770
Leu	Ser	Arg	Ile	Ala	Phe	Pro	Leu	Leu	Phe	Gly	Ile	Phe	Asn	Leu	Val	
422					427					432					437	
tac	tg	gct	acg	tat	tta	aac	aga	gag	cct	cag	cta	aaa	gcc	ccc	aca	1818
Tyr	Trp	Ala	Thr	Tyr	Leu	Asn	Arg	Glu	Pro	Gln	Leu	Lys	Ala	Pro	Thr	
438					443					448					453	
cca	cat	caa	tag	atc	ttttactcac	attctgttgt	tcagttcctc	tgcaactggga								1873
Pro	His	Gln	*													
454																
atttatttat	gttctcaacg	cagtaattcc	catctgcctt	tattgcctct	gtcttaaaga											1933
atttgaaagt	ttccttattt	tcataattca	tttaagacaa	gagaccctg	tctg											1987

```

<210> 332
<211> 6378
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (271)..(5037)

<220>
<221> misc_feature
<222> (1)...(6378)
<223> n = a,t,c or g

<400> 332

```

atttggccct cgaggccaag aattcggcac gaggaggaca gagtgcagcc ttttcctccc	60
ctaataaaaa agccattgcc ctcttttccct cccctaataag aaaagccatt gccctctttt	120
cctccaccct taagaagacc tgcacatgtt ggaccaacag acaactatcc ggcttacggc	180
caggggagcc cctgcagctg cacagaacca gtttcttatg tatctggcgg taattgggaa	240
agcttctgag aaagtccatg gggccgatgt	291
atg gga gat gaa tgt ggt ccc Met Gly Asp Glu Cys Gly Pro	
1 5	
gga ggc atc caa acg agg gct gtg tgg tgt gct cat gtg gag gga tgg	339
Gly Gly Ile Gln Thr Arg Ala Val Trp Cys Ala His Val Glu Gly Trp	
8 13 18 23	
act aca ctg cat act aac tgt aag cag gcc gag aga ccc aat aac cag	387
Thr Thr Leu His Thr Asn Cys Lys Gln Ala Glu Arg Pro Asn Asn Gln	
24 29 34 39	
cag aat tgt ttc aaa gtt tgc gat tgg cac aaa gag ttg tac gac tgg	435
Gln Asn Cys Phe Lys Val Cys Asp Trp His Lys Glu Leu Tyr Asp Trp	
40 45 50 55	
aga ctg gga cct tgg aat cag tgt cag ccc gtg att tca aaa agc cta	483
Arg Leu Gly Pro Trp Asn Gln Cys Gln Pro Val Ile Ser Lys Ser Leu	
56 61 66 71	
gag aaa cct ctt gag tgc att aag ggg gaa gaa ggt att cag gtg agg	531
Glu Lys Pro Leu Glu Cys Ile Lys Gly Glu Glu Gly Ile Gln Val Arg	
72 77 82 87	
gag ata gcg tgc atc cag aaa gac aaa gac att cct gcg gag gat atc	579
Glu Ile Ala Cys Ile Gln Lys Asp Lys Asp Ile Pro Ala Glu Asp Ile	
88 93 98 103	
atc tgt gag tac ttt gag ccc aag cct ctc ctg gag cag gct tgc ctc	627
Ile Cys Glu Tyr Phe Glu Pro Lys Pro Leu Leu Glu Gln Ala Cys Leu	
104 109 114 119	
att cct tgc cag caa gat tgc atc gtg tct gaa ttt tct gcc tgg tcc	675
Ile Pro Cys Gln Gln Asp Cys Ile Val Ser Glu Phe Ser Ala Trp Ser	
120 125 130 135	
gaa tgc tcc aag acc tgc ggc agc ggg ctc cag cac cgg acg cgt cat	723
Glu Cys Ser Lys Thr Cys Gly Ser Gly Leu Gln His Arg Thr Arg His	
136 141 146 151	
gtg gtg gcg ccc ccg cag ttc gga ggc tct ggc tgt cca aac ctg acg	771
Val Val Ala Pro Pro Gln Phe Gly Gly Ser Gly Cys Pro Asn Leu Thr	
152 157 162 167	
gag ttc cag gtg tgc caa tcc agt cca tgc gag gcc gag gag ctc agg	819
Glu Phe Gln Val Cys Gln Ser Ser Pro Cys Glu Ala Glu Glu Leu Arg	
168 173 178 183	
tac agc ctg cat gtg ggg ccc tgg agc acc tgc tca atg ccc cac tcc	867

Tyr	Ser	Leu	His	Val	Gly	Pro	Trp	Ser	Thr	Cys	Ser	Met	Pro	His	Ser		
184					189					194					199		
cga	caa	gta	aga	caa	gca	agg	aga	cgc	ggg	aag	aat	aaa	gaa	cgg	gaa		915
Arg	Gln	Val	Arg	Gln	Ala	Arg	Arg	Arg	Gly	Lys	Asn	Lys	Glu	Arg	Glu		
200					205					210					215		
aag	gac	cgc	agc	aaa	gga	gta	aag	gat	cca	gaa	gcc	cgc	gag	ctt	att		963
Lys	Asp	Arg	Ser	Lys	Gly	Val	Lys	Asp	Pro	Glu	Ala	Arg	Glu	Leu	Ile		
216					221					226					231		
aag	aaa	aag	aga	aac	aga	aac	agg	cag	aac	aga	caa	gag	aac	aaa	tat		1011
Lys	Lys	Lys	Arg	Asn	Arg	Asn	Arg	Gln	Asn	Arg	Gln	Glu	Asn	Lys	Tyr		
232					237					242					247		
tgg	gac	atc	cag	att	gga	tat	cag	acc	aga	gag	gtt	atg	tgc	att	aac		1059
Trp	Asp	Ile	Gln	Ile	Gly	Tyr	Gln	Thr	Arg	Glu	Val	Met	Cys	Ile	Asn		
248					253					258					263		
aag	acg	ggg	aaa	gct	gct	gat	tta	agc	ttt	tgc	cag	caa	gag	aag	ctt		1107
Lys	Thr	Gly	Lys	Ala	Ala	Asp	Leu	Ser	Phe	Cys	Gln	Gln	Glu	Lys	Leu		
264					269					274					279		
cca	atg	acc	ttc	cag	tcc	tgt	gtg	atc	acc	aaa	gag	tgc	cag	gtt	tcc		1155
Pro	Met	Thr	Phe	Gln	Ser	Cys	Val	Ile	Thr	Lys	Glu	Cys	Gln	Val	Ser		
280					285					290					295		
gag	tgg	tca	gag	tgg	agc	ccc	tgc	tca	aaa	aca	tgc	cat	gac	atg	gtg		1203
Glu	Trp	Ser	Glu	Trp	Ser	Pro	Cys	Ser	Lys	Thr	Cys	His	Asp	Met	Val		
296					301					306					311		
tcc	cct	gca	ggc	act	cgt	gta	agg	aca	cga	acc	atc	agg	cag	ttt	ccc		1251
Ser	Pro	Ala	Gly	Thr	Arg	Val	Arg	Thr	Arg	Thr	Ile	Arg	Gln	Phe	Pro		
312					317					322					327		
att	ggc	agt	gaa	aag	gag	tgt	cca	gaa	ttt	gaa	gaa	aaa	gaa	ccc	tgt		1299
Ile	Gly	Ser	Glu	Lys	Glu	Cys	Pro	Glu	Phe	Glu	Glu	Lys	Glu	Pro	Cys		
328					333					338					343		
ttg	tct	caa	gga	gat	gga	gtt	gtc	ccc	tgt	gcc	acg	tat	ggc	tgg	aga		1347
Leu	Ser	Gln	Gly	Asp	Gly	Val	Val	Pro	Cys	Ala	Thr	Tyr	Gly	Trp	Arg		
344					349					354					359		
act	aca	gag	tgg	act	gag	tgc	cgt	gtg	gac	cct	ttg	ctc	agt	cag	cag		1395
Thr	Thr	Glu	Trp	Thr	Glu	Cys	Arg	Val	Asp	Pro	Leu	Leu	Ser	Gln	Gln		
360					365					370					375		
gac	aag	agg	cgc	ggc	aac	cag	acg	gcc	ctc	tgt	gga	ggg	ggc	atc	cag		1443
Asp	Lys	Arg	Arg	Gly	Asn	Gln	Thr	Ala	Leu	Cys	Gly	Gly	Gly	Ile	Gln		
376					381					386					391		
acc	cga	gag	gtg	tac	tgc	gtg	cag	gcc	aac	gaa	aac	ctc	ctc	tca	caa		1491
Thr	Arg	Glu	Val	Tyr	Cys	Val	Gln	Ala	Asn	Glu	Asn	Leu	Leu	Ser	Gln		
392					397					402					407		
tta	agt	acc	cac	aag	aac	aaa	gaa	gcc	tca	aag	cca	atg	gac	tta	aaa		1539
Leu	Ser	Thr	His	Lys	Asn	Lys	Glu	Ala	Ser	Lys	Pro	Met	Asp	Leu	Lys		

408	413	418	423	
tta tgc act gga cct atc cct aat act aca cag ctg tgc cac att cct				1587
Leu Cys Thr Gly Pro Ile Pro Asn Thr Thr Gln Leu Cys His Ile Pro				
424	429	434	439	
tgt cca act gaa tgt gaa gtt tca cct tgg tca gct tgg gga cct tgt				1635
Cys Pro Thr Glu Cys Glu Val Ser Pro Trp Ser Ala Trp Gly Pro Cys				
440	445	450	455	
act tat gaa aac tgt aat gat cag caa ggg aaa aaa ggc ttc aaa ctg				1683
Thr Tyr Glu Asn Cys Asn Asp Gln Gln Gly Lys Lys Gly Phe Lys Leu				
456	461	466	471	
agg aag cgg cgc att acc aat gag ccc act gga ggc tct ggg gta acc				1731
Arg Lys Arg Arg Ile Thr Asn Glu Pro Thr Gly Gly Ser Gly Val Thr				
472	477	482	487	
gga aac tgc cct cac tta ctg gaa gcc att ccc tgt gaa gag cct gcc				1779
Gly Asn Cys Pro His Leu Leu Glu Ala Ile Pro Cys Glu Glu Pro Ala				
488	493	498	503	
tgt tat gac tgg aaa gca gtg aga ctg gga gac tgc gag cca gat aac				1827
Cys Tyr Asp Trp Lys Ala Val Arg Leu Gly Asp Cys Glu Pro Asp Asn				
504	509	514	519	
gga aag gag tgt ggt cca ggc acg caa gtt caa gag gtt gtg tgc atc				1875
Gly Lys Glu Cys Gly Pro Gly Thr Gln Val Gln Glu Val Val Cys Ile				
520	525	530	535	
aac agt gat gga gaa gaa gtt gac aga cag ctg tgc aga gat gcc atc				1923
Asn Ser Asp Gly Glu Glu Val Asp Arg Gln Leu Cys Arg Asp Ala Ile				
536	541	546	551	
ttc ccc atc cct gtg gcc tgt gat gcc cca tgc ccg aaa gac tgt gtg				1971
Phe Pro Ile Pro Val Ala Cys Asp Ala Pro Cys Pro Lys Asp Cys Val				
552	557	562	567	
ctc agc aca tgg tct acg tgg tcc tcc tgc tca cac acc tgc tca ggg				2019
Leu Ser Thr Trp Ser Thr Trp Ser Ser Cys Ser His Thr Cys Ser Gly				
568	573	578	583	
aaa acg aca gaa ggg aaa cag ata cga gca cga tcc att ctg gcc tat				2067
Lys Thr Thr Glu Gly Lys Gln Ile Arg Ala Arg Ser Ile Leu Ala Tyr				
584	589	594	599	
gcg ggt gaa gaa ggt gga att cgc tgt cca aat agc agt gct ttg caa				2115
Ala Gly Glu Glu Gly Gly Ile Arg Cys Pro Asn Ser Ser Ala Leu Gln				
600	605	610	615	
gaa gta cga agc tgt aat gag cat cct tgc aca gtg tac cac tgg caa				2163
Glu Val Arg Ser Cys Asn Glu His Pro Cys Thr Val Tyr His Trp Gln				
616	621	626	631	
act ggt ccc tgg ggc cag tgc att gag gac acc tca gta tcg tcc ttc				2211
Thr Gly Pro Trp Gly Gln Cys Ile Glu Asp Thr Ser Val Ser Ser Phe				
632	637	642	647	

aac aca act acg act tgg aat ggg gag gcc tcc tgc tct gtc ggc atg	2259
Asn Thr Thr Thr Thr Trp Asn Gly Glu Ala Ser Cys Ser Val Gly Met	
648 653 658 663	
cag aca aga aaa gtc atc tgt gtg cga gtc aat gtg ggc caa gtg gga	2307
Gln Thr Arg Lys Val Ile Cys Val Arg Val Asn Val Gly Gln Val Gly	
664 669 674 679	
ccc aaa aaa tgt cct gaa agc ctt cga cct gaa act gta agg cct tgt	2355
Pro Lys Lys Cys Pro Glu Ser Leu Arg Pro Glu Thr Val Arg Pro Cys	
680 685 690 695	
ctg ctt cct tgt aag aag gac tgt att gtg acc cca tat agt gac tgg	2403
Leu Leu Pro Cys Lys Lys Asp Cys Ile Val Thr Pro Tyr Ser Asp Trp	
696 701 706 711	
aca tca tgc ccc tct tcg tgt aaa gaa ggg gac tcc agt atc agg aag	2451
Thr Ser Cys Pro Ser Ser Cys Lys Glu Gly Asp Ser Ser Ile Arg Lys	
712 717 722 727	
cag tct agg cat cgg gtc atc att cag ctg cca gcc aac ggg ggc cga	2499
Gln Ser Arg His Arg Val Ile Ile Gln Leu Pro Ala Asn Gly Gly Arg	
728 733 738 743	
gac tgc aca gat ccc ctc tat gaa gag aag gcc tgt gag gca cct caa	2547
Asp Cys Thr Asp Pro Leu Tyr Glu Glu Lys Ala Cys Glu Ala Pro Gln	
744 749 754 759	
gcg tgc caa agc tac agg tgg aag act cac aaa tgg cgc aga tgc caa	2595
Ala Cys Gln Ser Tyr Arg Trp Lys Thr His Lys Trp Arg Arg Cys Gln	
760 765 770 775	
tta gtc cct tgg agc gtg caa caa gac agc cct gga gca cag gaa ggc	2643
Leu Val Pro Trp Ser Val Gln Gln Asp Ser Pro Gly Ala Gln Glu Gly	
776 781 786 791	
tgt ggg cct ggg cga cag gca aga gcc att act tgt cgc aag caa gat	2691
Cys Gly Pro Gly Arg Gln Ala Arg Ala Ile Thr Cys Arg Lys Gln Asp	
792 797 802 807	
gga gga cag gct gga atc cat gag tgc cta cag tat gca ggc cct gtg	2739
Gly Gly Gln Ala Gly Ile His Glu Cys Leu Gln Tyr Ala Gly Pro Val	
808 813 818 823	
cca gcc ctt acc cag gcc tgc cag atc ccc tgc cag gat gac tgt caa	2787
Pro Ala Leu Thr Gln Ala Cys Gln Ile Pro Cys Gln Asp Asp Cys Gln	
824 829 834 839	
ttg acc agc tgg tcc aag ttt tct tca tgc aat gga gac tgt ggt gca	2835
Leu Thr Ser Trp Ser Lys Phe Ser Ser Cys Asn Gly Asp Cys Gly Ala	
840 845 850 855	
gtt agg acc aga aag cgc act ctt gtt gga aaa agt aaa aaa aaa aaa	2883
Val Arg Thr Arg Lys Arg Thr Leu Val Gly Lys Ser Lys Lys Lys Lys	
856 861 866 871	

aaa tgt aaa aat tcc cat ttg tat ccc ctg att gag act cag tat tgt	2931
Lys Cys Lys Asn Ser His Leu Tyr Pro Leu Ile Glu Thr Gln Tyr Cys	
872 877 882 887	
cct tgt gac aaa tat aat gca caa cct gtg ggg aac tgg tca gac tgt	2979
Pro Cys Asp Lys Tyr Asn Ala Gln Pro Val Gly Asn Trp Ser Asp Cys	
888 893 898 903	
att tta cca gag gga aaa gtg gaa gtg ttg ctg gga atg aaa gta caa	3027
Ile Leu Pro Glu Gly Lys Val Glu Val Leu Leu Gly Met Lys Val Gln	
904 909 914 919	
gga gac atc aag gaa tgc gga caa gga tat cgt tac caa gca atg gca	3075
Gly Asp Ile Lys Glu Cys Gly Gln Gly Tyr Arg Tyr Gln Ala Met Ala	
920 925 930 935	
tgc tac gat caa aat ggc agg ctt gtg gaa aca tct aga tgt aac agc	3123
Cys Tyr Asp Gln Asn Gly Arg Leu Val Glu Thr Ser Arg Cys Asn Ser	
936 941 946 951	
cat ggt tac att gag gag gcc tgc atc atc ccc tgc ccc tca gac tgc	3171
His Gly Tyr Ile Glu Glu Ala Cys Ile Ile Pro Cys Pro Ser Asp Cys	
952 957 962 967	
aag ctc agt gag tgg tcc aac tgg tgc cgc tgc agc aag tcc tgt ggg	3219
Lys Leu Ser Glu Trp Ser Asn Trp Ser Arg Cys Ser Lys Ser Cys Gly	
968 973 978 983	
agt ggt gtg aag gtt cgt tct aaa tgg ctg cgt gaa aaa cca tat aat	3267
Ser Gly Val Lys Val Arg Ser Lys Trp Leu Arg Glu Lys Pro Tyr Asn	
984 989 994 999	
gga gga agg cct tgc ccc aaa ctg gac cat gtc aac cag gca cag gtg	3315
Gly Gly Arg Pro Cys Pro Lys Leu Asp His Val Asn Gln Ala Gln Val	
1000 1005 1010 1015	
tat gag gtt gtc cca tgc cac agt gac tgc aac cag tac cta tgg gtc	3363
Tyr Glu Val Val Pro Cys His Ser Asp Cys Asn Gln Tyr Leu Trp Val	
1016 1021 1026 1031	
aca gag ccc tgg agc atc tgc aag gtg acc ttt gtg aat atg cgg gag	3411
Thr Glu Pro Trp Ser Ile Cys Lys Val Thr Phe Val Asn Met Arg Glu	
1032 1037 1042 1047	
aac tgt gga gag ggc gtg caa acc cga aaa gtg aga tgc atg cag aat	3459
Asn Cys Gly Glu Gly Val Gln Thr Arg Lys Val Arg Cys Met Gln Asn	
1048 1053 1058 1063	
aca gca gat ggc cct tct gaa cat gta gag gat tac ctc tgt gac cca	3507
Thr Ala Asp Gly Pro Ser Glu His Val Glu Asp Tyr Leu Cys Asp Pro	
1064 1069 1074 1079	
gaa gag atg ccc ctg ggc tct aga gtg tgc aaa tta cca tgc cct gag	3555
Glu Glu Met Pro Leu Gly Ser Arg Val Cys Lys Leu Pro Cys Pro Glu	
1080 1085 1090 1095	
gac tgt gtg ata tct gaa tgg ggt cca tgg acc caa tgt gtt ttg cct	3603

Asp Cys Val Ile Ser Glu Trp Gly Pro Trp Thr Gln Cys Val Leu Pro	
1096 1101 1106 1111	
tgc aat caa agc agt ttc cgg caa agg tca gct gat ccc atc aga caa	3651
Cys Asn Gln Ser Ser Phe Arg Gln Arg Ser Ala Asp Pro Ile Arg Gln	
1112 1117 1122 1127	
cca gct gat gaa gga aga tct tgc cct aat gct gtt gag aaa gaa ccc	3699
Pro Ala Asp Glu Gly Arg Ser Cys Pro Asn Ala Val Glu Lys Glu Pro	
1128 1133 1138 1143	
tgt aac ctg aac aaa aac tgc tac cac tat gat tat aat gta aca gac	3747
Cys Asn Leu Asn Lys Asn Cys Tyr His Tyr Asp Tyr Asn Val Thr Asp	
1144 1149 1154 1159	
tgg agt aca tgt cag ctg agt gag aag gca gtt tgt gga aat gga ata	3795
Trp Ser Thr Cys Gln Leu Ser Glu Lys Ala Val Cys Gly Asn Gly Ile	
1160 1165 1170 1175	
aaa aca agg atg ttg gat tgt gtt cga agt gat ggc aag tca gtt gac	3843
Lys Thr Arg Met Leu Asp Cys Val Arg Ser Asp Gly Lys Ser Val Asp	
1176 1181 1186 1191	
ctg aaa tat tgt gaa gcg ctt ggc ttg gag aag aac tgg cag atg aac	3891
Leu Lys Tyr Cys Glu Ala Leu Gly Leu Glu Lys Asn Trp Gln Met Asn	
1192 1197 1202 1207	
acg tcc tgc atg gtg gaa tgc cct gtg aac tgt cag ctt tct gat tgg	3939
Thr Ser Cys Met Val Glu Cys Pro Val Asn Cys Gln Leu Ser Asp Trp	
1208 1213 1218 1223	
tct cct tgg tca gaa tgt tct caa aca tgt ggc ctc aca gga aaa atg	3987
Ser Pro Trp Ser Glu Cys Ser Gln Thr Cys Gly Leu Thr Gly Lys Met	
1224 1229 1234 1239	
atc cga aga cga aca gtg acc cag ccc ttt caa ggt gat gga aga cca	4035
Ile Arg Arg Arg Thr Val Thr Gln Pro Phe Gln Gly Asp Gly Arg Pro	
1240 1245 1250 1255	
tgc cct tcc ctg atg gac cag tcc aaa ccc tgc cca gtg aag cct tgt	4083
Cys Pro Ser Leu Met Asp Gln Ser Lys Pro Cys Pro Val Lys Pro Cys	
1256 1261 1266 1271	
tat cgg tgg caa tat ggc cag tgg tct cca tgc caa gtg cag gag gcc	4131
Tyr Arg Trp Gln Tyr Gly Gln Trp Ser Pro Cys Gln Val Gln Glu Ala	
1272 1277 1282 1287	
cag tgt gga gaa ggg acc aga aca agg aac att tct tgt gta gta agt	4179
Gln Cys Gly Glu Gly Thr Arg Thr Arg Asn Ile Ser Cys Val Val Ser	
1288 1293 1298 1303	
gat ggg tca gct gat gat ttc agc aaa gtg gtg gat gag gaa ttc tgt	4227
Asp Gly Ser Ala Asp Asp Phe Ser Lys Val Val Asp Glu Glu Phe Cys	
1304 1309 1314 1319	
gct gac att gaa ctc att ata gat ggt aat aaa aat atg gtt ctg gag	4275
Ala Asp Ile Glu Leu Ile Ile Asp Gly Asn Lys Asn Met Val Leu Glu	

1320	1325	1330	1335	
gaa tcc tgc agc cag cct tgc cca ggt gac tgt tat ttg aag gac tgg				4323
Glu Ser Cys Ser Gln Pro Cys Pro Gly Asp Cys Tyr Leu Lys Asp Trp				
1336	1341	1346	1351	
tct tcc tgg agc ctg tgt cag ctg acc tgt gtg aat ggt gag gat cta				4371
Ser Ser Trp Ser Leu Cys Gln Leu Thr Cys Val Asn Gly Glu Asp Leu				
1352	1357	1362	1367	
ggc ttt ggt gga ata cag gtc aga tcc aga ccg gtg att ata caa gaa				4419
Gly Phe Gly Gly Ile Gln Val Arg Ser Arg Pro Val Ile Ile Gln Glu				
1368	1373	1378	1383	
cta gag aat cag cat ctg tgc cca gag cag atg tta gaa aca aaa tca				4467
Leu Glu Asn Gln His Leu Cys Pro Glu Gln Met Leu Glu Thr Lys Ser				
1384	1389	1394	1399	
tgt tat gat gga cag tgc tat gaa tat aaa tgg atg gcc agt gct tgg				4515
Cys Tyr Asp Gly Gln Cys Tyr Glu Tyr Lys Trp Met Ala Ser Ala Trp				
1400	1405	1410	1415	
aag ggc tct tcc cga aca gtg tgg tgt caa agg tca gat ggt ata aat				4563
Lys Gly Ser Ser Arg Thr Val Trp Cys Gln Arg Ser Asp Gly Ile Asn				
1416	1421	1426	1431	
gta aca ggg ggc tgc ttg gtg atg agc cag cct gat gcc gac agg tct				4611
Val Thr Gly Gly Cys Leu Val Met Ser Gln Pro Asp Ala Asp Arg Ser				
1432	1437	1442	1447	
tgt aac cca ccg tgt agt caa ccc cac tcg tac tgt agc gag aca aaa				4659
Cys Asn Pro Pro Cys Ser Gln Pro His Ser Tyr Cys Ser Glu Thr Lys				
1448	1453	1458	1463	
aca tgc cat tgt gaa gaa ggg tac act gaa gtc atg tct tct aac agc				4707
Thr Cys His Cys Glu Glu Gly Tyr Thr Glu Val Met Ser Ser Asn Ser				
1464	1469	1474	1479	
acc ctt gag caa tgc aca ctt atc ccc gtg gtg gta tta ccc acc atg				4755
Thr Leu Glu Gln Cys Thr Leu Ile Pro Val Val Val Leu Pro Thr Met				
1480	1485	1490	1495	
gag gac aaa aga gga gat gtg aaa acc agt cgg gct gta cat cca acc				4803
Glu Asp Lys Arg Gly Asp Val Lys Thr Ser Arg Ala Val His Pro Thr				
1496	1501	1506	1511	
caa ccc tcc agt aac cca gca gga cgg gga agg acc tgg ttt cta cag				4851
Gln Pro Ser Ser Asn Pro Ala Gly Arg Gly Arg Thr Trp Phe Leu Gln				
1512	1517	1522	1527	
cca ttt ggg cca gat ggg aga cta aag acc tgg gtt tac ggt gta gca				4899
Pro Phe Gly Pro Asp Gly Arg Leu Lys Thr Trp Val Tyr Gly Val Ala				
1528	1533	1538	1543	
gct ggg gca ttt gtg tta ctc atc ttt att gtc tcc atg att tat cta				4947
Ala Gly Ala Phe Val Leu Leu Ile Phe Ile Val Ser Met Ile Tyr Leu				
1544	1549	1554	1559	

<210> 333
 <211> 8608
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(7785)

<400> 333

atg gca gat gtg gac cca gat aca ttg ctg gaa tgg cta cag atg gga	48
Met Ala Asp Val Asp Pro Asp Thr Leu Leu Glu Trp Leu Gln Met Gly	
1 5 10	
cag gga gat gaa agg gac atg caa cta ata gcc ctt gaa cag cta tgc	96
Gln Gly Asp Glu Arg Asp Met Gln Leu Ile Ala Leu Glu Gln Leu Cys	
17 22 27 32	
atg ctg ctt ttg atg tct gac aac gtg gat cgt tgt ttt gaa aca tgt	144
Met Leu Leu Leu Met Ser Asp Asn Val Asp Arg Cys Phe Glu Thr Cys	
33 38 43 48	
cct cct cgc act ttc tta cca gcc ctt tgc aaa att ttt ctt gat gaa	192
Pro Pro Arg Thr Phe Leu Pro Ala Leu Cys Lys Ile Phe Leu Asp Glu	
49 54 59 64	
agt gct cca gac aat gta tta gag gtg aca gcc cgt gcc ata aca tac	240
Ser Ala Pro Asp Asn Val Leu Glu Val Thr Ala Arg Ala Ile Thr Tyr	
65 70 75 80	
tac ctg gat gta tct gcg gaa tgt acc cga agg att gtt ggg gta gat	288
Tyr Leu Asp Val Ser Ala Glu Cys Thr Arg Arg Ile Val Gly Val Asp	
81 86 91 96	
gga gct ata aaa gca ctt tgt aat cgt ttg gtt gta gtt gaa ctt aac	336
Gly Ala Ile Lys Ala Leu Cys Asn Arg Leu Val Val Val Glu Leu Asn	
97 102 107 112	
aac agg act agc aga gac tta gcc gaa cag tgt gta aag gta tta gaa	384
Asn Arg Thr Ser Arg Asp Leu Ala Glu Gln Cys Val Lys Val Leu Glu	
113 118 123 128	
ctg ata tgt act cgt gag tca gga gca gtc ttt gag gct ggt ggt ttg	432
Leu Ile Cys Thr Arg Glu Ser Gly Ala Val Phe Glu Ala Gly Gly Leu	
129 134 139 144	
aat tgt gtg ctt acc ttc att cgt gac agt gga cat cta gtt cat aaa	480
Asn Cys Val Leu Thr Phe Ile Arg Asp Ser Gly His Leu Val His Lys	
145 150 155 160	
gac acc ttg cac tct gct atg gct gtg gta tca aga ctc tgt ggc aaa	528
Asp Thr Leu His Ser Ala Met Ala Val Val Ser Arg Leu Cys Gly Lys	
161 166 171 176	
atg gag cct caa gat tct tct tta gaa att tgt gta gaa tct ctg tct	576
Met Glu Pro Gln Asp Ser Ser Leu Glu Ile Cys Val Glu Ser Leu Ser	

177	182	187	192	
agt tta tta aag cat	gaa gat cat cag gtt	tca gat gga gct ctg cga		624
Ser Leu Leu Lys His	Glu Asp His Gln Val	Ser Asp Gly Ala Leu Arg		
193	198	203	208	
tgc ttt gca tca ctg	gct gac cga ttt acc	cgt cgt ggt gtt gac cca		672
Cys Phe Ala Ser Leu	Ala Asp Arg Phe Thr	Arg Arg Gly Val Asp Pro		
209	214	219	224	
gct cca tta gcc aag	cat gga tta act gag	gag ctg tta tct cga atg		720
Ala Pro Leu Ala Lys	His Gly Leu Thr Glu	Glu Leu Leu Ser Arg Met		
225	230	235	240	
gct gct gct ggt ggt	act gtt tca gga cca	tca tca gca tgc aaa cca		768
Ala Ala Ala Gly Gly	Thr Val Ser Gly Pro	Ser Ser Ala Cys Lys Pro		
241	246	251	256	
ggt cgc agc acc aca	gga gct cca tcc acc	act gca gat tcc aaa ttg		816
Gly Arg Ser Thr Thr	Gly Ala Pro Ser Thr	Thr Thr Ala Asp Ser Lys Leu		
257	262	267	272	
agt aat cag gtg tca	aca att gat ctt ctg	agg tcg gag ctt cca gat		864
Ser Asn Gln Val Ser	Thr Ile Asp Leu Leu	Arg Ser Glu Leu Pro Asp		
273	278	283	288	
tca att gaa agt gca	ttg cag ggt gat gaa	aga tgt gtg ctt gat act		912
Ser Ile Glu Ser Ala	Leu Gln Gly Asp Glu	Arg Cys Val Leu Asp Thr		
289	294	299	304	
atg cgt ttg gtt gac	ctt ctc ttg gtg cta	tta ttt gaa gga cga aaa		960
Met Arg Leu Val Asp	Leu Leu Leu Val Leu	Leu Phe Glu Gly Arg Lys		
305	310	315	320	
gct ttg cca aag tct	agt gct gga tct aca	ggc aga atc cca gga ctc		1008
Ala Leu Pro Lys Ser	Ser Ala Gly Ser Thr	Gly Arg Ile Pro Gly Leu		
321	326	331	336	
cgg aga tta gat agt	tct ggg gag cgc tca	cat cgg cag ctt ata gat		1056
Arg Arg Leu Asp Ser	Ser Gly Glu Arg Ser	His Arg Gln Leu Ile Asp		
337	342	347	352	
tgt att cga agt aaa	gat acc gat gca ctt	ata gat gca att gac aca		1104
Cys Ile Arg Ser Lys	Asp Thr Asp Ala Leu	Ile Asp Ala Ile Asp Thr		
353	358	363	368	
gga gcc ttt gaa gta	aat ttt atg gat gat	gta ggt cag act cta tta		1152
Gly Ala Phe Glu Val	Asn Phe Met Asp Asp	Val Gly Gln Thr Leu Leu		
369	374	379	384	
aac tgg gcc tct gct	ttt gga act cag gaa	atg gta gaa ttt ctt tgt		1200
Asn Trp Ala Ser Ala	Phe Gly Thr Gln Glu	Met Val Glu Phe Leu Cys		
385	390	395	400	
gag aga ggt gca gat	gtt aat aga ggt caa	agg tca tca tca tta cat		1248
Glu Arg Gly Ala Asp	Val Asn Arg Gly Gln	Arg Ser Ser Ser Leu His		
401	406	411	416	

tat gct gca tgt ttt gga aga cct caa gta gca aag act ctg tta cgg	1296
Tyr Ala Ala Cys Phe Gly Arg Pro Gln Val Ala Lys Thr Leu Leu Arg	
417 422 427 432	
cat ggt gca aat cca gat ctg aga gat gaa gat ggg aaa act cca tta	1344
His Gly Ala Asn Pro Asp Leu Arg Asp Glu Asp Gly Lys Thr Pro Leu	
433 438 443 448	
gat aaa gct cga gaa agg ggc cat agt gaa gtg gta gct att ctt cag	1392
Asp Lys Ala Arg Glu Arg Gly His Ser Glu Val Val Ala Ile Leu Gln	
449 454 459 464	
tct cca ggt gat tgg atg tgt cca gtt aat aaa gga gat gat aag aaa	1440
Ser Pro Gly Asp Trp Met Cys Pro Val Asn Lys Gly Asp Asp Lys Lys	
465 470 475 480	
aag aaa gat aca aac aaa gat gaa gaa gaa tgt aat gag ccc aaa gga	1488
Lys Lys Asp Thr Asn Lys Asp Glu Glu Glu Cys Asn Glu Pro Lys Gly	
481 486 491 496	
gat ccg gaa atg gca ccc ata tac ttg aaa agg tta ttg cca gtg ttt	1536
Asp Pro Glu Met Ala Pro Ile Tyr Leu Lys Arg Leu Leu Pro Val Phe	
497 502 507 512	
gca caa aca ttt cag caa act atg ctg cct tca ata agg aaa gca agt	1584
Ala Gln Thr Phe Gln Gln Thr Met Leu Pro Ser Ile Arg Lys Ala Ser	
513 518 523 528	
ctt gct cta att cga aaa atg att cat ttt tgc tct gaa gca ctg tta	1632
Leu Ala Leu Ile Arg Lys Met Ile His Phe Cys Ser Glu Ala Leu Leu	
529 534 539 544	
aaa gaa gtt tgt gat tct gat gtt ggt cac aat ttg cct aca ata cta	1680
Lys Glu Val Cys Asp Ser Asp Val Gly His Asn Leu Pro Thr Ile Leu	
545 550 555 560	
gtg gaa atc act gca act gtc ctg gat caa gag gat gat gat gat ggc	1728
Val Glu Ile Thr Ala Thr Val Leu Asp Gln Glu Asp Asp Asp Asp Gly	
561 566 571 576	
cac ttg ctg gct ttg cag atc ata agg gat tta gta gat aaa ggt ggt	1776
His Leu Leu Ala Leu Gln Ile Ile Arg Asp Leu Val Asp Lys Gly Gly	
577 582 587 592	
gat ata ttt ttg gat cag cta gcc aga ctt ggt gta att agc aaa gtg	1824
Asp Ile Phe Leu Asp Gln Leu Ala Arg Leu Gly Val Ile Ser Lys Val	
593 598 603 608	
tca acg ttg gca ggt cct tcc tct gat gat gag aat gaa gag gaa tca	1872
Ser Thr Leu Ala Gly Pro Ser Ser Asp Asp Glu Asn Glu Glu Glu Ser	
609 614 619 624	
aaa cca gaa aaa gaa gat gaa cca cag gaa gat gct aaa gaa ttg caa	1920
Lys Pro Glu Lys Glu Asp Glu Pro Gln Glu Asp Ala Lys Glu Leu Gln	
625 630 635 640	

caa ggt aaa cca tat cat tgg aga gac tgg tca atc att agg gga agg	1968
Gln Gly Lys Pro Tyr His Trp Arg Asp Trp Ser Ile Ile Arg Gly Arg	
641 646 651 656	
gac tgc tta tat att tgg agt gat gca gca gcc ttg gaa tta tct aat	2016
Asp Cys Leu Tyr Ile Trp Ser Asp Ala Ala Ala Leu Glu Leu Ser Asn	
657 662 667 672	
ggc agt aat gga tgg ttc aga ttt atc ttg gat gga aaa ctt gcc acc	2064
Gly Ser Asn Gly Trp Phe Arg Phe Ile Leu Asp Gly Lys Leu Ala Thr	
673 678 683 688	
atg tat tca agt ggt agt ccg gaa ggt gga tct gag agt tca gaa agc	2112
Met Tyr Ser Ser Gly Ser Pro Glu Gly Gly Ser Asp Ser Ser Glu Ser	
689 694 699 704	
cga agt gaa ttc tta gag aag tta caa aga gct cga ggc caa gta aag	2160
Arg Ser Glu Phe Leu Glu Lys Leu Gln Arg Ala Arg Gly Gln Val Lys	
705 710 715 720	
cca tct act tca agt caa cct ata ctg tca gca cca gga ccc act aaa	2208
Pro Ser Thr Ser Ser Gln Pro Ile Leu Ser Ala Pro Gly Pro Thr Lys	
721 726 731 736	
ctt act gta gga aat tgg tca ctg aca tgt ttg aaa gaa gga gaa att	2256
Leu Thr Val Gly Asn Trp Ser Leu Thr Cys Leu Lys Glu Gly Glu Ile	
737 742 747 752	
gct att cat aat tca gat ggt cag caa gct aca ata ttg aaa gaa gat	2304
Ala Ile His Asn Ser Asp Gly Gln Gln Ala Thr Ile Leu Lys Glu Asp	
753 758 763 768	
tta cct ggt ttt gta ttt gaa tct aat aga gga acc aaa cat tca ttt	2352
Leu Pro Gly Phe Val Phe Glu Ser Asn Arg Gly Thr Lys His Ser Phe	
769 774 779 784	
act gca gaa act tcc ctg ggt tca gaa ttt gtg act ggc tgg act ggc	2400
Thr Ala Glu Thr Ser Leu Gly Ser Glu Phe Val Thr Gly Trp Thr Gly	
785 790 795 800	
aaa aga ggc aga aaa ctg aaa tct aag tta gaa aaa aca aag caa aag	2448
Lys Arg Gly Arg Lys Leu Lys Ser Lys Leu Glu Lys Thr Lys Gln Lys	
801 806 811 816	
gta cga act atg gct cga gat tta tac gat gac cat ttt aaa gct gtt	2496
Val Arg Thr Met Ala Arg Asp Leu Tyr Asp Asp His Phe Lys Ala Val	
817 822 827 832	
gaa agc atg cct cgt gga gta gtg gta aca ctc aga aac ata gca act	2544
Glu Ser Met Pro Arg Gly Val Val Val Thr Leu Arg Asn Ile Ala Thr	
833 838 843 848	
cag tta gag tca tct tgg gaa ctt cat aca aat aga caa tgt att gag	2592
Gln Leu Glu Ser Ser Trp Glu Leu His Thr Asn Arg Gln Cys Ile Glu	
849 854 859 864	
agt gag aac act tgg aga gat tta atg aag aca gct tta gaa aac cta	2640

1089	1094	1099	1104	
gat aat tca gct tta aat	tgt cat agc aat gat	gat aag aat gcc tgg		3360
Asp Asn Ser Ala Leu Asn	Cys His Ser Asn Asp	Asp Lys Asn Ala Trp		
1105	1110	1115	1120	
ttt gcc ata gat ctg ggt	ctc tgg gtg ata cca	tca gca tat aca ctt		3408
Phe Ala Ile Asp Leu Gly	Leu Trp Val Ile Pro	Ser Ala Tyr Thr Leu		
1121	1126	1131	1136	
cgt cat gct cgt ggt tat	gga agg tct gca ctg	aga aat tgg gtt ttc		3456
Arg His Ala Arg Gly Tyr	Gly Arg Ser Ala Leu	Arg Asn Trp Val Phe		
1137	1142	1147	1152	
cag gta tcc aaa gat gga	cag aac tgg act tct	ttg tat acc cat gtt		3504
Gln Val Ser Lys Asp Gly	Gln Asn Trp Thr Ser	Leu Tyr Thr His Val		
1153	1158	1163	1168	
gat gac tgc agt ctc aat	gaa cca ggg tca act	gca act tgg cct ctt		3552
Asp Asp Cys Ser Leu Asn	Glu Pro Gly Ser Thr	Ala Thr Trp Pro Leu		
1169	1174	1179	1184	
gat cca cca aag gat gag	aaa caa ggg tgg aga	cat gtg aga att aaa		3600
Asp Pro Pro Lys Asp Glu	Lys Gln Gly Trp Arg	His Val Arg Ile Lys		
1185	1190	1195	1200	
cag atg ggg aaa aat gcc	agt gga caa aca cac	tac ctc tca tta tct		3648
Gln Met Gly Lys Asn Ala	Ser Gly Gln Thr His	Tyr Leu Ser Leu Ser		
1201	1206	1211	1216	
gga ttc gaa ctt tat ggc	act gta aat gga gta	tgt gaa gat cag cta		3696
Gly Phe Glu Leu Tyr Gly	Thr Val Asn Gly Val	Cys Glu Asp Gln Leu		
1217	1222	1227	1232	
ggg aaa gca gct aaa gaa	gca gaa gct aat ctt	aga cgg cag aga cgt		3744
Gly Lys Ala Ala Lys Glu	Ala Glu Ala Asn Leu	Arg Arg Gln Arg Arg		
1233	1238	1243	1248	
cta gta cgt tcc cag gtt	ctg aaa tac atg gtt	cca gga gct cgt gtt		3792
Leu Val Arg Ser Gln Val	Leu Lys Tyr Met Val	Pro Gly Ala Arg Val		
1249	1254	1259	1264	
atc aga ggc ctg gat tgg	aaa tgg cga gat cag	gat ggc agc cca cag		3840
Ile Arg Gly Leu Asp Trp	Lys Trp Arg Asp Gln	Asp Gly Ser Pro Gln		
1265	1270	1275	1280	
gga gaa ggc act gtc aca	gga gaa cta cac aat	ggc tgg att gat gtc		3888
Gly Glu Gly Thr Val Thr	Gly Glu Leu His Asn	Gly Trp Ile Asp Val		
1281	1286	1291	1296	
acc tgg gat gct ggt ggc	tca aac tct tac cgt	atg ggc gca gaa gga		3936
Thr Trp Asp Ala Gly Gly	Ser Asn Ser Tyr Arg	Met Gly Ala Glu Gly		
1297	1302	1307	1312	
aaa ttt gac ctc aag ctt	gca cca ggg tac gac	cct gat aca gtg gca		3984
Lys Phe Asp Leu Lys Leu	Ala Pro Gly Tyr Asp	Pro Asp Thr Val Ala		
1313	1318	1323	1328	

tca ccc aaa cct gtt tca tcc act gtt tca ggc aca acg caa tca tgg	4032
Ser Pro Lys Pro Val Ser Ser Thr Val Ser Gly Thr Thr Gln Ser Trp	
1329 1334 1339 1344	
agc agc ttg gtg aaa aac aac tgt cca gac aag aca tct gct gct gca	4080
Ser Ser Leu Val Lys Asn Asn Cys Pro Asp Lys Thr Ser Ala Ala Ala	
1345 1350 1355 1360	
ggc tcc tca agt aga aaa gga agc agc agt tct gtg tgt agc gtg gcc	4128
Gly Ser Ser Ser Arg Lys Gly Ser Ser Ser Ser Val Cys Ser Val Ala	
1361 1366 1371 1376	
agt agc agc gac atc agc ttg ggt tgc acc aaa acg gaa cgg aga tca	4176
Ser Ser Ser Asp Ile Ser Leu Gly Ser Thr Lys Thr Glu Arg Arg Ser	
1377 1382 1387 1392	
gaa att gta atg gaa cac agt ata gtt tca gga gct gat gtc cat gaa	4224
Glu Ile Val Met Glu His Ser Ile Val Ser Gly Ala Asp Val His Glu	
1393 1398 1403 1408	
cca att gtt gtt ctt tca tct gct gaa aac gtc cct caa aca gaa gta	4272
Pro Ile Val Val Leu Ser Ser Ala Glu Asn Val Pro Gln Thr Glu Val	
1409 1414 1419 1424	
ggg tca tct tcc agt gca agc acc agc acc tta aca gcg gaa acg gga	4320
Gly Ser Ser Ser Ser Ala Ser Thr Ser Thr Leu Thr Ala Glu Thr Gly	
1425 1430 1435 1440	
agt gaa aat gct gaa agg aag tta ggc cct gat agt tct gtt cgt act	4368
Ser Glu Asn Ala Glu Arg Lys Leu Gly Pro Asp Ser Ser Val Arg Thr	
1441 1446 1451 1456	
cct ggg gag tct agt gca ata tcc atg gga att gtc agt gtt agt tct	4416
Pro Gly Glu Ser Ser Ala Ile Ser Met Gly Ile Val Ser Val Ser Ser	
1457 1462 1467 1472	
cct gat gtt agt tca gta tct gaa tta act aat aaa gaa gca gct tca	4464
Pro Asp Val Ser Ser Val Ser Glu Leu Thr Asn Lys Glu Ala Ala Ser	
1473 1478 1483 1488	
caa cga cct ctt agc tct tca gca agt aac aga ctg tca gtg agt tct	4512
Gln Arg Pro Leu Ser Ser Ser Ala Ser Asn Arg Leu Ser Val Ser Ser	
1489 1494 1499 1504	
ttg ttg gct gct ggg gcc cct atg agc tct agt gca agt gta cct aac	4560
Leu Leu Ala Ala Gly Ala Pro Met Ser Ser Ser Ala Ser Val Pro Asn	
1505 1510 1515 1520	
ctg tcc tca aga gaa aca tct agc ttg gag agt ttt gta agg aga gtg	4608
Leu Ser Ser Arg Glu Thr Ser Ser Leu Glu Ser Phe Val Arg Arg Val	
1521 1526 1531 1536	
gca aac ata gca cgg act aat gcc acg aac aac atg aat cta agc cga	4656
Ala Asn Ile Ala Arg Thr Asn Ala Thr Asn Asn Met Asn Leu Ser Arg	
1537 1542 1547 1552	

agc agc agt gat aac aac act aat act ttg ggg agg aat gtg atg agc Ser Ser Ser Asp Asn Asn Thr Asn Thr Leu Gly Arg Asn Val Met Ser 1553 1558 1563 1568	4704
aca gca act tct cct ctt atg ggt gct cag agt ttc cct aat ttg acc Thr Ala Thr Ser Pro Leu Met Gly Ala Gln Ser Phe Pro Asn Leu Thr 1569 1574 1579 1584	4752
aca cct ggt act aca tca aca gtg act atg tca aca tcc agt gtt act Thr Pro Gly Thr Thr Ser Thr Val Thr Met Ser Thr Ser Ser Val Thr 1585 1590 1595 1600	4800
agc agc agc aat gta gct aca gca aca aca gtt tta tca gtt ggt caa Ser Ser Ser Asn Val Ala Thr Ala Thr Thr Val Leu Ser Val Gly Gln 1601 1606 1611 1616	4848
tct tta agt aac act tta acc acc agc ctc aca tca act tcc agt gag Ser Leu Ser Asn Thr Leu Thr Thr Ser Leu Thr Ser Thr Ser Ser Glu 1617 1622 1627 1632	4896
agt gac aca ggt cag gaa gca gaa tat tcc tta tat gat ttc ctt gat Ser Asp Thr Gly Gln Glu Ala Glu Tyr Ser Leu Tyr Asp Phe Leu Asp 1633 1638 1643 1648	4944
agc tgc cgt gcc agt act cta ttg gct gag ctc gat gat gat gag gac Ser Cys Arg Ala Ser Thr Leu Leu Ala Glu Leu Asp Asp Asp Glu Asp 1649 1654 1659 1664	4992
tta cct gag cca gat gaa gaa gat gat gag aat gaa gat gac aat cag Leu Pro Glu Pro Asp Glu Glu Asp Asp Glu Asn Glu Asp Asp Asn Gln 1665 1670 1675 1680	5040
gag gac caa gaa tac gag gag gtt atg att ctg aga cgc cca tcc ctg Glu Asp Gln Glu Tyr Glu Glu Val Met Ile Leu Arg Arg Pro Ser Leu 1681 1686 1691 1696	5088
caa cgt cga gct ggc tcc cgc tct gat gta acg cat cat gct gtt acc Gln Arg Arg Ala Gly Ser Arg Ser Asp Val Thr His His Ala Val Thr 1697 1702 1707 1712	5136
tcg cag cta cca cag gta cct gct gga gca ggg agc cga cct att ggg Ser Gln Leu Pro Gln Val Pro Ala Gly Ala Gly Ser Arg Pro Ile Gly 1713 1718 1723 1728	5184
gag cag gaa gaa gaa gag tac gaa act aaa gga gga cgc cgg aga aca Glu Gln Glu Glu Glu Glu Tyr Glu Thr Lys Gly Gly Arg Arg Arg Thr 1729 1734 1739 1744	5232
tgg gat gat gat tat gtg cta aag aga cag ttt tct gca ttg gtt cct Trp Asp Asp Asp Tyr Val Leu Lys Arg Gln Phe Ser Ala Leu Val Pro 1745 1750 1755 1760	5280
gct ttt gat cct aga cct ggt cgt act aat gtc cag cag aca act gat Ala Phe Asp Pro Arg Pro Gly Arg Thr Asn Val Gln Gln Thr Thr Asp 1761 1766 1771 1776	5328
cta gaa ata cca ccc cca ggg acc cct cat tca gag ctc ttg gaa gaa	5376

Leu Glu Ile Pro Pro Pro Gly Thr Pro His Ser Glu Leu Leu Glu Glu	
1777 1782 1787 1792	
gtc gaa tgt act ccg tca cct cga tta gct ctc act ttg aaa gta aca	5424
Val Glu Cys Thr Pro Ser Pro Arg Leu Ala Leu Thr Leu Lys Val Thr	
1793 1798 1803 1808	
ggt ctt gga acg act cgt gaa gtt gaa tta cca ctc acc aat ttc aga	5472
Gly Leu Gly Thr Thr Arg Glu Val Glu Leu Pro Leu Thr Asn Phe Arg	
1809 1814 1819 1824	
tca acc atc ttt tac tat gta caa aaa ttg ctt caa ttg tcc tgt aat	5520
Ser Thr Ile Phe Tyr Tyr Val Gln Lys Leu Leu Gln Leu Ser Cys Asn	
1825 1830 1835 1840	
ggc aat gtg aaa tca gat aaa ctt agg cgt att tgg gag ccc aca tac	5568
Gly Asn Val Lys Ser Asp Lys Leu Arg Arg Ile Trp Glu Pro Thr Tyr	
1841 1846 1851 1856	
aca atc atg tac aga gaa atg aag gat tct gat aaa gaa aag gaa aat	5616
Thr Ile Met Tyr Arg Glu Met Lys Asp Ser Asp Lys Glu Lys Glu Asn	
1857 1862 1867 1872	
gga aaa atg ggt tgc tgg tct ata gag cat gtg gag cag tac ctt ggc	5664
Gly Lys Met Gly Cys Trp Ser Ile Glu His Val Glu Gln Tyr Leu Gly	
1873 1878 1883 1888	
act gat gaa tta cca aag aat gac ttg ata acc tac ctg cag aag aat	5712
Thr Asp Glu Leu Pro Lys Asn Asp Leu Ile Thr Tyr Leu Gln Lys Asn	
1889 1894 1899 1904	
gca gac gct gct ttc ctg cgc cac tgg aaa tta act ggc act aat aaa	5760
Ala Asp Ala Ala Phe Leu Arg His Trp Lys Leu Thr Gly Thr Asn Lys	
1905 1910 1915 1920	
agt att agg aaa aac aga aat tgt tct cag ctc ata gct gca tat aag	5808
Ser Ile Arg Lys Asn Arg Asn Cys Ser Gln Leu Ile Ala Ala Tyr Lys	
1921 1926 1931 1936	
gat ttt tgt gag cat gga aca aag tct ggg tta aac cag ggg gcc att	5856
Asp Phe Cys Glu His Gly Thr Lys Ser Gly Leu Asn Gln Gly Ala Ile	
1937 1942 1947 1952	
tct act ctt caa agt agt gat att ctt aat tta aca aaa gaa caa cct	5904
Ser Thr Leu Gln Ser Ser Asp Ile Leu Asn Leu Thr Lys Glu Gln Pro	
1953 1958 1963 1968	
cag gcc aaa gca ggc aat gga cag aac tct tgt gga gta gaa gat gtc	5952
Gln Ala Lys Ala Gly Asn Gly Gln Asn Ser Cys Gly Val Glu Asp Val	
1969 1974 1979 1984	
ctt cag ctt ctg cgt att ctg tat ata gtt gca agt gac cct tat tca	6000
Leu Gln Leu Leu Arg Ile Leu Tyr Ile Val Ala Ser Asp Pro Tyr Ser	
1985 1990 1995 2000	
aga ata tcc cag gaa gat ggt gat gaa cag cct cag ttt act ttt cca	6048
Arg Ile Ser Gln Glu Asp Gly Asp Glu Gln Pro Gln Phe Thr Phe Pro	

2001	2006	2011	2016	
cca gat gaa ttc act agc aaa aaa att aca aca aaa ata tta cag cag				6096
Pro Asp Glu Phe Thr Ser Lys Lys Ile Thr Thr Lys Ile Leu Gln Gln				
2017	2022	2027	2032	
att gag gaa cca ttg gca ctg gca agt ggg gct ctg cca gac tgg tgt				6144
Ile Glu Glu Pro Leu Ala Leu Ala Ser Gly Ala Leu Pro Asp Trp Cys				
2033	2038	2043	2048	
gaa caa tta acc agc aaa tgt cct ttt cta ata cca ttt gaa act aga				6192
Glu Gln Leu Thr Ser Lys Cys Pro Phe Leu Ile Pro Phe Glu Thr Arg				
2049	2054	2059	2064	
cag ctt tat ttc aca tgt aca gca ttt ggc gcc tca aga gca ata gta				6240
Gln Leu Tyr Phe Thr Cys Thr Ala Phe Gly Ala Ser Arg Ala Ile Val				
2065	2070	2075	2080	
tgg tta cag aac cga cgt gaa gcc act gtg gag cga acg aga acc aca				6288
Trp Leu Gln Asn Arg Arg Glu Ala Thr Val Glu Arg Thr Arg Thr Thr				
2081	2086	2091	2096	
agc agt gtt agg cga gat gac cct gga gag ttt cga gtt ggt cgt ctc				6336
Ser Ser Val Arg Arg Asp Asp Pro Gly Glu Phe Arg Val Gly Arg Leu				
2097	2102	2107	2112	
aag cat gaa aga gta aaa gtt cca cgt ggc gag tca ctg atg gaa tgg				6384
Lys His Glu Arg Val Lys Val Pro Arg Gly Glu Ser Leu Met Glu Trp				
2113	2118	2123	2128	
gct gag aat gtc atg caa ata cat gca gat cgg aaa tca gtt ctt gag				6432
Ala Glu Asn Val Met Gln Ile His Ala Asp Arg Lys Ser Val Leu Glu				
2129	2134	2139	2144	
gtt gaa ttt tta gga gaa gaa gga act ggc ttg gga ccc aca tta gag				6480
Val Glu Phe Leu Gly Glu Glu Gly Thr Gly Leu Gly Pro Thr Leu Glu				
2145	2150	2155	2160	
ttt tat gct ctg gtg gca gca gaa ttc cag aga act gac ttg gga gct				6528
Phe Tyr Ala Leu Val Ala Ala Glu Phe Gln Arg Thr Asp Leu Gly Ala				
2161	2166	2171	2176	
tgg ctt tgt gat gat aat ttt cca gat gat gaa tct cgt cac gtt gat				6576
Trp Leu Cys Asp Asp Asn Phe Pro Asp Asp Glu Ser Arg His Val Asp				
2177	2182	2187	2192	
ctt gga ggt gga ttg aaa cct cct gga tat tat gtg cag agg tca tgt				6624
Leu Gly Gly Gly Leu Lys Pro Pro Gly Tyr Tyr Val Gln Arg Ser Cys				
2193	2198	2203	2208	
gga ctg ttc aca gca cca ttt cca cag gat agt gat gag ctt gaa agg				6672
Gly Leu Phe Thr Ala Pro Phe Pro Gln Asp Ser Asp Glu Leu Glu Arg				
2209	2214	2219	2224	
atc acg aaa ctg ttt cat ttg ctt gga att ttc ttg gcc aaa tgc att				6720
Ile Thr Lys Leu Phe His Phe Leu Gly Ile Phe Leu Ala Lys Cys Ile				
2225	2230	2235	2240	

caa gac aat aga ctt gtg gac tta cct att tct aaa cct ttt ttt aaa	6768
Gln Asp Asn Arg Leu Val Asp Leu Pro Ile Ser Lys Pro Phe Phe Lys	
2241 2246 2251 2256	
ctt atg tgt atg ggt gac att aaa agc aat atg agt aaa ctg att tat	6816
Leu Met Cys Met Gly Asp Ile Lys Ser Asn Met Ser Lys Leu Ile Tyr	
2257 2262 2267 2272	
gag tca cga ggt gat aga gac tta cac tgt act gaa agt cag tct gaa	6864
Glu Ser Arg Gly Asp Arg Asp Leu His Cys Thr Glu Ser Gln Ser Glu	
2273 2278 2283 2288	
gct tct aca gaa gaa ggt cat gat tca ctc tgc gta gga agc ttt gaa	6912
Ala Ser Thr Glu Glu Gly His Asp Ser Leu Ser Val Gly Ser Phe Glu	
2289 2294 2299 2304	
gag gat tca aaa tca gaa ttt att ctt gat ccc cct aaa cca aaa ccc	6960
Glu Asp Ser Lys Ser Glu Phe Ile Leu Asp Pro Pro Lys Pro Lys Pro	
2305 2310 2315 2320	
cca gct tgg ttt aat gga att ttg act tgg gaa gac ttt gaa tta gta	7008
Pro Ala Trp Phe Asn Gly Ile Leu Thr Trp Glu Asp Phe Glu Leu Val	
2321 2326 2331 2336	
aac cca cac aga gcc aga ttt tta aaa gaa att aaa gac ctt gct atc	7056
Asn Pro His Arg Ala Arg Phe Leu Lys Glu Ile Lys Asp Leu Ala Ile	
2337 2342 2347 2352	
aag agg cgc caa att tta agc aac aaa ggt ctt tct gaa gat gag aag	7104
Lys Arg Arg Gln Ile Leu Ser Asn Lys Gly Leu Ser Glu Asp Glu Lys	
2353 2358 2363 2368	
aac aca aaa tta cag gaa cta gtg ctg aag aat cca tca ggt tct ggg	7152
Asn Thr Lys Leu Gln Glu Leu Val Leu Lys Asn Pro Ser Gly Ser Gly	
2369 2374 2379 2384	
cct cca ctt agc ata gag gat tta ggt tta aat ttc cag ttt tgc cct	7200
Pro Pro Leu Ser Ile Glu Asp Leu Gly Leu Asn Phe Gln Phe Cys Pro	
2385 2390 2395 2400	
tcc tca aga ata tat ggt ttt aca gct gtg gat ctc aag cca agt ggt	7248
Ser Ser Arg Ile Tyr Gly Phe Thr Ala Val Asp Leu Lys Pro Ser Gly	
2401 2406 2411 2416	
gaa gat gag atg ata aca atg gat aat gca gaa gaa tat gtg gat ttg	7296
Glu Asp Glu Met Ile Thr Met Asp Asn Ala Glu Glu Tyr Val Asp Leu	
2417 2422 2427 2432	
atg ttt gac ttt tgt atg cat acg ggt att cag aaa caa atg gaa gcc	7344
Met Phe Asp Phe Cys Met His Thr Gly Ile Gln Lys Gln Met Glu Ala	
2433 2438 2443 2448	
ttt aga gat ggg ttt aat aaa gtt ttt cca atg gag aaa tta agt tcc	7392
Phe Arg Asp Gly Phe Asn Lys Val Phe Pro Met Glu Lys Leu Ser Ser	
2449 2454 2459 2464	

ttc agc cat gaa gaa gtc caa atg att ctt tgt gga aac cag tca cca	7440
Phe Ser His Glu Glu Val Gln Met Ile Leu Cys Gly Asn Gln Ser Pro	
2465 2470 2475 2480	
tcc tgg gca gca gag gat att atc aat tac act gaa cct aag ctg ggt	7488
Ser Trp Ala Ala Glu Asp Ile Ile Asn Tyr Thr Glu Pro Lys Leu Gly	
2481 2486 2491 2496	
tat aca cgt gac agc cct ggt ttc ctg agg ttt gtg agg gtt tta tgt	7536
Tyr Thr Arg Asp Ser Pro Gly Phe Leu Arg Phe Val Arg Val Leu Cys	
2497 2502 2507 2512	
ggc atg tct tct gat gaa agg aaa gca ttc ttg cag ttt acc act ggt	7584
Gly Met Ser Ser Asp Glu Arg Lys Ala Phe Leu Gln Phe Thr Thr Gly	
2513 2518 2523 2528	
tgt tca act cta ccc cca ggt gga ctg gct aac ctg cat ccc agg ctc	7632
Cys Ser Thr Leu Pro Pro Gly Gly Leu Ala Asn Leu His Pro Arg Leu	
2529 2534 2539 2544	
acg gtt gta cgc aag gtt gat gct act gat gca agc tat cca tca gtc	7680
Thr Val Val Arg Lys Val Asp Ala Thr Asp Ala Ser Tyr Pro Ser Val	
2545 2550 2555 2560	
aat aca tgt gtg cat tac ctt aag ttg cct gaa tat tct tcc gag gag	7728
Asn Thr Cys Val His Tyr Leu Lys Leu Pro Glu Tyr Ser Ser Glu Glu	
2561 2566 2571 2576	
atc atg aga gag cgc ctg cta gct gct aca atg gag aaa ggc ttt cat	7776
Ile Met Arg Glu Arg Leu Leu Ala Ala Thr Met Glu Lys Gly Phe His	
2577 2582 2587 2592	
ctc aat tga gctttga agtgcaatgg gagacatcag agactttaaa aatactagt	7832
Leu Asn *	
2593	
aagcctcttg tgtttgtgtg cagagaagta tatgatccac catgctaag acacttgcc	7892
ttttttccac cattaaggct ttaagaacat gtggaataag ttttttagct gctaagaca	7952
aaacaaatcc tgtaactacc cagccagcaa gtatatagca cagaacactg tgttacttta	8012
caagggctta tgtgactgga ataaggtggg cccacttgac tgttccaaag agcagcttct	8072
cagatcttca gtgttcaactg gtaaatttct aacagtgtat ttgtgtaaag tttgtcattt	8132
catactccat aactacagt tgctgtcact gatccctgtt ttgctggctt ttaagctact	8192
tggtcaaaaa tctgtcttcc ttaaaacata gagaattaat gagcatctca agctttttct	8252
tttctttttt aatgatgctt gcactatcaa gagtattcta gtgttctctc tttgtttggc	8312
atataatcat gcaccaaact ttttatttct ttaaggtggg agtatatttt tatttcctaa	8372
atgccatact atgaagatca aagtcttaag tgtgtttgca gctcaaaaat aaagatgtat	8432
taagggggga aaacctgggc taagtgaag gcacacttac agcgagtttt actttcgggt	8492

gtattttctt tgtatattat aaacatttat ttaacttggt gccgtttgaa gtaaaaaatt 8552
tccaaaatgt atgctcaaca ataatcatta aaatgtttgc agcgtaaaaa aaaaaa 8608

<210> 334
<211> 2163
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (869)..(1336)

<400> 334

aacttcgaaa cccgattacg ccaagcttgg cacgaggtgt gtggggagcg ggcgtcggat 60
ttgtccgtga ggatttttaa atggggccat ttgagccctg gcaaagttct gcctcctggg 120
ggcattgctg gccccatcc gagtgcttct ggcctttatc gtctcttttc tctctggcc 180
ctttgcctgg cttcaagtgg ccggtcttag tgaggagcag cttcaggagc caattacagg 240
atggaggaag actgtgtgcc acaacggggg gctaggcctg agccgcctgc tgtttttcct 300
gctgggcttc ctccgattc gcgttcgtgg ccagcgagcc tctcgcttc aagcccctgt 360
ccttgttgct gcccacact ccactttctt tgacccatt gttctgtgc cctgtgacct 420
gcccaaagtt gtgtcccgag ctgagaacct ttccgttctt gtcattggag cccttcttcg 480
attcaaccaa gccatcctgg tatcccgga tgacccggt tctcgacgca gagtgggtga 540
ggaggtccga aggcgggcca cctcaggagg caagtggcgg caggtgctat tctttcctga 600
gggcacctgt tccaacaaga aggctttgct taagttcaa ccaggagcct tcatcgagg 660
ggtgcctgtg cagcctgtcc tcatccgcta cccaacagt ctggacacca ccagctgggc 720
atggaggggt cctggagtag tcaaagtcct ctggctcaca gcctctcagc cctgcagcat 780
tgtggatgtg gagttccttc ctgtgtatca cccagccct gaggagagca gggacccac 840
cctctatgcc aacaatgttc agagggtc atg gca cag gct ctg ggc att cca 892
Met Ala Gln Ala Leu Gly Ile Pro
1 5
gcc acc gaa tgt gag ttt gta ggg agc tta cct gtg att gtg gtg ggc 940
Ala Thr Glu Cys Glu Phe Val Gly Ser Leu Pro Val Ile Val Val Gly
9 14 19 24
cgg ctg aag gtg gcg ttg gaa cca cag ctg tgg gaa ctg gga aaa gtg 988
Arg Leu Lys Val Ala Leu Glu Pro Gln Leu Trp Glu Leu Gly Lys Val
25 30 35 40

ctt cgg aag gct ggg ctg tcc gct ggc tat gtg gac gct ggg gca gag	1036
Leu Arg Lys Ala Gly Leu Ser Ala Gly Tyr Val Asp Ala Gly Ala Glu	
41 46 51 56	
cca ggc cgg agt cga atg atc agc cag gaa gag ttt gcc agg cag cta	1084
Pro Gly Arg Ser Arg Met Ile Ser Gln Glu Glu Phe Ala Arg Gln Leu	
57 62 67 72	
cag ctc tct gat cct cag acg gtg gct ggt gcc ttt ggc tac ttc cag	1132
Gln Leu Ser Asp Pro Gln Thr Val Ala Gly Ala Phe Gly Tyr Phe Gln	
73 78 83 88	
cag gat acc aag ggt ttg gtg gac ttc cga gat gtg gcc ctt gca cta	1180
Gln Asp Thr Lys Gly Leu Val Asp Phe Arg Asp Val Ala Leu Ala Leu	
89 94 99 104	
gca gct ctg gat ggg ggc agg agc ctg gaa gag cta act cgt ctg gcc	1228
Ala Ala Leu Asp Gly Gly Arg Ser Leu Glu Glu Leu Thr Arg Leu Ala	
105 110 115 120	
ttt gag gta atg ggg ggt ggc ggt ggt ggg ggg tgc tta gtg gct atg	1276
Phe Glu Val Met Gly Gly Gly Gly Gly Gly Gly Cys Leu Val Ala Met	
121 126 131 136	
ctc acc ccg ctc cag gag gcc tat ttt ggt atg ctg ttt cca gta gct	1324
Leu Thr Pro Leu Gln Glu Ala Tyr Phe Gly Met Leu Phe Pro Val Ala	
137 142 147 152	
tct aga tac tag gca tttggtatcc aacctagtgc cacagtgcct aaaactgcag	1379
Ser Arg Tyr *	
153	
acccccggcc tctatgttga gacctagctg ggcacaagaa gaaggaagaa gaaggaaaaa	1439
gctataaagt ctacagttct gcagaaaggg cactggaggg tcagggaaag cttgtgcacc	1499
acccttttgg aagaggagga gcctgtcagg ccagtctgtg gggcaggggtg aggccatggc	1559
atgaggagag aacttgactc ttatcccttt ctctcccaag ctctttgctg aagagcaagc	1619
agaggggtccc aaccgcctgc tgtacaaaga cggcttcagc accatcctgc acctgctgct	1679
gggttcaccc caccctgctg ccacagcttt gcatgctgag ctgtgccagg caggatccag	1739
ccaaggcctc tccctctgtc agttccagaa cttctccctc catgaccac tctatgggaa	1799
actcttcagc acctacctgc gccccccaca cacctctcga ggcacctccc agacacccaaa	1859
tgcctcatcc ccaggcaacc cactgctct ggccaatggg actgtgcaag caccgaagca	1919
gaaggagac tgagtgcctc agcctctcac cccctcctcc tcagggcagc gctagggggc	1979
tcccctatgc ctcagcccca tctctgctcc tgtttgaatt ttgttattgt tgtttggttg	2039
ttgttttttt aagttgattt taattttttg tttggttgat ttttttgtaa aaaactatatt	2099

tatatataaa tataaatcta tatctatatc tattaaaaaa atggaagtc aaaaaaaaaa 2159
 aaaa 2163

<210> 335
 <211> 2909
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (86)..(2302)

<400> 335
 taagcttgcg gccgccgagt cggctctgcgc agcctcctgc gttttctcgc ttggatcttg 60
 gcactgagag gcggtggccg gcggg atg gag aaa agt agg atg aac ctg ccc 112
 Met Glu Lys Ser Arg Met Asn Leu Pro
 1 5
 aag ggg ccg gac acg ctc tgc ttc gac aag gac gag ttc atg aag gaa 160
 Lys Gly Pro Asp Thr Leu Cys Phe Asp Lys Asp Glu Phe Met Lys Glu
 10 15 20 25
 gat ttc gat gtc gat cat ttt gtg tct gac tgt agg aag cgg gtc cag 208
 Asp Phe Asp Val Asp His Phe Val Ser Asp Cys Arg Lys Arg Val Gln
 26 31 36 41
 ctg gaa gaa ctg aga gat gac ctg gag ctc tac tat aaa ctt ctt aaa 256
 Leu Glu Glu Leu Arg Asp Asp Leu Glu Leu Tyr Tyr Lys Leu Leu Lys
 42 47 52 57
 aca gcc atg gtc gaa ctc atc aac aag gat tat gca gat ttt gtc aat 304
 Thr Ala Met Val Glu Leu Ile Asn Lys Asp Tyr Ala Asp Phe Val Asn
 58 63 68 73
 ctt tca aca aac ttg gtt ggc atg gac aaa gcc ctc aac cag ctt tct 352
 Leu Ser Thr Asn Leu Val Gly Met Asp Lys Ala Leu Asn Gln Leu Ser
 74 79 84 89
 gtg cct ttg gga caa tta cga gaa gag gtt ctg agc ctt aga tcg tct 400
 Val Pro Leu Gly Gln Leu Arg Glu Glu Val Leu Ser Leu Arg Ser Ser
 90 95 100 105
 gtc agt gaa gga att cgg gca gtt gat gaa cga atg tct aaa caa gag 448
 Val Ser Glu Gly Ile Arg Ala Val Asp Glu Arg Met Ser Lys Gln Glu
 106 111 116 121
 gac att agg aaa aaa aag atg tgt gta ttg agg ctt ata caa gtt att 496
 Asp Ile Arg Lys Lys Lys Met Cys Val Leu Arg Leu Ile Gln Val Ile
 122 127 132 137
 cgg tca gtt gag aaa att gaa aaa atc tta aac tct caa agt tct aaa 544
 Arg Ser Val Glu Lys Ile Glu Lys Ile Leu Asn Ser Gln Ser Ser Lys

138	143	148	153	
gaa acc tct gca cta	gaa gca agc agc ccc	ctt ttg act gga caa att		592
Glu Thr Ser Ala Leu	Glu Ala Ser Ser Pro	Leu Leu Thr Gly Gln Ile		
154	159	164	169	
ttg gag aga att gcc	aca gaa ttt aat cag	tta cag ttt cat gct gtt		640
Leu Glu Arg Ile Ala	Thr Glu Phe Asn Gln	Leu Gln Phe His Ala Val		
170	175	180	185	
caa agc aaa ggc atg	cct ctt ttg gac aaa	gta aga ccg cgt ata gct		688
Gln Ser Lys Gly Met	Pro Leu Leu Asp Lys	Val Arg Pro Arg Ile Ala		
186	191	196	201	
ggc att aca gcc atg	tta cag cag tca ctg	gaa ggt ctc cta tta gaa		736
Gly Ile Thr Ala Met	Leu Gln Gln Ser Leu	Glu Gly Leu Leu Leu Glu		
202	207	212	217	
ggc ctt cag acg tct	gac gtc gat ata ata	cgg cac tgc ttg cgg act		784
Gly Leu Gln Thr Ser	Asp Val Asp Ile Ile	Arg His Cys Leu Arg Thr		
218	223	228	233	
tac gcc acg att gac	aag aca cgg gac gcg	gag gcc tta gtt ggc caa		832
Tyr Ala Thr Ile Asp	Lys Thr Arg Asp Ala	Glu Ala Leu Val Gly Gln		
234	239	244	249	
gta cta gtg aaa cca	tac ata gac gag gtg	att ata gag cag ttt gtt		880
Val Leu Val Lys Pro	Tyr Ile Asp Glu Val	Ile Ile Glu Gln Phe Val		
250	255	260	265	
gaa tct cat ccc aat	ggc ctt cag gtc atg	tat aat aaa ctc ctg gag		928
Glu Ser His Pro Asn	Gly Leu Gln Val Met	Tyr Asn Lys Leu Leu Glu		
266	271	276	281	
ttt gtt cct cac cat	tgc cgc ctt ctt cga	gaa gtc aca gga ggt gcc		976
Phe Val Pro His His	Cys Arg Leu Leu Arg	Glu Val Thr Gly Gly Ala		
282	287	292	297	
atc tcc agt gaa aaa	ggc aat act gtt cct	gga tat gac ttt ttg gtg		1024
Ile Ser Ser Glu Lys	Gly Asn Thr Val Pro	Gly Tyr Asp Phe Leu Val		
298	303	308	313	
aat tct gtt tgg cca	caa ata gta caa gga	tta gaa gaa aag tta ccc		1072
Asn Ser Val Trp Pro	Gln Ile Val Gln Gly	Leu Glu Glu Lys Leu Pro		
314	319	324	329	
tgc ctt ttt aat cct	ggg aat ccc gat gca	ttt cat gag aaa tat acc		1120
Ser Leu Phe Asn Pro	Gly Asn Pro Asp Ala	Phe His Glu Lys Tyr Thr		
330	335	340	345	
ata agt atg gat ttt	gtc aga aga ttg gaa	cgg cag tgt gga tca cag		1168
Ile Ser Met Asp Phe	Val Arg Arg Leu Glu	Arg Gln Cys Gly Ser Gln		
346	351	356	361	
gct agt gta aag aga	tta aga gcc cat cct	gcc tat cac agc ttc aat		1216
Ala Ser Val Lys Arg	Leu Arg Ala His Pro	Ala Tyr His Ser Phe Asn		
362	367	372	377	

aag aag tgg aac ttg cct gtt tat ttt caa ata aga ttt aga gaa ata	1264
Lys Lys Trp Asn Leu Pro Val Tyr Phe Gln Ile Arg Phe Arg Glu Ile	
378 383 388 393	
gcg gga tcc tta gaa gca gca ctt aca gat gtc ctg gaa gat gcc cca	1312
Ala Gly Ser Leu Glu Ala Ala Leu Thr Asp Val Leu Glu Asp Ala Pro	
394 399 404 409	
gct gaa agt ccg tat tgc ctt ttg gct tct cat aga act tgg agc agc	1360
Ala Glu Ser Pro Tyr Cys Leu Leu Ala Ser His Arg Thr Trp Ser Ser	
410 415 420 425	
ctt agg agg tgt tgg tca gat gag atg ttc ttg cca tta ctg gtg cat	1408
Leu Arg Arg Cys Trp Ser Asp Glu Met Phe Leu Pro Leu Leu Val His	
426 431 436 441	
cgc ctg tgg aga ctc act ctg cag att ttg gca cga tac tct gtg ttt	1456
Arg Leu Trp Arg Leu Thr Leu Gln Ile Leu Ala Arg Tyr Ser Val Phe	
442 447 452 457	
gtc aat gag ctt tca ctc agg ccc att tct aat gaa agt ccc aag gag	1504
Val Asn Glu Leu Ser Leu Arg Pro Ile Ser Asn Glu Ser Pro Lys Glu	
458 463 468 473	
atc aag aaa cct ttg gta act ggt agc aaa gaa cct tcc atc acc caa	1552
Ile Lys Lys Pro Leu Val Thr Gly Ser Lys Glu Pro Ser Ile Thr Gln	
474 479 484 489	
gga aac act gaa gac caa gga agt ggt cct tcg gaa aca aag cct gtg	1600
Gly Asn Thr Glu Asp Gln Gly Ser Gly Pro Ser Glu Thr Lys Pro Val	
490 495 500 505	
gtt tcc att tcc cgc act cag ctc gtg tat gtg gtt gca gac ctg gac	1648
Val Ser Ile Ser Arg Thr Gln Leu Val Tyr Val Val Ala Asp Leu Asp	
506 511 516 521	
aag ctt cag gag cag ctt cca gaa ctc ttg gaa ata atc aag cca aaa	1696
Lys Leu Gln Glu Gln Leu Pro Glu Leu Leu Glu Ile Ile Lys Pro Lys	
522 527 532 537	
ctt gaa atg att ggc ttt aag aat ttt tct tct atc tca gca gcc ctg	1744
Leu Glu Met Ile Gly Phe Lys Asn Phe Ser Ser Ile Ser Ala Ala Leu	
538 543 548 553	
gag gac tcc cag agc tct ttt tca gcc tgt gtg ccc tcc ttg agt agc	1792
Glu Asp Ser Gln Ser Ser Phe Ser Ala Cys Val Pro Ser Leu Ser Ser	
554 559 564 569	
aag atc atc cag gat tta agt gac tct tgc ttc ggt ttc cta aaa agc	1840
Lys Ile Ile Gln Asp Leu Ser Asp Ser Cys Phe Gly Phe Leu Lys Ser	
570 575 580 585	
gcc ctg gag gtt ccc agg ctt tac cga aga acc aat aag gag gtc cca	1888
Ala Leu Glu Val Pro Arg Leu Tyr Arg Arg Thr Asn Lys Glu Val Pro	
586 591 596 601	

acc aca gct tcc tcc tat gtg gac agt gct ctg aag ccc tta ttc cag	1936
Thr Thr Ala Ser Ser Tyr Val Asp Ser Ala Leu Lys Pro Leu Phe Gln	
602 607 612 617	
ctt cag agc gga cac aag gat aag ctc aaa caa gca ata att cag cag	1984
Leu Gln Ser Gly His Lys Asp Lys Leu Lys Gln Ala Ile Ile Gln Gln	
618 623 628 633	
tgg cta gaa ggc act ctc agt gaa agc act cat aag tac tat gaa acc	2032
Trp Leu Glu Gly Thr Leu Ser Glu Ser Thr His Lys Tyr Tyr Glu Thr	
634 639 644 649	
gtg tca gat gta tta aac tct gtg aag aag atg gaa gag agc ctg aaa	2080
Val Ser Asp Val Leu Asn Ser Val Lys Lys Met Glu Glu Ser Leu Lys	
650 655 660 665	
agg ctg aaa caa gcc aga aaa acc act ccc gcc aac ccc gtc ggt ccc	2128
Arg Leu Lys Gln Ala Arg Lys Thr Thr Pro Ala Asn Pro Val Gly Pro	
666 671 676 681	
agt ggt ggc atg agc gac gac gac aaa atc agg ctg cag ttg gcc cta	2176
Ser Gly Gly Met Ser Asp Asp Asp Lys Ile Arg Leu Gln Leu Ala Leu	
682 687 692 697	
gat gtt gag tac ttg gga gag cag ata caa aag ttg gga cta caa gca	2224
Asp Val Glu Tyr Leu Gly Glu Gln Ile Gln Lys Leu Gly Leu Gln Ala	
698 703 708 713	
agt gac ata aaa agc ttc tca gct ctc gca gag ctt gtt gct gct gcc	2272
Ser Asp Ile Lys Ser Phe Ser Ala Leu Ala Glu Leu Val Ala Ala Ala	
714 719 724 729	
aag gac cag gca aca gca gag cag cct taa g catcttggaa gatccccgagg	2323
Lys Asp Gln Ala Thr Ala Glu Gln Pro *	
730 735	
ttagattcatt aagcaagaga agagttggac ttccaggctg aaggggagaa agtgactctg	2383
ttctcttagc aaccgtctgt agcaaagaag tgcttcacag atcactccag caacacgccc	2443
atgcgtcttc tctcagcgta tttgggtctt ctttgcccaa aagaacacaa aagccttttt	2503
ccattgtatg gaagatagtt ttttaagacat ttgaaacttt ctactatagt ttacagaaca	2563
aattatttta tttttattgt aaatcttagt gtggaagagc tgattttctaa aatatgatta	2623
aagtaaatat atacctatga atatcaagag tcgtctccct gagcctgtag ttggaagtga	2683
cgactgtaat ggaatgatgt cttgtataga aattcgaaat gcccttctct gaaataaaga	2743
gaactcctgg gctttctaaa gaggctgctg gaagccatcc tccactccca ctgtgtgtga	2803
gagcagtgtc tctgatcctg ctgtcaccct gacctctggc aggagccggc gccagtagga	2863
aagacctcct tcttaaataa aagaagtgtc tcccaaaaaa aaaaaa	2909

<210> 336
 <211> 2450
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (105)..(2258)

<400> 336
 gcgcccgtg taccgggtccg gaattcccgg gtcgacgatt tcgtccgcgc tgagctgaag 60
 gctgtgcgga gcggcgcggc acagagcctg ttgttgagct cagt atg tcg tgg gaa 116
 Met Ser Trp Glu
 1
 tcc ggg gcc ggg cca ggt cta ggt tcc cag ggg atg gat ctc gtg tgg 164
 Ser Gly Ala Gly Pro Gly Leu Gly Ser Gln Gly Met Asp Leu Val Trp
 5 10 15 20
 agt gcg tgg tac gga aag tgc gtt aaa ggg aaa ggg tcg ttg cca ctc 212
 Ser Ala Trp Tyr Gly Lys Cys Val Lys Gly Lys Gly Ser Leu Pro Leu
 21 26 31 36
 tcg gcc cac ggc atc gtg gtc gcc tgg ctc agc agg gcc gag tgg gac 260
 Ser Ala His Gly Ile Val Val Ala Trp Leu Ser Arg Ala Glu Trp Asp
 37 42 47 52
 cag gtg acg gtt tat ctg ttc tgt gac gac cat aag ttg cag cgg tac 308
 Gln Val Thr Val Tyr Leu Phe Cys Asp Asp His Lys Leu Gln Arg Tyr
 53 58 63 68
 gcg ctt aac cgc atc acg gtg tgg agg agc agg tca ggc aac gaa ctc 356
 Ala Leu Asn Arg Ile Thr Val Trp Arg Ser Arg Ser Gly Asn Glu Leu
 69 74 79 84
 cct ctg gca gtg gct tct act gct gac ctg ata cgc tgt aag ctc ttg 404
 Pro Leu Ala Val Ala Ser Thr Ala Asp Leu Ile Arg Cys Lys Leu Leu
 85 90 95 100
 gat gta act ggt ggc ttg ggc act gat gaa ctt aga ctg ctc tat ggc 452
 Asp Val Thr Gly Gly Leu Gly Thr Asp Glu Leu Arg Leu Leu Tyr Gly
 101 106 111 116
 atg gca ttg gtc agg ttt gtg aat ctt atc tca gag agg aag aca aag 500
 Met Ala Leu Val Arg Phe Val Asn Leu Ile Ser Glu Arg Lys Thr Lys
 117 122 127 132
 ttt gcc aag gtc ccc ctc aag tgt ctg gct caa gag gta aat att ccg 548
 Phe Ala Lys Val Pro Leu Lys Cys Leu Ala Gln Glu Val Asn Ile Pro
 133 138 143 148
 gat tgg att gtt gac ctt cgc cat gag ttg acc cac aag aaa atg ccc 596
 Asp Trp Ile Val Asp Leu Arg His Glu Leu Thr His Lys Lys Met Pro
 149 154 159 164

cat	ata	aat	gac	tgc	cgc	aga	ggc	tgc	tac	ttt	gtc	ctg	gat	tgg	ctc	644
His	Ile	Asn	Asp	Cys	Arg	Arg	Gly	Cys	Tyr	Phe	Val	Leu	Asp	Trp	Leu	
165					170					175					180	
cag	aag	acc	tat	tgg	tgc	cgc	caa	ctg	gag	aac	agc	ctg	aga	gag	acc	692
Gln	Lys	Thr	Tyr	Trp	Cys	Arg	Gln	Leu	Glu	Asn	Ser	Leu	Arg	Glu	Thr	
181					186					191					196	
tgg	gag	ttg	gag	gag	ttc	agg	gaa	ggg	ata	gag	gaa	gag	gat	caa	gag	740
Trp	Glu	Leu	Glu	Glu	Phe	Arg	Glu	Gly	Ile	Glu	Glu	Glu	Asp	Gln	Glu	
197					202					207					212	
gaa	gat	aag	aac	att	gtt	gtt	gat	gac	atc	aca	gaa	cag	aaa	cca	gag	788
Glu	Asp	Lys	Asn	Ile	Val	Val	Asp	Asp	Ile	Thr	Glu	Gln	Lys	Pro	Glu	
213					218					223					228	
cct	cag	gat	gat	ggg	aaa	agt	acg	gag	tca	gat	gta	aag	gcc	gat	gga	836
Pro	Gln	Asp	Asp	Gly	Lys	Ser	Thr	Glu	Ser	Asp	Val	Lys	Ala	Asp	Gly	
229					234					239					244	
gac	agc	aaa	ggc	agc	gaa	gag	gtg	gat	tct	cat	tgc	aaa	aag	gcc	ctg	884
Asp	Ser	Lys	Gly	Ser	Glu	Glu	Val	Asp	Ser	His	Cys	Lys	Lys	Ala	Leu	
245					250					255					260	
agt	cat	aaa	gag	cta	tat	gaa	aga	gcc	cga	gaa	ctg	ctg	gta	tca	tac	932
Ser	His	Lys	Glu	Leu	Tyr	Glu	Arg	Ala	Arg	Glu	Leu	Leu	Val	Ser	Tyr	
261					266					271					276	
gaa	gag	gag	cag	ttt	acg	gtg	ctg	gag	aaa	ttt	agg	tat	tta	cct	aag	980
Glu	Glu	Glu	Gln	Phe	Thr	Val	Leu	Glu	Lys	Phe	Arg	Tyr	Leu	Pro	Lys	
277					282					287					292	
gcc	att	aag	gag	tgg	aat	aac	ccg	tcc	cca	cgt	gta	gaa	tgt	gtc	ctg	1028
Ala	Ile	Lys	Ala	Trp	Asn	Asn	Pro	Ser	Pro	Arg	Val	Glu	Cys	Val	Leu	
293					298					303					308	
gca	gag	ctc	aag	ggc	gtt	aca	tgc	gag	aac	agg	gag	gct	gtg	ctg	gat	1076
Ala	Glu	Leu	Lys	Gly	Val	Thr	Cys	Glu	Asn	Arg	Glu	Ala	Val	Leu	Asp	
309					314					319					324	
gct	ttt	ctg	gat	gat	ggc	ttc	ctt	gtc	ccc	aca	ttt	gaa	cag	ttg	gca	1124
Ala	Phe	Leu	Asp	Asp	Gly	Phe	Leu	Val	Pro	Thr	Phe	Glu	Gln	Leu	Ala	
325					330					335					340	
gct	ttg	cag	ata	gaa	tat	gaa	gaa	aac	gtg	gac	ttg	aat	gac	gtc	ctg	1172
Ala	Leu	Gln	Ile	Glu	Tyr	Glu	Glu	Asn	Val	Asp	Leu	Asn	Asp	Val	Leu	
341					346					351					356	
gtg	cca	aag	ccg	ttc	tct	cag	ttc	tgg	cag	ccc	ctg	ctc	agg	ggc	ctg	1220
Val	Pro	Lys	Pro	Phe	Ser	Gln	Phe	Trp	Gln	Pro	Leu	Leu	Arg	Gly	Leu	
357					362					367					372	
cac	tcc	cag	aac	ttc	acg	cag	gcc	cta	ttg	gag	agg	atg	ctc	tct	gaa	1268
His	Ser	Gln	Asn	Phe	Thr	Gln	Ala	Leu	Leu	Glu	Arg	Met	Leu	Ser	Glu	
373					378					383					388	

ctg cca gcc ttg ggg atc agc ggg atc cgg cct acc tac atc ctc aga	1316
Leu Pro Ala Leu Gly Ile Ser Gly Ile Arg Pro Thr Tyr Ile Leu Arg	
389 394 399 404	
tgg acc gtt gaa ctg atc gtg gcc aac acc aag act gga cgg aat gct	1364
Trp Thr Val Glu Leu Ile Val Ala Asn Thr Lys Thr Gly Arg Asn Ala	
405 410 415 420	
cgc cga ttt tct gca ggc cag tgg gaa gca aga agg ggc tgg agg ctg	1412
Arg Arg Phe Ser Ala Gly Gln Trp Glu Ala Arg Arg Gly Trp Arg Leu	
421 426 431 436	
ttc aac tgc tcc gcc tcc ctt gac tgg ccc cgg atg gtt gag tcc tgc	1460
Phe Asn Cys Ser Ala Ser Leu Asp Trp Pro Arg Met Val Glu Ser Cys	
437 442 447 452	
ttg ggc tca cct tgc tgg gcc agc ccc caa ctc ctt cgg atc atc ttc	1508
Leu Gly Ser Pro Cys Trp Ala Ser Pro Gln Leu Leu Arg Ile Ile Phe	
453 458 463 468	
aaa gcc atg ggg cag ggc ctg cca gac gag gag cag gag aag ctg ctg	1556
Lys Ala Met Gly Gln Gly Leu Pro Asp Glu Glu Gln Glu Lys Leu Leu	
469 474 479 484	
cgc atc tgt tcc att tat acc cag agt gga gaa aac agc ctg gtg cag	1604
Arg Ile Cys Ser Ile Tyr Thr Gln Ser Gly Glu Asn Ser Leu Val Gln	
485 490 495 500	
gag ggc tct gag gcc tcc ccc att ggg aag tct cca tat aca cta gac	1652
Glu Gly Ser Glu Ala Ser Pro Ile Gly Lys Ser Pro Tyr Thr Leu Asp	
501 506 511 516	
agc ctg tat tgg agc gtc aag cca gcc agc tcc agc ttc ggg tct gaa	1700
Ser Leu Tyr Trp Ser Val Lys Pro Ala Ser Ser Ser Phe Gly Ser Glu	
517 522 527 532	
gca aag gcc cag caa cag gag gag cag ggc agt gtt aat gat gtc aag	1748
Ala Lys Ala Gln Gln Gln Glu Glu Gln Gly Ser Val Asn Asp Val Lys	
533 538 543 548	
gaa gag gag aag gag gag aaa gag gtc ttg cca gac cag gta gag gag	1796
Glu Glu Glu Lys Glu Glu Lys Glu Val Leu Pro Asp Gln Val Glu Glu	
549 554 559 564	
gag gaa gaa aat gat gac caa gag gag gaa gag gag gat gaa gat gat	1844
Glu Glu Glu Asn Asp Asp Gln Glu Glu Glu Glu Glu Asp Glu Asp Asp	
565 570 575 580	
gaa gat gat gaa gag gaa gac aga atg gag gtg ggg cct ttc tct aca	1892
Glu Asp Asp Glu Glu Glu Asp Arg Met Glu Val Gly Pro Phe Ser Thr	
581 586 591 596	
ggg caa gag tcc ccc act gcc gag aat gct agg ctt ctg gcc cag aaa	1940
Gly Gln Glu Ser Pro Thr Ala Glu Asn Ala Arg Leu Leu Ala Gln Lys	
597 602 607 612	
aga gga gct ttg cag ggc tct gca tgg cag gtt agc tca gaa gac gtg	1988

Arg Gly Ala Leu Gln Gly Ser Ala Trp Gln Val Ser Ser Glu Asp Val	
613 618 623 628	
cga tgg gac aca ttt ccc cta ggc cga atg cca ggt cag acc gag gac	2036
Arg Trp Asp Thr Phe Pro Leu Gly Arg Met Pro Gly Gln Thr Glu Asp	
629 634 639 644	
cca gca gag ctc atg ctg gag aat tat gac acc atg tat ctt ttg gac	2084
Pro Ala Glu Leu Met Leu Glu Asn Tyr Asp Thr Met Tyr Leu Leu Asp	
645 650 655 660	
cag cct gtg cta gag cag cgg ctg gaa ccc tca aca tgc aag act gac	2132
Gln Pro Val Leu Glu Gln Arg Leu Glu Pro Ser Thr Cys Lys Thr Asp	
661 666 671 676	
acc ttg ggc ctg agc tgt ggt gtc ggc agt ggc aac tgc agc aac agc	2180
Thr Leu Gly Leu Ser Cys Gly Val Gly Ser Gly Asn Cys Ser Asn Ser	
677 682 687 692	
agc agc agc aac ttc gag ggc ctt ctc tgg agc cag ggg cag ctg cat	2228
Ser Ser Ser Asn Phe Glu Gly Leu Leu Trp Ser Gln Gly Gln Leu His	
693 698 703 708	
ggg ctc aaa act ggc ctg cag ctc ttc tga t ggccatccct ggtgcaagt	2279
Gly Leu Lys Thr Gly Leu Gln Leu Phe *	
709 714	
ttcatccagc cgtgccaggg caacagccca cccctagta caactgatgc tccctgagac	2339
aacctgggag acagcctgga tcagccacat caactcagtt gtccaccaca ggggaatttt	2399
gaatgtcttt tgtttttgtt ttgttttgaa aaataataaa caggcaactg t	2450

<210> 337
 <211> 2513
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (105)..(2309)

<400> 337	
gcgcccgcgtg taccgggtccg gaattcccgg gtgcacgatt tcgtccgcgc tgagctgaag	60
gctgtgcgga gcggcgcggc acagagcctg ttgttgagct cagt atg tcg tgg gaa	116
Met Ser Trp Glu	
1	
tcc ggg gcc ggg cca ggt cta ggt tcc cag ggg atg gat ctc gtg tgg	164
Ser Gly Ala Gly Pro Gly Leu Gly Ser Gln Gly Met Asp Leu Val Trp	
5 10 15 20	
agt gcg tgg tac gga aag tgc gtt aaa ggg aaa ggg tcg ttg cca ctc	212

Ser	Ala	Trp	Tyr	Gly	Lys	Cys	Val	Lys	Gly	Lys	Gly	Ser	Leu	Pro	Leu		
21					26					31					36		
tcg	gcc	cac	ggc	atc	gtg	gtc	gcc	tgg	ctc	agc	agg	gcc	gag	tgg	gac	260	
Ser	Ala	His	Gly	Ile	Val	Val	Ala	Trp	Leu	Ser	Arg	Ala	Glu	Trp	Asp		
37					42					47					52		
cag	gtg	acg	gtt	tat	ctg	ttc	tgt	gac	gac	cat	aag	ttg	cag	cgg	tac	308	
Gln	Val	Thr	Val	Tyr	Leu	Phe	Cys	Asp	Asp	His	Lys	Leu	Gln	Arg	Tyr		
53					58					63					68		
gcg	ctt	aac	cgc	atc	acg	gtg	tgg	agg	agc	agg	tca	ggc	aac	gaa	ctc	356	
Ala	Leu	Asn	Arg	Ile	Thr	Val	Trp	Arg	Ser	Arg	Ser	Gly	Asn	Glu	Leu		
69					74					79					84		
cct	ctg	gca	gtg	gct	tct	act	gct	gac	ctg	ata	cgc	tgt	aag	ctc	ttg	404	
Pro	Leu	Ala	Val	Ala	Ser	Thr	Ala	Asp	Leu	Ile	Arg	Cys	Lys	Leu	Leu		
85					90					95					100		
gat	gta	act	ggg	ggc	ttg	ggc	act	gat	gaa	ctt	aga	ctg	ctc	tat	ggc	452	
Asp	Val	Thr	Gly	Gly	Leu	Gly	Thr	Asp	Glu	Leu	Arg	Leu	Leu	Tyr	Gly		
101					106					111					116		
atg	gca	ttg	gtc	agg	ttt	gtg	aat	ctt	atc	tca	gag	agg	aag	aca	aag	500	
Met	Ala	Leu	Val	Arg	Phe	Val	Asn	Leu	Ile	Ser	Glu	Arg	Lys	Thr	Lys		
117					122					127					132		
ttt	gcc	aag	gtc	ccc	ctc	aag	tgt	ctg	gct	caa	gag	gta	aat	att	ccg	548	
Phe	Ala	Lys	Val	Pro	Leu	Lys	Cys	Leu	Ala	Gln	Glu	Val	Asn	Ile	Pro		
133					138					143					148		
gat	tgg	att	gtt	gac	ctt	cgc	cat	gag	ttg	acc	cac	aag	aaa	atg	ccc	596	
Asp	Trp	Ile	Val	Asp	Leu	Arg	His	Glu	Leu	Thr	His	Lys	Lys	Met	Pro		
149					154					159					164		
cat	ata	aat	gac	tgc	cgc	aga	ggc	tgc	tac	ttt	gtc	ctg	gat	tgg	ctc	644	
His	Ile	Asn	Asp	Cys	Arg	Arg	Gly	Cys	Tyr	Phe	Val	Leu	Asp	Trp	Leu		
165					170					175					180		
cag	aag	acc	tat	tgg	tgc	cgc	caa	ctg	gag	aac	agc	ctg	aga	gag	acc	692	
Gln	Lys	Thr	Tyr	Trp	Cys	Arg	Gln	Leu	Glu	Asn	Ser	Leu	Arg	Glu	Thr		
181					186					191					196		
tgg	gag	ttg	gag	gag	ttc	agg	gaa	ggg	ata	gag	gaa	gag	gat	caa	gag	740	
Trp	Glu	Leu	Glu	Glu	Phe	Arg	Glu	Gly	Ile	Glu	Glu	Glu	Asp	Gln	Glu		
197					202					207					212		
gaa	gat	aag	aac	att	gtt	gtt	gat	gac	atc	aca	gaa	cag	aaa	cca	gag	788	
Glu	Asp	Lys	Asn	Ile	Val	Val	Asp	Asp	Ile	Thr	Glu	Gln	Lys	Pro	Glu		
213					218					223					228		
cct	cag	gat	gat	ggg	aaa	agt	acg	gag	tca	gat	gta	aag	gcc	gat	gga	836	
Pro	Gln	Asp	Asp	Gly	Lys	Ser	Thr	Glu	Ser	Asp	Val	Lys	Ala	Asp	Gly		
229					234					239					244		
gac	agc	aaa	ggc	agc	gaa	gag	gtg	gat	tct	cat	tgc	aaa	aag	gcc	ctg	884	
Asp	Ser	Lys	Gly	Ser	Glu	Glu	Val	Asp	Ser	His	Cys	Lys	Lys	Ala	Leu		

245	250	255	260	
agt cat aaa gag cta tat gaa aga gcc cga gaa ctg ctg gta tca tac				932
Ser His Lys Glu Leu Tyr Glu Arg Ala Arg Glu Leu Leu Val Ser Tyr				
261	266	271	276	
gaa gag gag cag ttt acg gtg ctg gag aaa ttt agg tat tta cct aag				980
Glu Glu Glu Gln Phe Thr Val Leu Glu Lys Phe Arg Tyr Leu Pro Lys				
277	282	287	292	
gcc att aag gcg tgg aat aac ccg tcc cca cgt gta gaa tgt gtc ctg				1028
Ala Ile Lys Ala Trp Asn Asn Pro Ser Pro Arg Val Glu Cys Val Leu				
293	298	303	308	
gca gag ctc aag ggc gtt aca tgc gag aac agg gag gct gtg ctg gat				1076
Ala Glu Leu Lys Gly Val Thr Cys Glu Asn Arg Glu Ala Val Leu Asp				
309	314	319	324	
gct ttt ctg gat gat ggc ttc ctt gtc ccc aca ttt gaa cag ttg gca				1124
Ala Phe Leu Asp Asp Gly Phe Leu Val Pro Thr Phe Glu Gln Leu Ala				
325	330	335	340	
gct ttg cag ata gaa tat gaa gat ggt cag act gag gtc cag aga ggg				1172
Ala Leu Gln Ile Glu Tyr Glu Asp Gly Gln Thr Glu Val Gln Arg Gly				
341	346	351	356	
gaa ggt act gac cca aag tca cac aaa aac gtg gac ttg aat gac gtc				1220
Glu Gly Thr Asp Pro Lys Ser His Lys Asn Val Asp Leu Asn Asp Val				
357	362	367	372	
ctg gtg cca aag ccg ttc tct cag ttc tgg cag ccc ctg ctc agg ggc				1268
Leu Val Pro Lys Pro Phe Ser Gln Phe Trp Gln Pro Leu Leu Arg Gly				
373	378	383	388	
ctg cac tcc cag aac ttc acg cag gcc cta ttg gag agg atg ctc tct				1316
Leu His Ser Gln Asn Phe Thr Gln Ala Leu Leu Glu Arg Met Leu Ser				
389	394	399	404	
gaa ctg cca gcc ttg ggg atc agc ggg atc cgg cct acc tac atc ctc				1364
Glu Leu Pro Ala Leu Gly Ile Ser Gly Ile Arg Pro Thr Tyr Ile Leu				
405	410	415	420	
aga tgg acc gtt gaa ctg atc gtg gcc aac acc aag act gga cgg aat				1412
Arg Trp Thr Val Glu Leu Ile Val Ala Asn Thr Lys Thr Gly Arg Asn				
421	426	431	436	
gct cgc cga ttt tct gca ggc cag tgg gaa gca aga agg ggc tgg agg				1460
Ala Arg Arg Phe Ser Ala Gly Gln Trp Glu Ala Arg Arg Gly Trp Arg				
437	442	447	452	
ctg ttc aac tgc tcc gcc tcc ctt gac tgg ccc cgg atg gtt gag tcc				1508
Leu Phe Asn Cys Ser Ala Ser Leu Asp Trp Pro Arg Met Val Glu Ser				
453	458	463	468	
tgc ttg ggc tca cct tgc tgg gcc agc ccc caa ctc ctt cgg atc atc				1556
Cys Leu Gly Ser Pro Cys Trp Ala Ser Pro Gln Leu Leu Arg Ile Ile				
469	474	479	484	

ttc aaa gcc atg ggg cag ggc ctg cca gac gag gag cag gag aag ctg	1604
Phe Lys Ala Met Gly Gln Gly Leu Pro Asp Glu Glu Gln Glu Lys Leu	
485 490 495 500	
ctg cgc atc tgt tcc att tat acc cag agt gga gaa aac agc ctg gtg	1652
Leu Arg Ile Cys Ser Ile Tyr Thr Gln Ser Gly Glu Asn Ser Leu Val	
501 506 511 516	
cag gag ggc tct gag gcc tcc ccc att ggg aag tct cca tat aca cta	1700
Gln Glu Gly Ser Glu Ala Ser Pro Ile Gly Lys Ser Pro Tyr Thr Leu	
517 522 527 532	
gac agc ctg tat tgg agc gtc aag cca gcc agc tcc agc ttc ggg tct	1748
Asp Ser Leu Tyr Trp Ser Val Lys Pro Ala Ser Ser Ser Phe Gly Ser	
533 538 543 548	
gaa gca aag gcc cag caa cag gag gag cag ggc agt gtt aat gat gtc	1796
Glu Ala Lys Ala Gln Gln Gln Glu Glu Gln Gly Ser Val Asn Asp Val	
549 554 559 564	
aag gaa gag gag aag gag gag aaa gag gtc ttg cca gac cag gta gag	1844
Lys Glu Glu Glu Lys Glu Glu Lys Glu Val Leu Pro Asp Gln Val Glu	
565 570 575 580	
gag gag gaa gaa aat gat gac caa gag gag gaa gag gag gat gaa gat	1892
Glu Glu Glu Glu Asn Asp Asp Gln Glu Glu Glu Glu Glu Asp Glu Asp	
581 586 591 596	
gat gaa gat gat gaa gag gaa gac aga atg gag gtg ggg cct ttc tct	1940
Asp Glu Asp Asp Glu Glu Glu Asp Arg Met Glu Val Gly Pro Phe Ser	
597 602 607 612	
aca ggg caa gag tcc ccc act gcc gag aat gct agg ctt ctg gcc cag	1988
Thr Gly Gln Glu Ser Pro Thr Ala Glu Asn Ala Arg Leu Leu Ala Gln	
613 618 623 628	
aaa aga gga gct ttg cag ggc tct gca tgg cag gtt agc tca gaa gac	2036
Lys Arg Gly Ala Leu Gln Gly Ser Ala Trp Gln Val Ser Ser Glu Asp	
629 634 639 644	
gtg cga tgg gac aca ttt ccc cta ggc cga atg cca ggt cag acc gag	2084
Val Arg Trp Asp Thr Phe Pro Leu Gly Arg Met Pro Gly Gln Thr Glu	
645 650 655 660	
gac cca gca gag ctc atg ctg gag aat tat gac acc atg tat ctt ttg	2132
Asp Pro Ala Glu Leu Met Leu Glu Asn Tyr Asp Thr Met Tyr Leu Leu	
661 666 671 676	
gac cag cct gtg cta gag cag cgg ctg gaa ccc tca aca tgc aag act	2180
Asp Gln Pro Val Leu Glu Gln Arg Leu Glu Pro Ser Thr Cys Lys Thr	
677 682 687 692	
gac acc ttg ggc ctg agc tgt ggt gtc ggc agt ggc aac tgc agc aac	2228
Asp Thr Leu Gly Leu Ser Cys Gly Val Gly Ser Gly Asn Cys Ser Asn	
693 698 703 708	

Gly Ile Gln Pro Val Ile Asp Lys Leu Arg Glu His Glu Asn Ser Thr	
312 317 322 327	
tta gat agg cat tta gac ttt ttt gaa atg ctc cga aat gaa gat gaa	1181
Leu Asp Arg His Leu Asp Phe Phe Glu Met Leu Arg Asn Glu Asp Glu	
328 333 338 343	
cta gaa ttt gcc aaa aga ttt gaa ctg gtt cac ata gac aca aaa agt	1229
Leu Glu Phe Ala Lys Arg Phe Glu Leu Val His Ile Asp Thr Lys Ser	
344 349 354 359	
gca act cag atg ttt gag ctg acc agg aag agg ctg aca cat agt gaa	1277
Ala Thr Gln Met Phe Glu Leu Thr Arg Lys Arg Leu Thr His Ser Glu	
360 365 370 375	
gct tac ccg cat ttc atg tcc atc ctg cac cac tgc ctc caa atg cct	1325
Ala Tyr Pro His Phe Met Ser Ile Leu His His Cys Leu Gln Met Pro	
376 381 386 391	
tac aag agg agt ggc aac act gtt cag tac tgg cta cta cta gat aga	1373
Tyr Lys Arg Ser Gly Asn Thr Val Gln Tyr Trp Leu Leu Leu Asp Arg	
392 397 402 407	
att ata cag cag ata gtt atc cag aat gac aaa gga cag gac cct gac	1421
Ile Ile Gln Gln Ile Val Ile Gln Asn Asp Lys Gly Gln Asp Pro Asp	
408 413 418 423	
tcc aca cct ttg gaa aac ttt aat att aag aat gtc gta cga atg ttg	1469
Ser Thr Pro Leu Glu Asn Phe Asn Ile Lys Asn Val Val Arg Met Leu	
424 429 434 439	
gtt aat gaa aat gaa gtt aag cag tgg aaa gaa caa gcg gaa aaa atg	1517
Val Asn Glu Asn Glu Val Lys Gln Trp Lys Glu Gln Ala Glu Lys Met	
440 445 450 455	
aga aaa gag cac aat gag cta caa cag aaa ctg gaa aag aaa gaa cga	1565
Arg Lys Glu His Asn Glu Leu Gln Gln Lys Leu Glu Lys Lys Glu Arg	
456 461 466 471	
gaa tgt gat gct aag act caa gag aag gaa gag atg atg cag acc tta	1613
Glu Cys Asp Ala Lys Thr Gln Glu Lys Glu Glu Met Met Gln Thr Leu	
472 477 482 487	
aat aaa atg aaa gag aaa ctt gaa aag gag act act gag cat aag caa	1661
Asn Lys Met Lys Glu Lys Leu Glu Lys Glu Thr Thr Glu His Lys Gln	
488 493 498 503	
gtc aag cag cag gtg gcg gac ctc aca gca cag ctc cat gag ctc agc	1709
Val Lys Gln Gln Val Ala Asp Leu Thr Ala Gln Leu His Glu Leu Ser	
504 509 514 519	
agg agg gcc gtc tgt gct tca atc cca ggt gga ccc tcg cct gga gca	1757
Arg Arg Ala Val Cys Ala Ser Ile Pro Gly Gly Pro Ser Pro Gly Ala	
520 525 530 535	
cca gga ggg ccc ttt cct tcc tct gtg cct gga tct ctc ctt cct ccc	1805
Pro Gly Gly Pro Phe Pro Ser Ser Val Pro Gly Ser Leu Leu Pro Pro	

536	541	546	551	
cca cca ccc cca cct cta cca ggt ggg atg ctt ccc cct cca ccg cct				1853
Pro Pro Pro Pro Pro Leu Pro Gly Gly Met Leu Pro Pro Pro Pro Pro				
552	557	562	567	
ccc ctc cct cca ggt ggc cct cct cct ccc cca ggg cct cct ccc tta				1901
Pro Leu Pro Pro Gly Gly Pro Pro Pro Pro Pro Gly Pro Pro Pro Leu				
568	573	578	583	
ggg gca atc atg cca cct cct ggt gct cca atg ggc cta gca ctg aag				1949
Gly Ala Ile Met Pro Pro Pro Gly Ala Pro Met Gly Leu Ala Leu Lys				
584	589	594	599	
aag aaa agc att cct cag ccc aca aat gcc ctg aaa tcc ttc aac tgg				1997
Lys Lys Ser Ile Pro Gln Pro Thr Asn Ala Leu Lys Ser Phe Asn Trp				
600	605	610	615	
tct aaa ctg ccc gag aac aaa ctg gaa gga aca gta tgg acc gaa att				2045
Ser Lys Leu Pro Glu Asn Lys Leu Glu Gly Thr Val Trp Thr Glu Ile				
616	621	626	631	
gat gat aca aaa gtc ttc aaa att cta gat ctt gaa gac ctg gaa aga				2093
Asp Asp Thr Lys Val Phe Lys Ile Leu Asp Leu Glu Asp Leu Glu Arg				
632	637	642	647	
acc ttc tct gcc tat caa aga cag cag gat ttc ttt gtg aac agt aac				2141
Thr Phe Ser Ala Tyr Gln Arg Gln Gln Asp Phe Phe Val Asn Ser Asn				
648	653	658	663	
tcc aag cag aaa gaa gca gat gcc att gat gac act ctg agt tcc aaa				2189
Ser Lys Gln Lys Glu Ala Asp Ala Ile Asp Asp Thr Leu Ser Ser Lys				
664	669	674	679	
ctt aaa gtt aaa gag ctt tcg gtg att gat ggt cgg aga gct cag aat				2237
Leu Lys Val Lys Glu Leu Ser Val Ile Asp Gly Arg Arg Ala Gln Asn				
680	685	690	695	
tgc aac atc ctt cta tcg agg ttg aaa tta tcc aat gac gaa atc aaa				2285
Cys Asn Ile Leu Leu Ser Arg Leu Lys Leu Ser Asn Asp Glu Ile Lys				
696	701	706	711	
cgg gca att cta aca atg gac gaa cag gaa gat ctg ccc aag gac atg				2333
Arg Ala Ile Leu Thr Met Asp Glu Gln Glu Asp Leu Pro Lys Asp Met				
712	717	722	727	
ttg gaa cag ctc ttg aaa ttt gtt cct gaa aaa agt gac att gac cta				2381
Leu Glu Gln Leu Leu Lys Phe Val Pro Glu Lys Ser Asp Ile Asp Leu				
728	733	738	743	
ttg gag gaa cat aaa cat gaa ctg gat cgg atg gcc aag gct gat agg				2429
Leu Glu Glu His Lys His Glu Leu Asp Arg Met Ala Lys Ala Asp Arg				
744	749	754	759	
ttc ctt ttt gag atg agc cga att aat cac tat cag caa agg ttg caa				2477
Phe Leu Phe Glu Met Ser Arg Ile Asn His Tyr Gln Gln Arg Leu Gln				
760	765	770	775	

tcg ctg tac ttc aaa aag aag ttt gca gag cgt gtg gca gaa gtg aaa Ser Leu Tyr Phe Lys Lys Lys Phe Ala Glu Arg Val Ala Glu Val Lys 776 781 786 791	2525
cct aaa gtg gaa gca att cgt tct ggc tca gaa gag gtg ttt agg agt Pro Lys Val Glu Ala Ile Arg Ser Gly Ser Glu Glu Val Phe Arg Ser 792 797 802 807	2573
ggg gcc ctg aag cag ttg ctg gag gtg gtt ttg gca ttt gga aat tat Gly Ala Leu Lys Gln Leu Leu Glu Val Val Leu Ala Phe Gly Asn Tyr 808 813 818 823	2621
atg aat aaa ggt caa aga ggg aat gca tat gga ttc aag ata tct agc Met Asn Lys Gly Gln Arg Gly Asn Ala Tyr Gly Phe Lys Ile Ser Ser 824 829 834 839	2669
cta aac aaa att gct gac aca aaa tcc agc atc gac aaa aac att acc Leu Asn Lys Ile Ala Asp Thr Lys Ser Ser Ile Asp Lys Asn Ile Thr 840 845 850 855	2717
ctt ttg cac tat ctg atc act att gtg gaa aat aag tac ccc agt gtt Leu Leu His Tyr Leu Ile Thr Ile Val Glu Asn Lys Tyr Pro Ser Val 856 861 866 871	2765
ctc aat cta aat gaa gaa ttg cga gat att cct caa gct gcg aaa gta Leu Asn Leu Asn Glu Glu Leu Arg Asp Ile Pro Gln Ala Ala Lys Val 872 877 882 887	2813
aac atg act gag ctg gac aaa gaa ata agt acc ttg aga agt ggc ttg Asn Met Thr Glu Leu Asp Lys Glu Ile Ser Thr Leu Arg Ser Gly Leu 888 893 898 903	2861
aaa gca gta gag aca gag ctg gaa tat cag aag tct cag ccc cca cag Lys Ala Val Glu Thr Glu Leu Glu Tyr Gln Lys Ser Gln Pro Pro Gln 904 909 914 919	2909
ccc gga gat aag ttt gtg tct gtt gtc agc cag ttc atc aca gta gcc Pro Gly Asp Lys Phe Val Ser Val Val Ser Gln Phe Ile Thr Val Ala 920 925 930 935	2957
agc ttc agc ttc tct gat gtt gaa gac ctt cta gca gaa gct aaa gac Ser Phe Ser Phe Ser Asp Val Glu Asp Leu Leu Ala Glu Ala Lys Asp 936 941 946 951	3005
ctg ttt act aaa gca gtg aag cac ttt ggg gaa gag gct ggc aaa ata Leu Phe Thr Lys Ala Val Lys His Phe Gly Glu Glu Ala Gly Lys Ile 952 957 962 967	3053
caa cca gat gag ttc ttt ggc att ttt gat caa ttt ctt caa gct gtg Gln Pro Asp Glu Phe Phe Gly Ile Phe Asp Gln Phe Leu Gln Ala Val 968 973 978 983	3101
tca gaa gcc aaa caa gaa aac gaa aat atg aga aag aaa aag gag gaa Ser Glu Ala Lys Gln Glu Asn Glu Asn Met Arg Lys Lys Lys Glu Glu 984 989 994 999	3149

gaa gaa cgt cga gct cgc atg gaa gct cag ctc aaa gaa caa cgt gaa	3197
Glu Glu Arg Arg Ala Arg Met Glu Ala Gln Leu Lys Glu Gln Arg Glu	
1000 1005 1010 1015	
agg gaa cgt aaa atg aga aaa gct aaa gag aat agt gaa gaa agc gga	3245
Arg Glu Arg Lys Met Arg Lys Ala Lys Glu Asn Ser Glu Glu Ser Gly	
1016 1021 1026 1031	
gag ttt gat gac ctt gtt tca gct tta cgc tca gga gaa gtg ttt gac	3293
Glu Phe Asp Asp Leu Val Ser Ala Leu Arg Ser Gly Glu Val Phe Asp	
1032 1037 1042 1047	
aaa gac ctt tct aaa ttg aaa cgg aat cgc aaa cgt att acc aac cag	3341
Lys Asp Leu Ser Lys Leu Lys Arg Asn Arg Lys Arg Ile Thr Asn Gln	
1048 1053 1058 1063	
atg act gac agc agc aga gag aga cca atc aca aaa ctt aat ttc taa	3389
Met Thr Asp Ser Ser Arg Glu Arg Pro Ile Thr Lys Leu Asn Phe *	
1064 1069 1074 1079	
ttttccatga atactttttt ttagaaagct cattagcagc cctctaaagt gactagaacg	3449
tttcattaca ctgccttgca atccaaacag tggcaatttt ttccttcac tgtgagtga	3509
tgtgtgaacg tgtgtatgta aatgtatgtg tgtatatatt aaaaaatgta tatagatgtc	3569
tgagtgttgt ctggagacct atacgtatgg ttaaaaagat ttatgttaat gtatgtgctc	3629
caaaaccttt cgtgtatgca ttcacattga gtgtggctca ttttctttcc ccgaacgcc	3689
tgactgttca gaagcacaat actatctcct gaaagagata agagacattc cctagattca	3749
aaggcaaaac agaagaaaca aacaaacaaa caaacaaagc ttgcaaaata ttttatgggt	3809
tccaagcttg atatccttta aaattatttt cattgatgga actggagttg ttggaaaaac	3869
atagatttaa aatgattttt gatagctgac attgtgatgt tgatgtatca catcagtaat	3929
aggaccagct ttgaatttct gacattgggtg tggggatata gtctgtaaat gtttattgag	3989
aacatcttgc acacaatttg aattatgtag aatgtcaatc aagtttttgt atatttaaaa	4049
gttgacatc aattttttcc cctgatttca tcaagttatc tctgccaagt gctcttgata	4109
atttcttcag atttttggaa aaaaacacta tataaatgca atccatgctt tttttaaga	4169
acaacattgc cagagtatgc ttgttctaac aatatagata tataaacctt aaaaataata	4229
aaatatctca cccaagactt aaaggaagaa ttctctgaag ggataaagat tactaaaaaa	4289
aaaaaa	4295

<210> 339
<211> 4091

```
<220>  
<221> CDS  
<222> (77)..(2515)
```

attggatcga tgactattag ccagagcggg cggaattcgg cggcggcgcg aggcagtatg 60

ccc cag tgt gtg ccg gag aac acg ggc tac acg tat gcg ctc agt tcc 157
Pro Gln Cys Val Pro Glu Asn Thr Gly Tyr Thr Tyr Ala Leu Ser Ser
12 17 22 27

cct gta ttt gat tct cca cgg atg tcc cgc cgt agt ttg cgc ctg gcc 253
Pro Val Phe Asp Ser Pro Arg Met Ser Arg Arg Ser Leu Arg Leu Ala
44 49 54 59

ggc acc agc agc gct gtc tcc ctg aag aac cga gcg gcc aga aca aca 349
Gly Thr Ser Ser Ala Val Ser Leu Lys Asn Arg Ala Ala Arg Thr Thr
76 81 86 91

tca agg cag gtc acg tcc tct ggc gtc agc tac ggc ggc act gtc agc 445
Ser Arg Gln Val Thr Ser Ser Gly Val Ser Tyr Gly Gly Thr Val Ser
108 113 118 123

ctg cag gat gct gtg act cga cgg cct cct gta ttg gac gag tct tgg 493
Leu Gln Asp Ala Val Thr Arg Arg Pro Pro Val Leu Asp Glu Ser Trp
124 129 134 139

att cgt gaa cag acc aca gtg gac cac ttc tgg ggt ctt gat gat gat 541
Ile Arg Glu Gln Thr Thr Val Asp His Phe Trp Gly Leu Asp Asp Asp
140 145 150 155

ggt gat ctt aaa ggt gga aat aaa gct gcc att cag gga aac ggg gat 589
Gly Asp Leu Lys Gly Gly Asn Lys Ala Ala Ile Gln Gly Asn Gly Asp
156 161 166 171

gtg gga gtc gcc gcc gcc acc gcg cac aac ggc ttc tcc tgc agc aac 637
Val Gly Val Ala Ala Ala Thr Ala His Asn Gly Phe Ser Cys Ser Asn
172 177 182 187

tgc agc atg ctg tcc gag cgc aag gac gtg ctc acg gcg cac ccc gcg	685
Cys Ser Met Leu Ser Glu Arg Lys Asp Val Leu Thr Ala His Pro Ala	
188 193 198 203	
gcc ccc ggg ccc gtg tcg aga gtt tat tct agg gac agg aat caa aaa	733
Ala Pro Gly Pro Val Ser Arg Val Tyr Ser Arg Asp Arg Asn Gln Lys	
204 209 214 219	
tgc gac gac tgt aag ggc aag agg cac ctc gac gcg cac ccc ggt cgg	781
Cys Asp Asp Cys Lys Gly Lys Arg His Leu Asp Ala His Pro Gly Arg	
220 225 230 235	
gca ggg acc ctc tgg cac atc tgg gca tgt gca ggt ³ tac ttc ttg ctg	829
Ala Gly Thr Leu Trp His Ile Trp Ala Cys Ala Gly Tyr Phe Leu Leu	
236 241 246 251	
cag att ctg cgc agg atc gga gct gtg ggc cag gct gtg tcc agg acg	877
Gln Ile Leu Arg Arg Ile Gly Ala Val Gly Gln Ala Val Ser Arg Thr	
252 257 262 267	
gcg tgg tcg gcc ctt tgg ctg gcc gtg gtt gct cca ggg aag gca gcc	925
Ala Trp Ser Ala Leu Trp Leu Ala Val Val Ala Pro Gly Lys Ala Ala	
268 273 278 283	
tct gga gtg ttc tgg tgg ctg ggg att gga tgg tac cag ttt gtt act	973
Ser Gly Val Phe Trp Trp Leu Gly Ile Gly Trp Tyr Gln Phe Val Thr	
284 289 294 299	
ttg att tct tgg ctg aat gtg ttt ctt ctt acc agg tgc ctt cga aac	1021
Leu Ile Ser Trp Leu Asn Val Phe Leu Leu Thr Arg Cys Leu Arg Asn	
300 305 310 315	
atc tgc aag ttt tta gtc ttg ctc atc cca ctc ttc ctt tta cta gca	1069
Ile Cys Lys Phe Leu Val Leu Leu Ile Pro Leu Phe Leu Leu Leu Ala	
316 321 326 331	
ggg ctc tcc tta cgg ggc cag ggc aat ttc ttt tcg ttc ttg ccc gtg	1117
Gly Leu Ser Leu Arg Gly Gln Gly Asn Phe Phe Ser Phe Leu Pro Val	
332 337 342 347	
ttg aac tgg gca agc atg cat aga aca cag cgg gtg gat gac ccc cag	1165
Leu Asn Trp Ala Ser Met His Arg Thr Gln Arg Val Asp Asp Pro Gln	
348 353 358 363	
gac gtg ttt aaa ccc acg act tct cgc ctg aag cag cct ctg cag ggt	1213
Asp Val Phe Lys Pro Thr Thr Ser Arg Leu Lys Gln Pro Leu Gln Gly	
364 369 374 379	
gac agt gag gct ttt ccg tgg cat tgg atg agt ggc gtg gag cag cag	1261
Asp Ser Glu Ala Phe Pro Trp His Trp Met Ser Gly Val Glu Gln Gln	
380 385 390 395	
gtg gcc tct ctg tct gga cag tgc cac cac cat ggt gag aat ctc cga	1309
Val Ala Ser Leu Ser Gly Gln Cys His His His Gly Glu Asn Leu Arg	
396 401 406 411	

gag ctg acc act ttg cta cag aag ctg cag gct cgg gtg gac cag atg	1357
Glu Leu Thr Thr Leu Leu Gln Lys Leu Gln Ala Arg Val Asp Gln Met	
412 417 422 427	
gaa ggc ggc gct gcc ggg ccg tca gct tcc gtc aga gac gct gtg gga	1405
Glu Gly Gly Ala Ala Gly Pro Ser Ala Ser Val Arg Asp Ala Val Gly	
428 433 438 443	
cag ccc ccg agg gag act gac ttt atg gcc ttt cac caa gaa cat gaa	1453
Gln Pro Pro Arg Glu Thr Asp Phe Met Ala Phe His Gln Glu His Glu	
444 449 454 459	
gtg cgt atg tca cac ttg gaa gat att ctg gga aaa ctg aga gaa aaa	1501
Val Arg Met Ser His Leu Glu Asp Ile Leu Gly Lys Leu Arg Glu Lys	
460 465 470 475	
tct gag gcc atc cag aag gaa cta gaa cag acc aag caa aaa aca atc	1549
Ser Glu Ala Ile Gln Lys Glu Leu Glu Gln Thr Lys Gln Lys Thr Ile	
476 481 486 491	
agt gcg gtt ggt gag cag ctc ctg ccc aca gtc gag cac ctc cag ctg	1597
Ser Ala Val Gly Glu Gln Leu Leu Pro Thr Val Glu His Leu Gln Leu	
492 497 502 507	
gag ctg gat cag cta aag tca gag ctg tcc agc tgg cga cac gtg aag	1645
Glu Leu Asp Gln Leu Lys Ser Glu Leu Ser Ser Trp Arg His Val Lys	
508 513 518 523	
acc ggc tgt gag aca gtg gat gcc gta caa gaa aga gtg gac gtg caa	1693
Thr Gly Cys Glu Thr Val Asp Ala Val Gln Glu Arg Val Asp Val Gln	
524 529 534 539	
gtc aga gaa atg gtg aaa ctc ctg ttt tcc gaa gat cag caa ggc ggt	1741
Val Arg Glu Met Val Lys Leu Leu Phe Ser Glu Asp Gln Gln Gly Gly	
540 545 550 555	
tct ctg gaa cag ctg ctg cag agg ttc tca tca cag ttt gtg agc aaa	1789
Ser Leu Glu Gln Leu Leu Gln Arg Phe Ser Ser Gln Phe Val Ser Lys	
556 561 566 571	
ggc gac ttg cag acg atg ctg cga gac ctg cag ctg cag atc ctg cgg	1837
Gly Asp Leu Gln Thr Met Leu Arg Asp Leu Gln Leu Gln Ile Leu Arg	
572 577 582 587	
aac gtc acc cac cac gtt tcc gtg acc aag cag ctc cca acc tca gaa	1885
Asn Val Thr His His Val Ser Val Thr Lys Gln Leu Pro Thr Ser Glu	
588 593 598 603	
gcc gtg gtg tct gct gtg agc gag gcg ggg gcg tct gga ata aca gag	1933
Ala Val Val Ser Ala Val Ser Glu Ala Gly Ala Ser Gly Ile Thr Glu	
604 609 614 619	
gcg caa gca cgt gcc atc gtg aac agc gcc ttg aag ctg tat tcc caa	1981
Ala Gln Ala Arg Ala Ile Val Asn Ser Ala Leu Lys Leu Tyr Ser Gln	
620 625 630 635	
gat aag acc ggg atg gtg gac ttt gct ctg gaa tct ggt ggt ggc agc	2029

Asp Lys Thr Gly Met Val Asp Phe Ala Leu Glu Ser Gly Gly Gly Ser	
636 641 646 651	
atc ttg agt act cgc tgt tct gaa act tac gaa acc aaa acg gcg ctg	2077
Ile Leu Ser Thr Arg Cys Ser Glu Thr Tyr Glu Thr Lys Thr Ala Leu	
652 657 662 667	
atg agt ctg ttt ggg atc ccg ctg tgg tac ttc tcg cag tcc ccg cgc	2125
Met Ser Leu Phe Gly Ile Pro Leu Trp Tyr Phe Ser Gln Ser Pro Arg	
668 673 678 683	
gtg gtc atc cag cct gac att tac ccc ggt aac tgc tgg gca ttt aaa	2173
Val Val Ile Gln Pro Asp Ile Tyr Pro Gly Asn Cys Trp Ala Phe Lys	
684 689 694 699	
ggc tcc cag ggg tac ctg gtg gtg agg ctc tcc atg atg atc cac cca	2221
Gly Ser Gln Gly Tyr Leu Val Val Arg Leu Ser Met Met Ile His Pro	
700 705 710 715	
gcc gcc ttc act ctg gag cac atc cct aag acg ctg tcg cca aca ggc	2269
Ala Ala Phe Thr Leu Glu His Ile Pro Lys Thr Leu Ser Pro Thr Gly	
716 721 726 731	
aac atc agc agc gcc ccc aag gac ttc gcc gtc tat gga tta gaa aat	2317
Asn Ile Ser Ser Ala Pro Lys Asp Phe Ala Val Tyr Gly Leu Glu Asn	
732 737 742 747	
gag tat cag gaa gaa ggg cag ctt ctg gga cag ttc acg tat gat cag	2365
Glu Tyr Gln Glu Glu Gly Gln Leu Leu Gly Gln Phe Thr Tyr Asp Gln	
748 753 758 763	
gat ggg gag tcg ctc cag atg ttc cag gcc ctg aaa aga ccc gac gac	2413
Asp Gly Glu Ser Leu Gln Met Phe Gln Ala Leu Lys Arg Pro Asp Asp	
764 769 774 779	
aca gct ttc caa ata gtg gaa ctt cgg att ttt tct aac tgg ggc cat	2461
Thr Ala Phe Gln Ile Val Glu Leu Arg Ile Phe Ser Asn Trp Gly His	
780 785 790 795	
cct gag tat acc tgt ctg tat cgg ttc aga gtt cat ggc gaa cct gtc	2509
Pro Glu Tyr Thr Cys Leu Tyr Arg Phe Arg Val His Gly Glu Pro Val	
796 801 806 811	
aag tga agacactact cattatTTTT gtacatTTTT gtatatactg ggacagcgtg	2565
Lys *	
812	
aaacactgga atccttcatg gacgagggca tatacaatga tgggacagtg ccacactcct	2625
tcaataaaacg tggctgctgg ccagaggacg tgagcgtgtg acgggcgccct tggcgccacc	2685
tgttggggtgc tcaactgcctc tgcaggtgca gaggggtcag cagcaggaga agcgtgttga	2745
acacgtggct ctacagacact ccttgTTTTT aacgggaagc tctttgcatt tgcatttcct	2805
caacaaagga gcaaagcaga ggaagctgag agtctggcgt gttcttgacg ctttgggtctt	2865

cagccttgca ctggctcttc taaaggactt ttggagggca gataatttca tctgttaa	2925
ccaacacaca tttctttcag ggaaaaacaa tgtcaccaaa ttttcagagt tctaaactcc	2985
tttccttcaa gccggaatth tccttttttc agcaccagta ggtactaagt ctccagatgg	3045
ggaaataact aaaatgtggt tttctgcttt gttogetctt acttctgagg aaggtttcca	3105
gtcaggactc gotgtaccaa tatccatgga ggaatatggg agcgtttcgc tctccttgta	3165
ggctgaagtc agtctgactt gaaggggcct ggtttgatc taagcaaaca cccagatggg	3225
gttctctggt ctgagcaagg cttttcctgt tgggagtcac agtaaacaga aacccaaaaa	3285
tctcatcttg ggtgttttca gggcttggtt tgagttttgc tgaataggga gcgcaagacg	3345
ccctgagcct ccctctcact ggtggtgata agaggagccg tctggtgtgt cagggtcacg	3405
aaccogttac atttcaggac gatccttttt ccttcagcag catttcttac tggctgtggc	3465
tggaatctgc cttttatcac agctgtcacc attctcacgt gattcttggt agactctttt	3525
tggttataat tactatttaa tatttagact attttactga gcagacttta taaatgagat	3585
atctacaagg cacttaaagt gttacagatg ttttacctta agaattatth aagttgtggt	3645
gggttaagac agttttcagt gtaccgtaaa tgttggtgtt tcagaaaaag acaaaacgat	3705
ggtgctgact ggttttctgt atattgcaca acagtcctca aatacactga tgtatgaaac	3765
tattcataca tcaagcagca tttttttcac tctccttaga attggaacta tgcagttaag	3825
gcagataaaa tgtacagatg tttcatatat tacaggttac atatataaat caaaatttcc	3885
tatataaaac tgatttgga tttggggtgg aaatattttg aatattaatt tattttttaa	3945
gatgcaagat aggactttgt gcaatgtatt tttgtaaag cttttcaaaa tatctgtctt	4005
tggtagtgct tctgctgctg ccaccaaatt gataagatgc tattaagagg tttaaataaa	4065
gagttttaat ttttaaaaaa aaaaaa	4091

<210> 340
 <211> 2553
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (551)..(1456)

<400> 340	60
gcaacgcctg caggaattcg gcacgagcag gcatcgaga ccctgacgcc actggctgta	

caagctgccc	cccagttattg	cagggtcaagt	ggctgggtcag	caggggctgg	ccgtgtggac	120
aattcctaca	gcaactgtgg	ctgccctccc	aggaetgacc	gctgcttctc	ctacggggggg	180
agtgttcaag	ccacctttag	ccggtctcca	agcagctgct	gtgtggaaca	ccgctcttcc	240
ggcaccggta	caagctgccg	caccagtaca	ggcctcctcg	acggcccaac	cccggccacc	300
agcccagccc	cagacgctgt	tccagaccca	gcccgtgctg	cagaccacac	ctgccatcct	360
cccgcagccc	actgctgcca	ccgctgctgc	ccctaccccc	aagccagtgg	acaccccccc	420
acagatcacc	gtccagcctg	cagcgttcgc	atttagccca	ggaatcatca	gtgctgcttc	480
cctcggggga	cagaccaga	tcttgggggc	cctcactaca	gctccagtca	ttaccagcgc	540
cattcccagc	atg cca ggg atc agc agt cag atc ctc acc aat gct cag					589
	Met Pro Gly Ile Ser Ser Gln Ile Leu Thr Asn Ala Gln					
	1	5		10		
gga cag gtt att gga acc ctt cca tgg gta gtg aac tca gct agt gtg						637
Gly Gln Val Ile Gly Thr Leu Pro Trp Val Val Asn Ser Ala Ser Val						
14	19		24		29	
gcg gcc cca gca cca gcc caa agc ctg cag gtc cag gcc gtg acc ccc						685
Ala Ala Pro Ala Pro Ala Gln Ser Leu Gln Val Gln Ala Val Thr Pro						
30	35		40		45	
cag ctg ttg ttg aac gcc cag ggc cag gtg att gcg acc ctg gct agc						733
Gln Leu Leu Leu Asn Ala Gln Gly Gln Val Ile Ala Thr Leu Ala Ser						
46	51		56		61	
agc ccc ctg cct cca cct gtg gct gtc cgg aag cca agc aca cct gag						781
Ser Pro Leu Pro Pro Pro Val Ala Val Arg Lys Pro Ser Thr Pro Glu						
62	67		72		77	
tcc cct gct aag agt gag gtg cag ccc atc cag ccc aca cca acc gtg						829
Ser Pro Ala Lys Ser Glu Val Gln Pro Ile Gln Pro Thr Pro Thr Val						
78	83		88		93	
ccc cag cct gct gtg gtc att gcc agc cca gct cca gcc gcc aag cca						877
Pro Gln Pro Ala Val Val Ile Ala Ser Pro Ala Pro Ala Ala Lys Pro						
94	99		104		109	
tct gcc tct gct cct atc cca att acc tgc tca gag acc ccc acc gtc						925
Ser Ala Ser Ala Pro Ile Pro Ile Thr Cys Ser Glu Thr Pro Thr Val						
110	115		120		125	
agc cag ttg gtg tcc aag cca cat act cca agt ctg gat gag gat ggg						973
Ser Gln Leu Val Ser Lys Pro His Thr Pro Ser Leu Asp Glu Asp Gly						
126	131		136		141	
atc aac tta gaa gag atc cgg gag ttt gcc aag aac ttt aag atc cgg						1021
Ile Asn Leu Glu Glu Ile Arg Glu Phe Ala Lys Asn Phe Lys Ile Arg						
142	147		152		157	
cgg ctc tcg ctg ggc ctt aca cag acc cag gtg ggt cag gct ctg act						1069

Arg Leu Ser Leu Gly Leu Thr Gln Thr Gln Val Gly Gln Ala Leu Thr	
158 163 168 173	
gca acg gaa ggt cca gcc tac agc cag tca gcc atc tgc cgg ttc gag	1117
Ala Thr Glu Gly Pro Ala Tyr Ser Gln Ser Ala Ile Cys Arg Phe Glu	
174 179 184 189	
aag cta gac atc aca ccc aag agt gcc cag aag cta aag ccg gtg ctg	1165
Lys Leu Asp Ile Thr Pro Lys Ser Ala Gln Lys Leu Lys Pro Val Leu	
190 195 200 205	
gaa aag tgg cta aac gaa gct gaa ctg cgg aac cag gaa ggc cag cag	1213
Glu Lys Trp Leu Asn Glu Ala Glu Leu Arg Asn Gln Glu Gly Gln Gln	
206 211 216 221	
aac ctg atg gag ttt gtg gga ggc gag ccc tcc aag aaa cgc aaa cgc	1261
Asn Leu Met Glu Phe Val Gly Gly Glu Pro Ser Lys Lys Arg Lys Arg	
222 227 232 237	
cgc acc tcc ttc acc ccc cag gcc ata gag gct ctc aat gcc tat ttt	1309
Arg Thr Ser Phe Thr Pro Gln Ala Ile Glu Ala Leu Asn Ala Tyr Phe	
238 243 248 253	
gag aag aac cca ctg ccc aca ggc cag gag atc act gaa att gct aag	1357
Glu Lys Asn Pro Leu Pro Thr Gly Gln Glu Ile Thr Glu Ile Ala Lys	
254 259 264 269	
gag ctc aac tac gac cgt gag gta gtg cgg gtc tgg ttc tgc aat cgg	1405
Glu Leu Asn Tyr Asp Arg Glu Val Val Arg Val Trp Phe Cys Asn Arg	
270 275 280 285	
cgc cag acg ctc aag aac acc agc aag ctg aac gtc ttt cag atc cct	1453
Arg Gln Thr Leu Lys Asn Thr Ser Lys Leu Asn Val Phe Gln Ile Pro	
286 291 296 301	
tag ggct cagcccctgg ccctgtgttc tagcactttg tccatttccc gtggcatccg	1510
* 302	
gctgcagcca ctgccatgac agcacctgtc attttgccac gtgcagctgt gctcacccca	1570
ggatcatcaga ctccaccgtg tgcattgtgca tcaatgtccc tcttttctcc cacacatctc	1630
acatcatggg gaggccagag ggggccacac gagagctcca ggctctgggc tggtcactcc	1690
gaagaagagg atttgtgacg tcaacttagag aagcaccttg ctagcatggg ttctgaaggg	1750
tgaattctgg tggggaacca gaaactccct gtctttgggg cagggctaaa gcagctccta	1810
aggaccactg gccattagct cttgcttttg atggcattct ctttccacct tgtcttctcc	1870
tttgcctctc tgtgttagtg tggcaggtat gacaactcat ccagtggaaa cacagcctca	1930
cactgccctt ccgcccccca cactttgcct gcaggtgcac cgaaaggact tgggagataa	1990
aattcaaaaa agtgtgatgt gctgctcaga aggtcagact ccatgtctgc cttgacctca	2050

```

aggtcagaag gttcccaaac ccttggggct ggaacatggg atctctcttt ccacctcttc 2110
ctgggttcctt tgcggggaaa attgcactaa aacagaacct tttcttaatc catgttgga 2170
ggaagcaaca gtgaactcta cctgttctgg agttctcttg ggtctgcaga aggttgggaa 2230
tttagaaaat aaggctgttc tttcatatct taatttaatc tctgtcaatg gccatccctc 2290
ccacaaaaaa acgtgggtta agagaacttg cagactggat atgcaagcaa acgggcaact 2350
ctggagaaaa ataaggaaag gaatgctgac tttctctttc tttctcttgt cccacacccc 2410
attcccaacc caatactggg gccttctcaa aaggagcaaa ttaaacaata aaccagacag 2470
caaggccctg ggggaaagga caacatcttg aaataaatga tggagcccag gaaggtctct 2530
tgtggaagtt gaaaaaaaaa aaa 2553

```

```

<210> 341
<211> 3136
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (439)..(2304)

```

```

<400> 341
atacgactgg aagtaaatag ttctcttctg gaatattaca ctgaattaga tgcagttgtg 60
ctacatgggtg tgaaggacaa gccagtgtt tctctcaaga accggcccg aattcccg 120
tcgacccacg cgtccgggcg gttgtgccgc atctagagag tcggggagcc gccccgcac 180
ccaggccttc tcgcgctgcc tggctgctgg tgaagccgc ggcgcgcgcc tctcccgac 240
cctgcagggt aaaagaatgt cacatgtcag catttgtacc tgaagtcagc atgcaaagtt 300
cagggtacat ggatgaatgc caacttttgc atttcccatg tgtatctgt gaccattcta 360
tctgggaaca tcttcaaag agttcatgca tcttactgag gacacctgac cttttgaagc 420
ttcataattc acatctag atg tca ccg gtc ttt ccc atg tta aca gtt ctg 471
Met Ser Pro Val Phe Pro Met Leu Thr Val Leu
1 5

acc atg ttt tat tat ata tgc ctt cgg cgc cga gcc agg aca gct aca 519
Thr Met Phe Tyr Tyr Ile Cys Leu Arg Arg Arg Ala Arg Thr Ala Thr
12 17 22 27

aga gga gaa atg atg aac acc cat aga gct ata gaa tca aac agc cag 567
Arg Gly Glu Met Met Asn Thr His Arg Ala Ile Glu Ser Asn Ser Gln
28 33 38 43

```

act tcc cct ctc aat gca gag gta gtc cag tat gcc aaa gaa gta gtg	615
Thr Ser Pro Leu Asn Ala Glu Val Val Gln Tyr Ala Lys Glu Val Val	
44 49 54 59	
gat ttc agt tcc cat tat gga agt gag aat agt atg tcc tat act atg	663
Asp Phe Ser Ser His Tyr Gly Ser Glu Asn Ser Met Ser Tyr Thr Met	
60 65 70 75	
tgg aat ttg gct ggt gta cca aat gta ttc cca agt tct ggt gac ttt	711
Trp Asn Leu Ala Gly Val Pro Asn Val Phe Pro Ser Ser Gly Asp Phe	
76 81 86 91	
act cag aca gct gtg ttt cga act tat ggg aca tgg tgg gat cag tgt	759
Thr Gln Thr Ala Val Phe Arg Thr Tyr Gly Thr Trp Trp Asp Gln Cys	
92 97 102 107	
cct agt gct tcc ttg cca ttc aag agg acg cca cct aat ttt cag agc	807
Pro Ser Ala Ser Leu Pro Phe Lys Arg Thr Pro Pro Asn Phe Gln Ser	
108 113 118 123	
cag gac tat gtg gaa ctt act ttt gaa caa cag gtg tat cct aca gct	855
Gln Asp Tyr Val Glu Leu Thr Phe Glu Gln Gln Val Tyr Pro Thr Ala	
124 129 134 139	
gta cat gtt cta gaa acc tat cat ccc gga gca gtc att aga att ctc	903
Val His Val Leu Glu Thr Tyr His Pro Gly Ala Val Ile Arg Ile Leu	
140 145 150 155	
gct tgt tct gca aat cct tat tcc cca aat cca cca gct gaa gta aga	951
Ala Cys Ser Ala Asn Pro Tyr Ser Pro Asn Pro Pro Ala Glu Val Arg	
156 161 166 171	
tgg gag att ctt tgg tca gag aga cct acg aag gtt aat gct tcc caa	999
Trp Glu Ile Leu Trp Ser Glu Arg Pro Thr Lys Val Asn Ala Ser Gln	
172 177 182 187	
gct cgc cag ttt aaa cct tgt att aag cag ata aat ttc ccc aca aat	1047
Ala Arg Gln Phe Lys Pro Cys Ile Lys Gln Ile Asn Phe Pro Thr Asn	
188 193 198 203	
ctt ata cga ctg gaa gta aat agt tct ctt ctg gaa tat tac act gaa	1095
Leu Ile Arg Leu Glu Val Asn Ser Ser Leu Leu Glu Tyr Tyr Thr Glu	
204 209 214 219	
tta gat gca gtt gtg cta cat ggt gtg aag gac aag cca gtg ctt tct	1143
Leu Asp Ala Val Val Leu His Gly Val Lys Asp Lys Pro Val Leu Ser	
220 225 230 235	
ctc aag act tca ctt att gac atg aat gat ata gaa gat gat gcc tat	1191
Leu Lys Thr Ser Leu Ile Asp Met Asn Asp Ile Glu Asp Asp Ala Tyr	
236 241 246 251	
gca gaa aag gat ggt tgt gga atg gac agt ctt aac aaa aag ttt agc	1239
Ala Glu Lys Asp Gly Cys Gly Met Asp Ser Leu Asn Lys Lys Phe Ser	
252 257 262 267	
agt gct gtc ctc ggg gaa ggg cca aat aat ggg tat ttt gat aaa cta	1287

Ser Ala Val Leu Gly	Glu Gly Pro Asn Asn Gly Tyr Phe Asp Lys Leu	
268	273	278 283
cct tat gag ctt att	cag ctg att ctg aat cat ctt aca cta cca gac	1335
Pro Tyr Glu Leu Ile	Gln Leu Ile Leu Asn His Leu Thr Leu Pro Asp	
284	289 294 299	
ctg tgt aga tta gca	cag act tgc aaa cta ctg agc cag cat tgc tgt	1383
Leu Cys Arg Leu Ala	Gln Thr Cys Lys Leu Leu Ser Gln His Cys Cys	
300	305 310 315	
gat cct ctg caa tac	atc cac ctc aat ctg caa cca tac tgg gca aaa	1431
Asp Pro Leu Gln Tyr	Ile His Leu Asn Leu Gln Pro Tyr Trp Ala Lys	
316	321 326 331	
cta gat gac act tct	ctg gaa ttt cta cag tct cgc tgc act ctt gtc	1479
Leu Asp Asp Thr Ser	Leu Glu Phe Leu Gln Ser Arg Cys Thr Leu Val	
332	337 342 347	
cag tgg ctt aat tta	tct tgg act ggc aat aga ggc ttc atc tct gtt	1527
Gln Trp Leu Asn Leu	Ser Trp Thr Gly Asn Arg Gly Phe Ile Ser Val	
348	353 358 363	
gca gga ttt agc agg	ttt ctg aag gtt tgt gga tcc gaa tta gta cgc	1575
Ala Gly Phe Ser Arg	Phe Leu Lys Val Cys Gly Ser Glu Leu Val Arg	
364	369 374 379	
ctt gaa ttg tct tgc	agc cac ttt ctt aat gaa act tgc tta gaa gtt	1623
Leu Glu Leu Ser Cys	Ser His Phe Leu Asn Glu Thr Cys Leu Glu Val	
380	385 390 395	
att tct gag atg tgt	cca aat cta cag gcc tta aat ctc tcc tcc tgt	1671
Ile Ser Glu Met Cys	Pro Asn Leu Gln Ala Leu Asn Leu Ser Ser Cys	
396	401 406 411	
gat aag cta cca cct	caa gct ttc aac cac att gcc aag tta tgc agc	1719
Asp Lys Leu Pro Pro	Gln Ala Phe Asn His Ile Ala Lys Leu Cys Ser	
412	417 422 427	
ctt aaa cga ctt gtt	ctc tat cga aca aaa gta gag caa aca gca ctg	1767
Leu Lys Arg Leu Val	Leu Tyr Arg Thr Lys Val Glu Gln Thr Ala Leu	
428	433 438 443	
ctc agc att ttg aac	ttc tgt tca gag ctt cag cac ctc agt tta ggc	1815
Leu Ser Ile Leu Asn	Phe Cys Ser Glu Leu Gln His Leu Ser Leu Gly	
444	449 454 459	
agt tgt gtc atg att	gaa gac tat gat gtg ata gct agc atg ata gga	1863
Ser Cys Val Met Ile	Glu Asp Tyr Asp Val Ile Ala Ser Met Ile Gly	
460	465 470 475	
gcc aag tgt aaa aaa	ctc cgg acc ctg gat ctg tgg aga tgt aag aat	1911
Ala Lys Cys Lys Lys	Leu Arg Thr Leu Asp Leu Trp Arg Cys Lys Asn	
476	481 486 491	
att act gag aat gga	ata gca gaa ctg gct tct ggg tgt cca cta ctg	1959
Ile Thr Glu Asn Gly	Ile Ala Glu Leu Ala Ser Gly Cys Pro Leu Leu	

492	497	502	507	
gag gag ctt gac ctt ggc tgg tgc cca act ctg cag agc agc acc ggg				2007
Glu Glu Leu Asp Leu Gly Trp Cys Pro Thr Leu Gln Ser Ser Thr Gly				
508	513	518	523	
tgc ttc acc aga ctg gca cac cag ctc cca aac ttg caa aaa ctc ttt				2055
Cys Phe Thr Arg Leu Ala His Gln Leu Pro Asn Leu Gln Lys Leu Phe				
524	529	534	539	
ctt aca gct aat aga tct gtg tgt gac aca gac att gat gaa ttg gca				2103
Leu Thr Ala Asn Arg Ser Val Cys Asp Thr Asp Ile Asp Glu Leu Ala				
540	545	550	555	
tgt aat tgt acc agg tta cag cag ctg gac ata tta gga aca aga atg				2151
Cys Asn Cys Thr Arg Leu Gln Gln Leu Asp Ile Leu Gly Thr Arg Met				
556	561	566	571	
gta agt ccg gca tcc tta aga aaa ctc ctg gaa tct tgt aaa gat ctt				2199
Val Ser Pro Ala Ser Leu Arg Lys Leu Leu Glu Ser Cys Lys Asp Leu				
572	577	582	587	
tct tta ctt gat gtg tcc ttc tgt tgc cag att gat aac aga gct gtg				2247
Ser Leu Leu Asp Val Ser Phe Cys Ser Gln Ile Asp Asn Arg Ala Val				
588	593	598	603	
cta gaa ctg aat gca agc ttt cca aaa gtg ttc ata aaa aag agc ttt				2295
Leu Glu Leu Asn Ala Ser Phe Pro Lys Val Phe Ile Lys Lys Ser Phe				
604	609	614	619	
act cag tga ctttaata tatgtttctgt attaaaatta atgtgctttg ttgggggttta				2351
Thr Gln *				
620				
attttgggat tgggttttggg ttttgttttt agttgtttta atggtaagaa ttaagacatt				2411
tgtagatttt aaagaaaaat atgaaattgt ccattaaatc aagtaaaaaat gtgcacaaat				2471
gttttcataa aatactgcaa gcacttctct tcaagaatat gagtggatat tatttttacc				2531
ttatgttaat cagtgatatg ctttagtcaa taatatgatt gataaaagaa taacatggaa				2591
tcatgctaac ttatttttcaa aggaacactg agcaataaag tatcgtggca tttatgcaaa				2651
aaaaaaagtt aatttttttac accttcatgt aaggatgtct tattaagcct gtgacctggc				2711
aagtgttttg tttggatatgt acaaaatggc cagagctagt tggagaatga gacatgcttt				2771
tccagctgtt tggttatttc tctggattaa ctgttcaact ggaaaatttt tagtttttct				2831
agccaggtgt ggtggcacac actttagtgc ctagcgacac gggagggtgga ggcaggagga				2891
ttacttgaga tgggattttg agactctagt gtaqttatga ttgcacctgt gagcagccac				2951
tgcactocaa cctgggcaat atagcgagtc cctttctctt aaaaaaatt gtagtgtttc				3011
cacttttctt ctgatatttt tgtctatttc actactggat aatgccaata taaaaatttg				3071

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

Thr	Gln	Thr	Ala	Val	Phe	Arg	Thr	Tyr	Gly	Thr	Trp	Trp	Asp	Gln	Cys	
92					97					102					107	
cct	agt	gct	tcc	ttg	cca	ttc	aag	agg	acg	cca	cct	aat	ttt	cag	agc	807
Pro	Ser	Ala	Ser	Leu	Pro	Phe	Lys	Arg	Thr	Pro	Pro	Asn	Phe	Gln	Ser	
108					113					118					123	
cag	gac	tat	gtg	gaa	ctt	act	ttt	gaa	caa	cag	gtg	tat	cct	aca	gct	855
Gln	Asp	Tyr	Val	Glu	Leu	Thr	Phe	Glu	Gln	Gln	Val	Tyr	Pro	Thr	Ala	
124					129					134					139	
gta	cat	gtt	cta	gaa	acc	tat	cat	ccc	gga	gca	gtc	att	aga	att	ctc	903
Val	His	Val	Leu	Glu	Thr	Tyr	His	Pro	Gly	Ala	Val	Ile	Arg	Ile	Leu	
140					145					150					155	
gct	tgt	tct	gca	aat	cct	tat	tcc	cca	aat	cca	cca	gct	gaa	gta	aga	951
Ala	Cys	Ser	Ala	Asn	Pro	Tyr	Ser	Pro	Asn	Pro	Pro	Ala	Glu	Val	Arg	
156					161					166					171	
tgg	gag	att	ctt	tgg	tca	gag	aga	cct	acg	aag	gtt	aat	gct	tcc	caa	999
Trp	Glu	Ile	Leu	Trp	Ser	Glu	Arg	Pro	Thr	Lys	Val	Asn	Ala	Ser	Gln	
172					177					182					187	
gct	cgc	cag	ttt	aaa	cct	tgt	att	aag	cag	ata	aat	ttc	ccc	aca	aat	1047
Ala	Arg	Gln	Phe	Lys	Pro	Cys	Ile	Lys	Gln	Ile	Asn	Phe	Pro	Thr	Asn	
188					193					198					203	
ctt	ata	cga	ctg	gaa	gta	aat	agt	tct	ctt	ctg	gaa	tat	tac	act	gaa	1095
Leu	Ile	Arg	Leu	Glu	Val	Asn	Ser	Ser	Leu	Leu	Glu	Tyr	Tyr	Thr	Glu	
204					209					214					219	
tta	gat	gca	gtt	gtg	cta	cat	ggt	gtg	aag	gac	aag	cca	gtg	ctt	tct	1143
Leu	Asp	Ala	Val	Val	Leu	His	Gly	Val	Lys	Asp	Lys	Pro	Val	Leu	Ser	
220					225					230					235	
ctc	aag	act	tca	ctt	att	gac	atg	aat	gat	ata	gaa	gat	gat	gcc	tat	1191
Leu	Lys	Thr	Ser	Leu	Ile	Asp	Met	Asn	Asp	Ile	Glu	Asp	Asp	Ala	Tyr	
236					241					246					251	
gca	gaa	aag	gat	ggt	tgt	gga	atg	gac	agt	ctt	aac	aaa	aag	ttt	agc	1239
Ala	Glu	Lys	Asp	Gly	Cys	Gly	Met	Asp	Ser	Leu	Asn	Lys	Lys	Phe	Ser	
252					257					262					267	
agt	gct	gtc	ctc	ggg	gaa	ggg	cca	aat	aat	ggg	tat	ttt	gat	aaa	cta	1287
Ser	Ala	Val	Leu	Gly	Glu	Gly	Pro	Asn	Asn	Gly	Tyr	Phe	Asp	Lys	Leu	
268					273					278					283	
cct	tat	gag	ctt	att	cag	ctg	att	ctg	aat	cat	ctt	aca	cta	cca	gac	1335
Pro	Tyr	Glu	Leu	Ile	Gln	Leu	Ile	Leu	Asn	His	Leu	Thr	Leu	Pro	Asp	
284					289					294					299	
ctg	tgt	aga	tta	gca	cag	act	tgc	aaa	cta	ctg	agc	cag	cat	tgc	tgt	1383
Leu	Cys	Arg	Leu	Ala	Gln	Thr	Cys	Lys	Leu	Leu	Ser	Gln	His	Cys	Cys	
300					305					310					315	
gat	cct	ctg	caa	tac	atc	cac	ctc	aat	ctg	caa	cca	tac	tgg	gca	aaa	1431
Asp	Pro	Leu	Gln	Tyr	Ile	His	Leu	Asn	Leu	Gln	Pro	Tyr	Trp	Ala	Lys	

316	321	326	331	
cta gat gac act tct ctg gaa ttt cta cag tct cgc tgc act ctt gtc				1479
Leu Asp Asp Thr Ser Leu Glu Phe Leu Gln Ser Arg Cys Thr Leu Val				
332	337	342	347	
cag tgg ctt aat tta tct tgg act ggc aat aga ggc ttc atc tct gtt				1527
Gln Trp Leu Asn Leu Ser Trp Thr Gly Asn Arg Gly Phe Ile Ser Val				
348	353	358	363	
gca gga ttt agc agg ttt ctg aag gtt tgt gga tcc gaa tta gta cgc				1575
Ala Gly Phe Ser Arg Phe Leu Lys Val Cys Gly Ser Glu Leu Val Arg				
364	369	374	379	
ctt gaa ttg tct tgc agc cac ttt ctt aat gaa act tgc tta gaa gtt				1623
Leu Glu Leu Ser Cys Ser His Phe Leu Asn Glu Thr Cys Leu Glu Val				
380	385	390	395	
att tct gag atg tgt cca aat cta cag gcc tta aat ctc tcc tcc tgt				1671
Ile Ser Glu Met Cys Pro Asn Leu Gln Ala Leu Asn Leu Ser Ser Cys				
396	401	406	411	
gat aag cta cca cct caa gct ttc aac cac att gcc aag tta tgc agc				1719
Asp Lys Leu Pro Pro Gln Ala Phe Asn His Ile Ala Lys Leu Cys Ser				
412	417	422	427	
ctt aaa cga ctt gtt ctc tat cga aca aaa gta gag att gaa gac tat				1767
Leu Lys Arg Leu Val Leu Tyr Arg Thr Lys Val Glu Ile Glu Asp Tyr				
428	433	438	443	
gat gtg ata gct agc atg ata gga gcc aag tgt aaa aaa ctc cgg acc				1815
Asp Val Ile Ala Ser Met Ile Gly Ala Lys Cys Lys Lys Leu Arg Thr				
444	449	454	459	
ctg gat ctg tgg aga tgt aag aat att act gag aat gga ata gca gaa				1863
Leu Asp Leu Trp Arg Cys Lys Asn Ile Thr Glu Asn Gly Ile Ala Glu				
460	465	470	475	
ctg gct tct ggg tgt cca cta ctg gag gag ctt gac ctt ggc tgg tgc				1911
Leu Ala Ser Gly Cys Pro Leu Leu Glu Glu Leu Asp Leu Gly Trp Cys				
476	481	486	491	
cca act ctg cag agc agc acc ggg tgc ttc acc aga ctg gca cac cag				1959
Pro Thr Leu Gln Ser Ser Thr Gly Cys Phe Thr Arg Leu Ala His Gln				
492	497	502	507	
ctc cca aac ttg caa aaa ctc ttt ctt aca gct aat aga tct gtg tgt				2007
Leu Pro Asn Leu Gln Lys Leu Phe Leu Thr Ala Asn Arg Ser Val Cys				
508	513	518	523	
gac aca gac att gat gaa ttg gca tgt aat tgt acc agg tta cag cag				2055
Asp Thr Asp Ile Asp Glu Leu Ala Cys Asn Cys Thr Arg Leu Gln Gln				
524	529	534	539	
ctg gac ata tta gga aca aga atg gta agt ccg gca tcc tta aga aaa				2103
Leu Asp Ile Leu Gly Thr Arg Met Val Ser Pro Ala Ser Leu Arg Lys				
540	545	550	555	

ctc ctg gaa tct tgt aaa gat ctt tct tta ctt gat gtg tcc ttc tgt	2151
Leu Leu Glu Ser Cys Lys Asp Leu Ser Leu Leu Asp Val Ser Phe Cys	
556 561 566 571	
tcg cag att gat aac aga gct gtg cta gaa ctg aat gca agc ttt cca	2199
Ser Gln Ile Asp Asn Arg Ala Val Leu Glu Leu Asn Ala Ser Phe Pro	
572 577 582 587	
aaa gtg ttc ata aaa aag agc ttt act cag tga cttaatat atgttctgta	2250
Lys Val Phe Ile Lys Lys Ser Phe Thr Gln *	
588 593 598	
ttaaaattaa tgtgctttgt tgggggttaa ttttgggatt ggttttgggt tttgttttta	2310
gttgttttaa tggaagaat taagacattt gtagatttta aagaaaaata tgaaattgtc	2370
cattaaatca agtaaaaatg tgcacaaatg ttttcataaa atactgcaag cacttctctt	2430
caagaatatg agtggatatt atttttacct tatgttaatc agtgatatgc tttagtcaat	2490
aatatgattg ataaaaagaat aacatggaat catgctaact tattttcaaa ggaacactga	2550
gcaataaagt atcgtggcat ttatgcaaaa aaaaaagtta attttttaca ccttcatgta	2610
aggatgtctt attaagcctg tgacctggca agtgttttgt ttggatatgta caaaatggtc	2670
agagctagtt ggagaatgag acatgctttt ccagctgttt ggttatttct ctggattaac	2730
tgttcaactg gaaaattttt agtttttcta gccagggtgtg gtggcacaca cttgtagtcc	2790
tagcgacacg ggaggtggag gcaggaggat tacttgagat gggattttga gactctagtg	2850
tacttatgat tgcacctgtg agcagccact gcactccaac ctgggcaata tagcgagtcc	2910
ctttctctta aaaaaaattg tagtgtttcc acttttcttc tgatattttt gtctatttca	2970
ctactggata atgccaatat aaaaatttgg gtataatcaa gaataagagg taaactacta	3030
aataaaaaaa gctttccaac tgaaaaaaa aaaa	3064

<210> 343
 <211> 5273
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (328) .. (4728)

<400> 343	
tcttcgggaa ctggggctgc atcatatata gtaaacacag gagaaacaga ggtaggcttt	60
gttccaacgt ttggaccttg ttacctgaat ctttatggaa gccccagaga gtacacggga	120

185	190	195	200	
aga ctg gcc tat gca cga att ccc gca cat cag gtc ttg tac tcc acc				975
Arg Leu Ala Tyr Ala Arg Ile Pro Ala His Gln Val Leu Tyr Ser Thr				
201	206	211	216	
agt ggt gag aat gca tct gga aaa tac tgt ggg aaa acc caa acc atc				1023
Ser Gly Glu Asn Ala Ser Gly Lys Tyr Cys Gly Lys Thr Gln Thr Ile				
217	222	227	232	
ttt ctg aag tat cca cag gag aaa aac aac ggg cca aag gtg cct gtg				1071
Phe Leu Lys Tyr Pro Gln Glu Lys Asn Asn Gly Pro Lys Val Pro Val				
233	238	243	248	
gag ttg cga gtg aac atc tgg cta ggc tta agt gct gtg gag aag aag				1119
Glu Leu Arg Val Asn Ile Trp Leu Gly Leu Ser Ala Val Glu Lys Lys				
249	254	259	264	
ttt aac agc ttc gca gaa gga act ttc acc gtc ttt gct gaa atg tat				1167
Phe Asn Ser Phe Ala Glu Gly Thr Phe Thr Val Phe Ala Glu Met Tyr				
265	270	275	280	
gaa aat caa gct ctc atg ttt gga aaa tgg ggt act tct gga tta gta				1215
Glu Asn Gln Ala Leu Met Phe Gly Lys Trp Gly Thr Ser Gly Leu Val				
281	286	291	296	
gga cgt cat aag ttt tct gat gtc aca gga aaa ata aaa ctc aag agg				1263
Gly Arg His Lys Phe Ser Asp Val Thr Gly Lys Ile Lys Leu Lys Arg				
297	302	307	312	
gaa ttt ttt ctg cct cca aaa ggc tgg gaa tgg gaa gga gag tgg ata				1311
Glu Phe Phe Leu Pro Pro Lys Gly Trp Glu Trp Glu Gly Glu Trp Ile				
313	318	323	328	
gtt gat cct gaa aga agc ttg ctg act gag gca gat gca ggt cac acg				1359
Val Asp Pro Glu Arg Ser Leu Leu Thr Glu Ala Asp Ala Gly His Thr				
329	334	339	344	
gag ttc act gat gaa gtc tat cag aac gag agc cgc tac ccc ggg ggc				1407
Glu Phe Thr Asp Glu Val Tyr Gln Asn Glu Ser Arg Tyr Pro Gly Gly				
345	350	355	360	
gac tgg aag ccg gcc gag gac acc tac acg gat gcg aac ggc gat aaa				1455
Asp Trp Lys Pro Ala Glu Asp Thr Tyr Thr Asp Ala Asn Gly Asp Lys				
361	366	371	376	
gca gca tca ccc agc gag ttg act tgt cct cca ggt tgg gaa tgg gaa				1503
Ala Ala Ser Pro Ser Glu Leu Thr Cys Pro Pro Gly Trp Glu Trp Glu				
377	382	387	392	
gat gat gca tgg tct tat gac ata aat cga gcg gtg gat gag aaa ggc				1551
Asp Asp Ala Trp Ser Tyr Asp Ile Asn Arg Ala Val Asp Glu Lys Gly				
393	398	403	408	
tgg gaa tat gga atc acc att cct cct gat cat aag ccc aaa tcc tgg				1599
Trp Glu Tyr Gly Ile Thr Ile Pro Pro Asp His Lys Pro Lys Ser Trp				
409	414	419	424	

gtt gca gca gag aaa atg tac cac act cat aga cgg cga agg ctg gtc	1647
Val Ala Ala Glu Lys Met Tyr His Thr His Arg Arg Arg Arg Leu Val	
425 430 435 440	
cga aaa cgc aag aaa gat tta aca cag act gct tca agc acc gca agg	1695
Arg Lys Arg Lys Lys Asp Leu Thr Gln Thr Ala Ser Ser Thr Ala Arg	
441 446 451 456	
gcc atg gag gaa ttg caa gac caa gag ggc tgg gaa tat gct tct cta	1743
Ala Met Glu Glu Leu Gln Asp Gln Glu Gly Trp Glu Tyr Ala Ser Leu	
457 462 467 472	
att ggc tgg aaa ttt cac tgg aaa caa cgt agt tca gat acc ttc cgc	1791
Ile Gly Trp Lys Phe His Trp Lys Gln Arg Ser Ser Asp Thr Phe Arg	
473 478 483 488	
cgc aga cgc tgg agg aga aaa atg gct cct tca gaa aca cat ggt gca	1839
Arg Arg Arg Trp Arg Arg Lys Met Ala Pro Ser Glu Thr His Gly Ala	
489 494 499 504	
gct gcc atc ttt aaa ctt gaa ggt gcc ctt ggg gca gac act acc gaa	1887
Ala Ala Ile Phe Lys Leu Glu Gly Ala Leu Gly Ala Asp Thr Thr Glu	
505 510 515 520	
gat ggg gat gag aag agc ctg gag aaa cag aag cac agt gcc acc act	1935
Asp Gly Asp Glu Lys Ser Leu Glu Lys Gln Lys His Ser Ala Thr Thr	
521 526 531 536	
gtg ttc gga gca aac acc ccc att gtt tcc tgc aat ttt gac aga gac	1983
Val Phe Gly Ala Asn Thr Pro Ile Val Ser Cys Asn Phe Asp Arg Asp	
537 542 547 552	
tac atc tac cat ctg cgc tgc tat gtc tat caa gcc aga aac ctc ttg	2031
Tyr Ile Tyr His Leu Arg Cys Tyr Val Tyr Gln Ala Arg Asn Leu Leu	
553 558 563 568	
gct tta gat aag gat agc ttt tca gat cca ttt gct cat atc tgt ttc	2079
Ala Leu Asp Lys Asp Ser Phe Ser Asp Pro Phe Ala His Ile Cys Phe	
569 574 579 584	
ctc cat cgg agc aaa acc act gag atc atc cat tca acc ctg aat ccc	2127
Leu His Arg Ser Lys Thr Thr Glu Ile Ile His Ser Thr Leu Asn Pro	
585 590 595 600	
acg tgg gac caa aca att ata ttc gat gaa gtt gaa atc tat ggg gaa	2175
Thr Trp Asp Gln Thr Ile Ile Phe Asp Glu Val Glu Ile Tyr Gly Glu	
601 606 611 616	
ccc caa aca gtt cta cag aat cca ccc aaa gtt atc atg gaa ctt ttt	2223
Pro Gln Thr Val Leu Gln Asn Pro Pro Lys Val Ile Met Glu Leu Phe	
617 622 627 632	
gac aat gac caa gtg ggc aaa gat gaa ttt tta gga cga agc att ttc	2271
Asp Asn Asp Gln Val Gly Lys Asp Glu Phe Leu Gly Arg Ser Ile Phe	
633 638 643 648	

tct cct gtg gtg aaa ctg aac tca gaa atg gac atc aca ccc aaa ctt	2319
Ser Pro Val Val Lys Leu Asn Ser Glu Met Asp Ile Thr Pro Lys Leu	
649 654 659 664	
ctc tgg cac cca gta atg aat gga gac aaa gcc tgc ggg gat gtt ctt	2367
Leu Trp His Pro Val Met Asn Gly Asp Lys Ala Cys Gly Asp Val Leu	
665 670 675 680	
gta act gca gag ctg att ctg agg ggc aag gat ggc tcc aac ctt ccc	2415
Val Thr Ala Glu Leu Ile Leu Arg Gly Lys Asp Gly Ser Asn Leu Pro	
681 686 691 696	
att ctt ccc cct caa agg gcg cca aat cta tac atg gtc ccc cag ggg	2463
Ile Leu Pro Pro Gln Arg Ala Pro Asn Leu Tyr Met Val Pro Gln Gly	
697 702 707 712	
atc agg cct gtg gtc cag ctc act gcc att gag att cta gct tgg ggc	2511
Ile Arg Pro Val Val Gln Leu Thr Ala Ile Glu Ile Leu Ala Trp Gly	
713 718 723 728	
tta aga aat atg aaa aac ttc cag atg gct tct atc aca tcc ccc agt	2559
Leu Arg Asn Met Lys Asn Phe Gln Met Ala Ser Ile Thr Ser Pro Ser	
729 734 739 744	
ctt gtt gtg gag tgt gga gga gaa agg gtg gaa tcg gtg gtg atc aaa	2607
Leu Val Val Glu Cys Gly Gly Glu Arg Val Glu Ser Val Val Ile Lys	
745 750 755 760	
aac ctt aag aag aca ccc aac ttt cca agt tct gtt ctc ttc atg aaa	2655
Asn Leu Lys Lys Thr Pro Asn Phe Pro Ser Ser Val Leu Phe Met Lys	
761 766 771 776	
gtg ttc ttg ccc aag gag gaa ttg tac atg ccc cca ctg gtg atc aag	2703
Val Phe Leu Pro Lys Glu Glu Leu Tyr Met Pro Pro Leu Val Ile Lys	
777 782 787 792	
gtc atc gac cac agg cag ttt ggg cgg aag cct gtc gta ggc cag tgc	2751
Val Ile Asp His Arg Gln Phe Gly Arg Lys Pro Val Val Gly Gln Cys	
793 798 803 808	
acc atc gag cgc ctg gat cgc ttt cgc tgt gac cct tat gca ggg aaa	2799
Thr Ile Glu Arg Leu Asp Arg Phe Arg Cys Asp Pro Tyr Ala Gly Lys	
809 814 819 824	
gag gac atc gtc cca cag ctc aaa gcc tcc ctt ctg tct gcc cca cca	2847
Glu Asp Ile Val Pro Gln Leu Lys Ala Ser Leu Leu Ser Ala Pro Pro	
825 830 835 840	
tgc cgg gac atc gtt atc gaa atg gaa gac acc aaa cca tta ctg gct	2895
Cys Arg Asp Ile Val Ile Glu Met Glu Asp Thr Lys Pro Leu Leu Ala	
841 846 851 856	
tct aag tgc tta agc agt atg tca aca gca ctc agc aaa atg gct tct	2943
Ser Lys Cys Leu Ser Ser Met Ser Thr Ala Leu Ser Lys Met Ala Ser	
857 862 867 872	
cca gcg aca gtg cat ctg aca gaa aag gag gaa gaa atc gtg gac tgg	2991

Pro Ala Thr Val His Leu Thr Glu Lys Glu Glu Glu Ile Val Asp Trp	
873 878 883 888	
tgg agt aaa ttt tat gct tcc tca ggg gaa cat gaa aaa tgc gga cag	3039
Trp Ser Lys Phe Tyr Ala Ser Ser Gly Glu His Glu Lys Cys Gly Gln	
889 894 899 904	
tat att cag aaa ggc tat tcc aag ctc aag ata tat aat tgt gaa cta	3087
Tyr Ile Gln Lys Gly Tyr Ser Lys Leu Lys Ile Tyr Asn Cys Glu Leu	
905 910 915 920	
gaa aat gta gca gaa ttt gag ggc ctg aca gac ttc tca gat acg ttc	3135
Glu Asn Val Ala Glu Phe Glu Gly Leu Thr Asp Phe Ser Asp Thr Phe	
921 926 931 936	
aag ttg tac cga ggc aag tcg gat gaa aat gaa gat cct tct gtg gtt	3183
Lys Leu Tyr Arg Gly Lys Ser Asp Glu Asn Glu Asp Pro Ser Val Val	
937 942 947 952	
gga gag ttt aag ggc tcc ttt cgg atc tac cct ctg ccg gat gac ccc	3231
Gly Glu Phe Lys Gly Ser Phe Arg Ile Tyr Pro Leu Pro Asp Asp Pro	
953 958 963 968	
agc gtg cca gcc cct ccc aga cag ttt cgg gaa tta cct gac agc gtc	3279
Ser Val Pro Ala Pro Pro Arg Gln Phe Arg Glu Leu Pro Asp Ser Val	
969 974 979 984	
cca cag gaa tgc acg gtt agg att tac att gtt cga ggc tta gag ctc	3327
Pro Gln Glu Cys Thr Val Arg Ile Tyr Ile Val Arg Gly Leu Glu Leu	
985 990 995 1000	
cag ccc cag gac aac aat ggc ctg tgt gac cct tac ata aaa ata aca	3375
Gln Pro Gln Asp Asn Asn Gly Leu Cys Asp Pro Tyr Ile Lys Ile Thr	
1001 1006 1011 1016	
ctg ggc aaa aaa gtc att gaa gac cga gat cac tac att ccc aac act	3423
Leu Gly Lys Lys Val Ile Glu Asp Arg Asp His Tyr Ile Pro Asn Thr	
1017 1022 1027 1032	
ctc aac cca gtc ttt ggc agg atg tac gaa ctg agc tgc tac tta cct	3471
Leu Asn Pro Val Phe Gly Arg Met Tyr Glu Leu Ser Cys Tyr Leu Pro	
1033 1038 1043 1048	
caa gaa aaa gac ctg aaa att tct gtc tat gat tat gac acc ttt acc	3519
Gln Glu Lys Asp Leu Lys Ile Ser Val Tyr Asp Tyr Asp Thr Phe Thr	
1049 1054 1059 1064	
cgg gat gaa aaa gta gga gaa aca att att gat ctg gaa aac cga ttc	3567
Arg Asp Glu Lys Val Gly Glu Thr Ile Ile Asp Leu Glu Asn Arg Phe	
1065 1070 1075 1080	
ctt tcc cgc ttt ggg tcc cac tgc ggc ata cca gag gag tac tgt gtt	3615
Leu Ser Arg Phe Gly Ser His Cys Gly Ile Pro Glu Glu Tyr Cys Val	
1081 1086 1091 1096	
tct gga gtc aat acc tgg cga gat caa ctg aga cca aca cag ctg ctt	3663
Ser Gly Val Asn Thr Trp Arg Asp Gln Leu Arg Pro Thr Gln Leu Leu	

1097	1102	1107	1112	
caa aat gtc gcc aga ttc aaa ggc ttc cca caa ccc atc ctt tcc gaa				3711
Gln Asn Val Ala Arg Phe Lys Gly Phe Pro Gln Pro Ile Leu Ser Glu				
1113	1118	1123	1128	
gat ggg agt aga atc ata tat gga gga cga gac tac agc ttg gat gaa				3759
Asp Gly Ser Arg Ile Ile Tyr Gly Gly Arg Asp Tyr Ser Leu Asp Glu				
1129	1134	1139	1144	
ttt gaa gcc aac aaa atc ctg cac cag cac ctc ggg gcc cct gaa gag				3807
Phe Glu Ala Asn Lys Ile Leu His Gln His Leu Gly Ala Pro Glu Glu				
1145	1150	1155	1160	
cgg ctt gct ctt cac atc ctc agg act cag ggg ctg gtc cct gag cac				3855
Arg Leu Ala Leu His Ile Leu Arg Thr Gln Gly Leu Val Pro Glu His				
1161	1166	1171	1176	
gtg gaa aca agg act ttg cac agc acc ttc cag ccc aac att tcc aga				3903
Val Glu Thr Arg Thr Leu His Ser Thr Phe Gln Pro Asn Ile Ser Arg				
1177	1182	1187	1192	
tac tac ctg cgt gtg atc atc tgg aac acc aag gac gtt atc ttg gac				3951
Tyr Tyr Leu Arg Val Ile Ile Trp Asn Thr Lys Asp Val Ile Leu Asp				
1193	1198	1203	1208	
gag aaa agc atc aca gga gag gaa atg agt gac atc tac gtc aaa ggc				3999
Glu Lys Ser Ile Thr Gly Glu Glu Met Ser Asp Ile Tyr Val Lys Gly				
1209	1214	1219	1224	
tgg att cct ggc aat gaa gaa aac aaa cag aaa aca gat gtc cgt tac				4047
Trp Ile Pro Gly Asn Glu Glu Asn Lys Gln Lys Thr Asp Val Arg Tyr				
1225	1230	1235	1240	
aga tct ttg gat ggt gaa ggg aat ttt aac tgg cga ttt gtt ttc ccg				4095
Arg Ser Leu Asp Gly Glu Gly Asn Phe Asn Trp Arg Phe Val Phe Pro				
1241	1246	1251	1256	
ttt gac tac ctt cca gcc gaa caa ctc tgt atc gtt gcg aaa aaa gag				4143
Phe Asp Tyr Leu Pro Ala Glu Gln Leu Cys Ile Val Ala Lys Lys Glu				
1257	1262	1267	1272	
cat ttc tgg agt att gac caa acg gaa ttt cga atc cca ccc agg ctg				4191
His Phe Trp Ser Ile Asp Gln Thr Glu Phe Arg Ile Pro Pro Arg Leu				
1273	1278	1283	1288	
atc att cag ata tgg gac aat gac aag ttt tct ctg gat gac tac ttg				4239
Ile Ile Gln Ile Trp Asp Asn Asp Lys Phe Ser Leu Asp Asp Tyr Leu				
1289	1294	1299	1304	
ggt ttc cta gaa ctt gac ttg cgt cac acg atc att cct gca aaa tca				4287
Gly Phe Leu Glu Leu Asp Leu Arg His Thr Ile Ile Pro Ala Lys Ser				
1305	1310	1315	1320	
cca gag aaa tgc aga ttg gac atg att ccg gac ctc aaa gcc atg aac				4335
Pro Glu Lys Cys Arg Leu Asp Met Ile Pro Asp Leu Lys Ala Met Asn				
1321	1326	1331	1336	

cag atc cga aag ctg cgg tcc agg tct ctc tcc caa ata cat gag gcg	783
Gln Ile Arg Lys Leu Arg Ser Arg Ser Leu Ser Gln Ile His Glu Ala	
137 142 147 152	
gct gtg agg atg agg tcg gaa gcc aca gat gtg aag tcc aca ctg gca	831
Ala Val Arg Met Arg Ser Glu Ala Thr Asp Val Lys Ser Thr Leu Ala	
153 158 163 168	
gaa att gag gac tgg ctt gat aaa tta atg cag ctg act gaa gag cca	879
Glu Ile Glu Asp Trp Leu Asp Lys Leu Met Gln Leu Thr Glu Glu Pro	
169 174 179 184	
cag aac agc atg cct gac atc atc atc tgg atg atc cgg gga gag aag	927
Gln Asn Ser Met Pro Asp Ile Ile Ile Trp Met Ile Arg Gly Glu Lys	
185 190 195 200	
aga ctg gcc tat gca cga att ccc gca cat cag gtc ttg tac tcc acc	975
Arg Leu Ala Tyr Ala Arg Ile Pro Ala His Gln Val Leu Tyr Ser Thr	
201 206 211 216	
agt ggt gag aat gca tct gga aaa tac tgt ggg aaa acc caa acc atc	1023
Ser Gly Glu Asn Ala Ser Gly Lys Tyr Cys Gly Lys Thr Gln Thr Ile	
217 222 227 232	
ttt ctg aag tat cca cag gag aaa aac aac ggg cca aag gtg oct gtg	1071
Phe Leu Lys Tyr Pro Gln Glu Lys Asn Asn Gly Pro Lys Val Pro Val	
233 238 243 248	
gag ttg cga gtg aac atc tgg cta ggc tta agt gct gtg gag aag aag	1119
Glu Leu Arg Val Asn Ile Trp Leu Gly Leu Ser Ala Val Glu Lys Lys	
249 254 259 264	
ttt aac agc ttc gca gaa gga act ttc acc gtc ttt gct gaa atg tat	1167
Phe Asn Ser Phe Ala Glu Gly Thr Phe Thr Val Phe Ala Glu Met Tyr	
265 270 275 280	
gaa aat caa gct ctc atg ttt gga aaa tgg ggt act tct gga tta gta	1215
Glu Asn Gln Ala Leu Met Phe Gly Lys Trp Gly Thr Ser Gly Leu Val	
281 286 291 296	
gga cgt cat aag ttt tct gat gtc aca gga aaa ata aaa ctc aag agg	1263
Gly Arg His Lys Phe Ser Asp Val Thr Gly Lys Ile Lys Leu Lys Arg	
297 302 307 312	
gaa ttt ttt ctg cct cca aaa ggc tgg gaa tgg gaa gga gag tgg ata	1311
Glu Phe Phe Leu Pro Pro Lys Gly Trp Glu Trp Glu Gly Glu Trp Ile	
313 318 323 328	
gtt gat cct gaa aga agc ttg ctg act gag gca gat gca ggt cac acg	1359
Val Asp Pro Glu Arg Ser Leu Leu Thr Glu Ala Asp Ala Gly His Thr	
329 334 339 344	
gag ttc act gat gaa gtc tat cag aac gag agc cgc tac ccc ggg ggc	1407
Glu Phe Thr Asp Glu Val Tyr Gln Asn Glu Ser Arg Tyr Pro Gly Gly	
345 350 355 360	
gac tgg aag ccg gcc gag gac acc tac acg gat gcg aac ggc gat aaa	1455

Asp Trp Lys Pro Ala Glu Asp Thr Tyr Thr Asp Ala Asn Gly Asp Lys	
361 366 371 376	
gca gca tca ccc agc gag ttg act tgt cct cca ggt tgg gaa tgg gaa	1503
Ala Ala Ser Pro Ser Glu Leu Thr Cys Pro Pro Gly Trp Glu Trp Glu	
377 382 387 392	
gat gat gca tgg tct tat gac ata aat cga gcg gtg gat gag aaa ggc	1551
Asp Asp Ala Trp Ser Tyr Asp Ile Asn Arg Ala Val Asp Glu Lys Gly	
393 398 403 408	
tgg gaa tat gga atc acc att cct cct gat cat aag ccc aaa tcc tgg	1599
Trp Glu Tyr Gly Ile Thr Ile Pro Pro Asp His Lys Pro Lys Ser Trp	
409 414 419 424	
gtt gca gca gag aaa atg tac cac act cat aga cgg cga agg ctg gtc	1647
Val Ala Ala Glu Lys Met Tyr His Thr His Arg Arg Arg Arg Leu Val	
425 430 435 440	
cga aaa cgc aag aaa gat tta aca cag act gct tca agc acc gca agg	1695
Arg Lys Arg Lys Lys Asp Leu Thr Gln Thr Ala Ser Ser Thr Ala Arg	
441 446 451 456	
gcc atg gag gaa ttg caa gac caa gag ggc tgg gaa tat gct tct cta	1743
Ala Met Glu Glu Leu Gln Asp Gln Glu Gly Trp Glu Tyr Ala Ser Leu	
457 462 467 472	
att ggc tgg aaa ttt cac tgg aaa caa cgt agt tca gat acc ttc cgc	1791
Ile Gly Trp Lys Phe His Trp Lys Gln Arg Ser Ser Asp Thr Phe Arg	
473 478 483 488	
cgc aga cgc tgg agg aga aaa atg gct cct tca gaa aca cat ggt gca	1839
Arg Arg Arg Trp Arg Arg Lys Met Ala Pro Ser Glu Thr His Gly Ala	
489 494 499 504	
gct gcc atc ttt aaa ctt gaa ggt gcc ctt ggg gca gac act acc gaa	1887
Ala Ala Ile Phe Lys Leu Glu Gly Ala Leu Gly Ala Asp Thr Thr Glu	
505 510 515 520	
gat ggg gat gag aag agc ctg gag aaa cag aag cac agt gcc acc act	1935
Asp Gly Asp Glu Lys Ser Leu Glu Lys Gln Lys His Ser Ala Thr Thr	
521 526 531 536	
gtg ttc gga gca aac acc ccc att gtt tcc tgc aat ttt gac aga gac	1983
Val Phe Gly Ala Asn Thr Pro Ile Val Ser Cys Asn Phe Asp Arg Asp	
537 542 547 552	
tac atc tac cat ctg cgc tgc tat gtc tat caa gcc aga aac ctc ttg	2031
Tyr Ile Tyr His Leu Arg Cys Tyr Val Tyr Gln Ala Arg Asn Leu Leu	
553 558 563 568	
gct tta gat aag gat agc ttt tca gat cca ttt gct cat atc tgt ttc	2079
Ala Leu Asp Lys Asp Ser Phe Ser Asp Pro Phe Ala His Ile Cys Phe	
569 574 579 584	
ctc cat cgg agc aaa acc act gag atc atc cat tca acc ctg aat ccc	2127
Leu His Arg Ser Lys Thr Thr Glu Ile Ile His Ser Thr Leu Asn Pro	

585	590	595	600	
acg tgg gac caa aca att ata ttc gat gaa gtt gaa atc tat ggg gaa				2175
Thr Trp Asp Gln Thr Ile Ile Phe Asp Glu Val Glu Ile Tyr Gly Glu				
601	606	611	616	
ccc caa aca gtt cta cag aat cca ccc aaa gtt atc atg gaa ctt ttt				2223
Pro Gln Thr Val Leu Gln Asn Pro Pro Lys Val Ile Met Glu Leu Phe				
617	622	627	632	
gac aat gac caa gtg ggc aaa gat gaa ttt tta gga cga agc att ttc				2271
Asp Asn Asp Gln Val Gly Lys Asp Glu Phe Leu Gly Arg Ser Ile Phe				
633	638	643	648	
tct cct gtg gtg aaa ctg aac tca gaa atg gac atc aca ccc aaa ctt				2319
Ser Pro Val Val Lys Leu Asn Ser Glu Met Asp Ile Thr Pro Lys Leu				
649	654	659	664	
ctc tgg cac cca gta atg aat gga gac aaa gcc tgc ggg gat gtt ctt				2367
Leu Trp His Pro Val Met Asn Gly Asp Lys Ala Cys Gly Asp Val Leu				
665	670	675	680	
gta act gca gag ctg att ctg agg ggc aag gat ggc tcc aac ctt ccc				2415
Val Thr Ala Glu Leu Ile Leu Arg Gly Lys Asp Gly Ser Asn Leu Pro				
681	686	691	696	
att ctt ccc cct caa agg gcg cca aat cta tac atg gtc ccc cag ggg				2463
Ile Leu Pro Pro Gln Arg Ala Pro Asn Leu Tyr Met Val Pro Gln Gly				
697	702	707	712	
atc agg cct gtg gtc cag ctc act gcc att gag att cta gct tgg ggc				2511
Ile Arg Pro Val Val Gln Leu Thr Ala Ile Glu Ile Leu Ala Trp Gly				
713	718	723	728	
tta aga aat atg aaa aac ttc cag atg gct tct atc aca tcc ccc agt				2559
Leu Arg Asn Met Lys Asn Phe Gln Met Ala Ser Ile Thr Ser Pro Ser				
729	734	739	744	
ctt gtt gtg gag tgt gga gga gaa agg gtg gaa tcg gtg gtg atc aaa				2607
Leu Val Val Glu Cys Gly Gly Glu Arg Val Glu Ser Val Val Ile Lys				
745	750	755	760	
aac ctt aag aag aca ccc aac ttt cca agt tct gtt ctc ttc atg aaa				2655
Asn Leu Lys Lys Thr Pro Asn Phe Pro Ser Ser Val Leu Phe Met Lys				
761	766	771	776	
gtg ttc ttg ccc aag gag gaa ttg tac atg ccc cca ctg gtg atc aag				2703
Val Phe Leu Pro Lys Glu Glu Leu Tyr Met Pro Pro Leu Val Ile Lys				
777	782	787	792	
gtc atc gac cac agg cag ttt ggg cgg aag cct gtc gta ggc cag tgc				2751
Val Ile Asp His Arg Gln Phe Gly Arg Lys Pro Val Val Gly Gln Cys				
793	798	803	808	
acc atc gag cgc ctg gat cgc ttt cgc tgt gac cct tat gca ggg aaa				2799
Thr Ile Glu Arg Leu Asp Arg Phe Arg Cys Asp Pro Tyr Ala Gly Lys				
809	814	819	824	

gag gac atc gtc cca cag ctc aaa gcc tcc ctt ctg tct gcc cca cca	2847
Glu Asp Ile Val Pro Gln Leu Lys Ala Ser Leu Leu Ser Ala Pro Pro	
825 830 835 840	
tgc cgg gac atc gtt atc gaa atg gaa gac acc aaa cca tta ctg gct	2895
Cys Arg Asp Ile Val Ile Glu Met Glu Asp Thr Lys Pro Leu Leu Ala	
841 846 851 856	
tct aag ctg aca gaa aag gag gaa gaa atc gtg gac tgg tgg agt aaa	2943
Ser Lys Leu Thr Glu Lys Glu Glu Glu Ile Val Asp Trp Trp Ser Lys	
857 862 867 872	
ttt tat gct tcc tca ggg gaa cat gaa aaa tgc gga cag tat att cag	2991
Phe Tyr Ala Ser Ser Gly Glu His Glu Lys Cys Gly Gln Tyr Ile Gln	
873 878 883 888	
aaa ggc tat tcc aag ctc aag ata tat aat tgt gaa cta gaa aat gta	3039
Lys Gly Tyr Ser Lys Leu Lys Ile Tyr Asn Cys Glu Leu Glu Asn Val	
889 894 899 904	
gca gaa ttt gag ggc ctg aca gac ttc tca gat acg ttc aag ttg tac	3087
Ala Glu Phe Glu Gly Leu Thr Asp Phe Ser Asp Thr Phe Lys Leu Tyr	
905 910 915 920	
cga ggc aag tcg gat gaa aat gaa gat cct tct gtg gtt gga gag ttt	3135
Arg Gly Lys Ser Asp Glu Asn Glu Asp Pro Ser Val Val Gly Glu Phe	
921 926 931 936	
aag ggc tcc ttt cgg atc tac cct ctg ccg gat gac ccc agc gtg cca	3183
Lys Gly Ser Phe Arg Ile Tyr Pro Leu Pro Asp Asp Pro Ser Val Pro	
937 942 947 952	
gcc cct ccc aga cag ttt cgg gaa tta cct gac agc gtc cca cag gaa	3231
Ala Pro Pro Arg Gln Phe Arg Glu Leu Pro Asp Ser Val Pro Gln Glu	
953 958 963 968	
tgc acg gtt agg att tac att gtt cga ggc tta gag ctc cag ccc cag	3279
Cys Thr Val Arg Ile Tyr Ile Val Arg Gly Leu Glu Leu Gln Pro Gln	
969 974 979 984	
gac aac aat ggc ctg tgt gac cct tac ata aaa ata aca ctg ggc aaa	3327
Asp Asn Asn Gly Leu Cys Asp Pro Tyr Ile Lys Ile Thr Leu Gly Lys	
985 990 995 1000	
aaa gtc att gaa gac cga gat cac tac att ccc aac act ctc aac cca	3375
Lys Val Ile Glu Asp Arg Asp His Tyr Ile Pro Asn Thr Leu Asn Pro	
1001 1006 1011 1016	
gtc ttt ggc agg atg tac gaa ctg agc tgc tac tta cct caa gaa aaa	3423
Val Phe Gly Arg Met Tyr Glu Leu Ser Cys Tyr Leu Pro Gln Glu Lys	
1017 1022 1027 1032	
gac ctg aaa att tct gtc tat gat tat gac acc ttt acc cgg gat gaa	3471
Asp Leu Lys Ile Ser Val Tyr Asp Tyr Asp Thr Phe Thr Arg Asp Glu	
1033 1038 1043 1048	

aaa gta gga gaa aca att att gat ctg gaa aac cga ttc ctt tcc cgc	3519
Lys Val Gly Glu Thr Ile Ile Asp Leu Glu Asn Arg Phe Leu Ser Arg	
1049 1054 1059 1064	
ttt ggg tcc cac tgc ggc ata cca gag gag tac tgt gtt tct gga gtc	3567
Phe Gly Ser His Cys Gly Ile Pro Glu Glu Tyr Cys Val Ser Gly Val	
1065 1070 1075 1080	
aat acc tgg cga gat caa ctg aga cca aca cag ctg ctt caa aat gtc	3615
Asn Thr Trp Arg Asp Gln Leu Arg Pro Thr Gln Leu Leu Gln Asn Val	
1081 1086 1091 1096	
gcc aga ttc aaa ggc ttc cca caa ccc atc ctt tcc gaa gat ggg agt	3663
Ala Arg Phe Lys Gly Phe Pro Gln Pro Ile Leu Ser Glu Asp Gly Ser	
1097 1102 1107 1112	
aga atc ata tat gga gga cga gac tac agc ttg gat gaa ttt gaa gcc	3711
Arg Ile Ile Tyr Gly Gly Arg Asp Tyr Ser Leu Asp Glu Phe Glu Ala	
1113 1118 1123 1128	
aac aaa atc ctg cac cag cac ctc ggg gcc cct gaa gag cgg ctt gct	3759
Asn Lys Ile Leu His Gln His Leu Gly Ala Pro Glu Glu Arg Leu Ala	
1129 1134 1139 1144	
ctt cac atc ctc agg act cag ggg ctg gtc cct gag cac gtg gaa aca	3807
Leu His Ile Leu Arg Thr Gln Gly Leu Val Pro Glu His Val Glu Thr	
1145 1150 1155 1160	
agg act ttg cac agc acc ttc cag ccc aac att tcc aga tac tac ctg	3855
Arg Thr Leu His Ser Thr Phe Gln Pro Asn Ile Ser Arg Tyr Tyr Leu	
1161 1166 1171 1176	
cgt gtg atc atc tgg aac acc aag gac gtt atc ttg gac gag aaa agc	3903
Arg Val Ile Ile Trp Asn Thr Lys Asp Val Ile Leu Asp Glu Lys Ser	
1177 1182 1187 1192	
atc aca gga gag gaa atg agt gac atc tac gtc aaa ggc tgg att cct	3951
Ile Thr Gly Glu Glu Met Ser Asp Ile Tyr Val Lys Gly Trp Ile Pro	
1193 1198 1203 1208	
ggc aat gaa gaa aac aaa cag aaa aca gat gtc cgt tac aga tct ttg	3999
Gly Asn Glu Glu Asn Lys Gln Lys Thr Asp Val Arg Tyr Arg Ser Leu	
1209 1214 1219 1224	
gat ggt gaa ggg aat ttt aac tgg cga ttt gtt ttc ccg ttt gac tac	4047
Asp Gly Glu Gly Asn Phe Asn Trp Arg Phe Val Phe Pro Phe Asp Tyr	
1225 1230 1235 1240	
ctt cca gcc gaa caa ctc tgt atc gtt gcg aaa aaa gag cat ttc tgg	4095
Leu Pro Ala Glu Gln Leu Cys Ile Val Ala Lys Lys Glu His Phe Trp	
1241 1246 1251 1256	
agt att gac caa acg gaa ttt cga atc cca ccc agg ctg atc att cag	4143
Ser Ile Asp Gln Thr Glu Phe Arg Ile Pro Pro Arg Leu Ile Ile Gln	
1257 1262 1267 1272	
ata tgg gac aat gac aag ttt tct ctg gat gac tac ttg ggt ttc cta	4191

Ile Trp Asp Asn Asp Lys Phe Ser Leu Asp Asp Tyr Leu Gly Phe Leu	
1273 1278 1283 1288	
gaa ctt gac ttg cgt cac acg atc att cct gca aaa tca cca gag aaa	4239
Glu Leu Asp Leu Arg His Thr Ile Ile Pro Ala Lys Ser Pro Glu Lys	
1289 1294 1299 1304	
tgc aga ttg gac atg att ccg gac ctc aaa gcc atg aac ccc ctt aaa	4287
Cys Arg Leu Asp Met Ile Pro Asp Leu Lys Ala Met Asn Pro Leu Lys	
1305 1310 1315 1320	
gcc aag aca gcc tcc ctc ttt gag cag aag tcc atg aaa gga tgg tgg	4335
Ala Lys Thr Ala Ser Leu Phe Glu Gln Lys Ser Met Lys Gly Trp Trp	
1321 1326 1331 1336	
cca tgc tac gca gag aaa gat ggc gcc cgc gta atg gct ggg aaa gtg	4383
Pro Cys Tyr Ala Glu Lys Asp Gly Ala Arg Val Met Ala Gly Lys Val	
1337 1342 1347 1352	
gag atg aca ttg gaa atc ctc aac gag aag gag gcc gac gag agg cca	4431
Glu Met Thr Leu Glu Ile Leu Asn Glu Lys Glu Ala Asp Glu Arg Pro	
1353 1358 1363 1368	
gcc ggg aag ggg cgg gac gaa ccc aac atg aac ccc aag ctg gac tta	4479
Ala Gly Lys Gly Arg Asp Glu Pro Asn Met Asn Pro Lys Leu Asp Leu	
1369 1374 1379 1384	
cca aat cga cca gaa acc tcc ttc ctc tgg ttc acc aac cca tgc aag	4527
Pro Asn Arg Pro Glu Thr Ser Phe Leu Trp Phe Thr Asn Pro Cys Lys	
1385 1390 1395 1400	
acc atg aag ttc atc gtg tgg cgc cgc ttt aag tgg gtc atc atc ggc	4575
Thr Met Lys Phe Ile Val Trp Arg Arg Phe Lys Trp Val Ile Ile Gly	
1401 1406 1411 1416	
ttg ctg ttc ctg ctt atc ctg ctg ctc ttc gtg gcc gtg ctc ctc tac	4623
Leu Leu Phe Leu Leu Ile Leu Leu Leu Phe Val Ala Val Leu Leu Tyr	
1417 1422 1427 1432	
tct ttg ccg aac tat ttg tca atg aag att gta aag cca aat gtg taa	4671
Ser Leu Pro Asn Tyr Leu Ser Met Lys Ile Val Lys Pro Asn Val *	
1433 1438 1443 1448	
caaaggcaaa ggcttcattt caagagtcac ccagcaatga gagaatcctg cctctgtaga	4731
ccaacatcca gtgtgatttt gtgtctgaga ccacacccca gtagcagggtt acgccatgtc	4791
accgagcccc attgattccc agagggtctt agtcctggaa agtcaggcca acaagcaacg	4851
tttgcacatcat gttatctctt aagtattaaa agttttattt tctaaagttt aaatcatggt	4911
tttcaaaata tttttcaagg tggctgggttc catttaaaaa tcatcttttt atatgtgtct	4971
tcggttctag acttcagctt ttggaaattg ctaaatagaa ttcaaaaatc tctgcatoct	5031
gaggtgatata acttcatatt tgtaatcaac tgaaagagct gtgcattata aaatcagtta	5091

gaatagttag aacaattctt atttatgccc acaaccattg ctatatatttg tatggatgtc 5151
ataaaagtct atttaacctc tgtaatgaaa ctaaataaaaa atgtttcacc tttaaaaaaa 5211
aaaaa 5216

<210> 345
<211> 5364
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (328)..(4818)

<400> 345
tcttcgggaa ctggggctgc atcatataca gtaaacacag gagaaacaga ggtaggcttt 60
gttccaacgt ttggaccttg ttacctgaat ctttatggaa gcccagaga gtacacggga 120
ttcccagacc cctatgatga gctgaatact ggaaaggggg aaggagtgtc ctacagaggc 180
aggatcttgg ttgaattagc cacttttctt gagaagacac caccagataa aaagcttgag 240
cccatttcaa atgatgacct gctggttggt gagaaatacc agcgaaggcg gaagtacagc 300
ctgtctgccg tgtttcattc agccacc atg ttg caa gat gtt ggt gag gcc 351
Met Leu Gln Asp Val Gly Glu Ala
1 5
att cag ttt gaa gtc agc att ggg aac tat ggc aac aag ttt gac acc 399
Ile Gln Phe Glu Val Ser Ile Gly Asn Tyr Gly Asn Lys Phe Asp Thr
9 14 19 24
acc tgt aag cct ttg gca tca aca act cag tac agc cgt gct gta ttt 447
Thr Cys Lys Pro Leu Ala Ser Thr Thr Gln Tyr Ser Arg Ala Val Phe
25 30 35 40
gat ggc aac tac tat tat tac ttg cct tgg gcc cac acc aag cca gtt 495
Asp Gly Asn Tyr Tyr Tyr Tyr Leu Pro Trp Ala His Thr Lys Pro Val
41 46 51 56
gtt acc ctg act tca tac tgg gag gat att agt cat cgc ctg gat gcg 543
Val Thr Leu Thr Ser Tyr Trp Glu Asp Ile Ser His Arg Leu Asp Ala
57 62 67 72
gtg aac act ctc cta gct atg gca gaa cgg ctg caa aca aat ata gaa 591
Val Asn Thr Leu Leu Ala Met Ala Glu Arg Leu Gln Thr Asn Ile Glu
73 78 83 88
gct cta aaa tca ggg ata caa ggt aaa att cct gca aac cag ctg gct 639
Ala Leu Lys Ser Gly Ile Gln Gly Lys Ile Pro Ala Asn Gln Leu Ala
89 94 99 104

gaa ttg tgg ctg aag ctg ata gat gaa gtt ata gaa gac acg aga tac	687
Glu Leu Trp Leu Lys Leu Ile Asp Glu Val Ile Glu Asp Thr Arg Tyr	
105 110 115 120	
acg ttg cct ctc aca gaa gga aaa gcc aac gtc aca gtt ctc gat act	735
Thr Leu Pro Leu Thr Glu Gly Lys Ala Asn Val Thr Val Leu Asp Thr	
121 126 131 136	
cag atc cga aag ctg cgg tcc agg tct ctc tcc caa ata cat gag gcg	783
Gln Ile Arg Lys Leu Arg Ser Arg Ser Leu Ser Gln Ile His Glu Ala	
137 142 147 152	
gct gtg agg atg agg tcg gaa gcc aca gat gtg aag tcc aca ctg gca	831
Ala Val Arg Met Arg Ser Glu Ala Thr Asp Val Lys ¹¹ Ser Thr Leu Ala	
153 158 163 168	
gaa att gag gac tgg ctt gat aaa tta atg cag ctg act gaa gag cca	879
Glu Ile Glu Asp Trp Leu Asp Lys Leu Met Gln Leu Thr Glu Glu Pro	
169 174 179 184	
cag aac agc atg cct gac atc atc atc tgg atg atc cgg gga gag aag	927
Gln Asn Ser Met Pro Asp Ile Ile Ile Trp Met Ile Arg Gly Glu Lys	
185 190 195 200	
aga ctg gcc tat gca cga att ccc gca cat cag gtc ttg tac tcc acc	975
Arg Leu Ala Tyr Ala Arg Ile Pro Ala His Gln Val Leu Tyr Ser Thr	
201 206 211 216	
agt ggt gag aat gca tct gga aaa tac tgt ggg aaa acc caa acc atc	1023
Ser Gly Glu Asn Ala Ser Gly Lys Tyr Cys Gly Lys Thr Gln Thr Ile	
217 222 227 232	
ttt ctg aag tat cca cag gag aaa aac aac ggg cca aag gtg cct gtg	1071
Phe Leu Lys Tyr Pro Gln Glu Lys Asn Asn Gly Pro Lys Val Pro Val	
233 238 243 248	
gag ttg cga gtg aac atc tgg cta ggc tta agt gct gtg gag aag aag	1119
Glu Leu Arg Val Asn Ile Trp Leu Gly Leu Ser Ala Val Glu Lys Lys	
249 254 259 264	
ttt aac agc ttc gca gaa gga act ttc acc gtc ttt gct gaa atg tat	1167
Phe Asn Ser Phe Ala Glu Gly Thr Phe Thr Val Phe Ala Glu Met Tyr	
265 270 275 280	
gaa aat caa gct ctc atg ttt gga aaa tgg ggt act tct gga tta gta	1215
Glu Asn Gln Ala Leu Met Phe Gly Lys Trp Gly Thr Ser Gly Leu Val	
281 286 291 296	
gga cgt cat aag ttt tct gat gtc aca gga aaa ata aaa ctc aag agg	1263
Gly Arg His Lys Phe Ser Asp Val Thr Gly Lys Ile Lys Leu Lys Arg	
297 302 307 312	
gaa ttt ttt ctg cct cca aaa ggc tgg gaa tgg gaa gga gag tgg ata	1311
Glu Phe Phe Leu Pro Pro Lys Gly Trp Glu Trp Glu Gly Glu Trp Ile	
313 318 323 328	
gtt gat cct gaa aga agc ttg ctg act gag gca gat gca ggt cac acg	1359

Val	Asp	Pro	Glu	Arg	Ser	Leu	Leu	Thr	Glu	Ala	Asp	Ala	Gly	His	Thr		
329					334					339					344		
gag	ttc	act	gat	gaa	gtc	tat	cag	aac	gag	agc	cgc	tac	ccc	ggg	ggc	1407	
Glu	Phe	Thr	Asp	Glu	Val	Tyr	Gln	Asn	Glu	Ser	Arg	Tyr	Pro	Gly	Gly		
345					350					355					360		
gac	tgg	aag	ccg	gcc	gag	gac	acc	tac	acg	gat	gcg	aac	ggc	gat	aaa	1455	
Asp	Trp	Lys	Pro	Ala	Glu	Asp	Thr	Tyr	Thr	Asp	Ala	Asn	Gly	Asp	Lys		
361					366					371					376		
gca	gca	tca	ccc	agc	gag	ttg	act	tgt	cct	cca	ggt	tgg	gaa	tgg	gaa	1503	
Ala	Ala	Ser	Pro	Ser	Glu	Leu	Thr	Cys	Pro	Pro	Gly	Trp	Glu	Trp	Glu		
377					382					387					392		
gat	gat	gca	tgg	tct	tat	gac	ata	aat	cga	gcg	gtg	gat	gag	aaa	ggc	1551	
Asp	Asp	Ala	Trp	Ser	Tyr	Asp	Ile	Asn	Arg	Ala	Val	Asp	Glu	Lys	Gly		
393					398					403					408		
tgg	gaa	tat	gga	atc	acc	att	cct	cct	gat	cat	aag	ccc	aaa	tcc	tgg	1599	
Trp	Glu	Tyr	Gly	Ile	Thr	Ile	Pro	Pro	Asp	His	Lys	Pro	Lys	Ser	Trp		
409					414					419					424		
gtt	gca	gca	gag	aaa	atg	tac	cac	act	cat	aga	cgg	cga	agg	ctg	gtc	1647	
Val	Ala	Ala	Glu	Lys	Met	Tyr	His	Thr	His	Arg	Arg	Arg	Arg	Leu	Val		
425					430					435					440		
cga	aaa	cgc	aag	aaa	gat	tta	aca	cag	act	gct	tca	agc	acc	gca	agg	1695	
Arg	Lys	Arg	Lys	Lys	Asp	Leu	Thr	Gln	Thr	Ala	Ser	Ser	Thr	Ala	Arg		
441					446					451					456		
gcc	atg	gag	gaa	ttg	caa	gac	caa	gag	ggc	tgg	gaa	tat	gct	tct	cta	1743	
Ala	Met	Glu	Glu	Leu	Gln	Asp	Gln	Glu	Gly	Trp	Glu	Tyr	Ala	Ser	Leu		
457					462					467					472		
att	ggc	tgg	aaa	ttt	cac	tgg	aaa	caa	cgt	agt	tca	gat	acc	ttc	cgc	1791	
Ile	Gly	Trp	Lys	Phe	His	Trp	Lys	Gln	Arg	Ser	Ser	Asp	Thr	Phe	Arg		
473					478					483					488		
cgc	aga	cgc	tgg	agg	aga	aaa	atg	gct	cct	tca	gaa	aca	cat	ggt	gca	1839	
Arg	Arg	Arg	Trp	Arg	Arg	Lys	Met	Ala	Pro	Ser	Glu	Thr	His	Gly	Ala		
489					494					499					504		
gct	gcc	atc	ttt	aaa	ctt	gaa	ggt	gcc	ctt	ggg	gca	gac	act	acc	gaa	1887	
Ala	Ala	Ile	Phe	Lys	Leu	Glu	Gly	Ala	Leu	Gly	Ala	Asp	Thr	Thr	Glu		
505					510					515					520		
gat	ggg	gat	gag	aag	agc	ctg	gag	aaa	cag	aag	cac	agt	gcc	acc	act	1935	
Asp	Gly	Asp	Glu	Lys	Ser	Leu	Glu	Lys	Gln	Lys	His	Ser	Ala	Thr	Thr		
521					526					531					536		
gtg	ttc	gga	gca	aac	acc	ccc	att	gtt	tcc	tgc	aat	ttt	gac	aga	gac	1983	
Val	Phe	Gly	Ala	Asn	Thr	Pro	Ile	Val	Ser	Cys	Asn	Phe	Asp	Arg	Asp		
537					542					547					552		
tac	atc	tac	cat	ctg	cgc	tgc	tat	gtc	tat	caa	gcc	aga	aac	ctc	ttg	2031	
Tyr	Ile	Tyr	His	Leu	Arg	Cys	Tyr	Val	Tyr	Gln	Ala	Arg	Asn	Leu	Leu		

553	558	563	568	
gct tta gat aag gat agc ttt tca gat cca ttt gct cat atc tgt ttc				2079
Ala Leu Asp Lys Asp Ser Phe Ser Asp Pro Phe Ala His Ile Cys Phe				
569	574	579	584	
ctc cat cgg agc aaa acc act gag atc atc cat tca acc ctg aat ccc				2127
Leu His Arg Ser Lys Thr Thr Glu Ile Ile His Ser Thr Leu Asn Pro				
585	590	595	600	
acg tgg gac caa aca att ata ttc gat gaa gtt gaa atc tat ggg gaa				2175
Thr Trp Asp Gln Thr Ile Ile Phe Asp Glu Val Glu Ile Tyr Gly Glu				
601	606	611	616	
ccc caa aca gtt cta cag aat cca ccc aaa gtt atc atg gaa ctt ttt				2223
Pro Gln Thr Val Leu Gln Asn Pro Pro Lys Val Ile Met Glu Leu Phe				
617	622	627	632	
gac aat gac caa gtg ggc aaa gat gaa ttt tta gga cga agc att ttc				2271
Asp Asn Asp Gln Val Gly Lys Asp Glu Phe Leu Gly Arg Ser Ile Phe				
633	638	643	648	
tct cct gtg gtg aaa ctg aac tca gaa atg gac atc aca ccc aaa ctt				2319
Ser Pro Val Val Lys Leu Asn Ser Glu Met Asp Ile Thr Pro Lys Leu				
649	654	659	664	
ctc tgg cac cca gta atg aat gga gac aaa gcc tgc ggg gat gtt ctt				2367
Leu Trp His Pro Val Met Asn Gly Asp Lys Ala Cys Gly Asp Val Leu				
665	670	675	680	
gta act gca gag ctg att ctg agg ggc aag gat ggc tcc aac ctt ccc				2415
Val Thr Ala Glu Leu Ile Leu Arg Gly Lys Asp Gly Ser Asn Leu Pro				
681	686	691	696	
att ctt ccc cct caa agg gcg cca aat cta tac atg gtc ccc cag ggg				2463
Ile Leu Pro Pro Gln Arg Ala Pro Asn Leu Tyr Met Val Pro Gln Gly				
697	702	707	712	
atc agg cct gtg gtc cag ctc act gcc att gag att cta gct tgg ggc				2511
Ile Arg Pro Val Val Gln Leu Thr Ala Ile Glu Ile Leu Ala Trp Gly				
713	718	723	728	
tta aga aat atg aaa aac ttc cag atg gct tct atc aca tcc ccc agt				2559
Leu Arg Asn Met Lys Asn Phe Gln Met Ala Ser Ile Thr Ser Pro Ser				
729	734	739	744	
ctt gtt gtg gag tgt gga gga gaa agg gtg gaa tcg gtg gtg atc aaa				2607
Leu Val Val Glu Cys Gly Gly Glu Arg Val Glu Ser Val Val Ile Lys				
745	750	755	760	
aac ctt aag aag aca ccc aac ttt cca agt tct gtt ctc ttc atg aaa				2655
Asn Leu Lys Lys Thr Pro Asn Phe Pro Ser Ser Val Leu Phe Met Lys				
761	766	771	776	
gtg ttc ttg ccc aag gag gaa ttg tac atg ccc cca ctg gtg atc aag				2703
Val Phe Leu Pro Lys Glu Glu Leu Tyr Met Pro Pro Leu Val Ile Lys				
777	782	787	792	

gtc atc gac cac agg cag ttt ggg cgg aag cct gtc gta ggc cag tgc	2751
Val Ile Asp His Arg Gln Phe Gly Arg Lys Pro Val Val Gly Gln Cys	
793 798 803 808	
acc atc gag cgc ctg gat cgc ttt cgc tgt gac cct tat gca ggg aaa	2799
Thr Ile Glu Arg Leu Asp Arg Phe Arg Cys Asp Pro Tyr Ala Gly Lys	
809 814 819 824	
gag gac atc gtc cca cag ctc aaa gcc tcc ctt ctg tct gcc cca cca	2847
Glu Asp Ile Val Pro Gln Leu Lys Ala Ser Leu Leu Ser Ala Pro Pro	
825 830 835 840	
tgc cgg gac atc gtt atc gaa atg gaa gac acc aaa ⁺ cca tta ctg gct	2895
Cys Arg Asp Ile Val Ile Glu Met Glu Asp Thr Lys Pro Leu Leu Ala	
841 846 851 856	
tct aag tgc tta agc agt atg tca aca gca ctc agc aaa atg gct tct	2943
Ser Lys Cys Leu Ser Ser Met Ser Thr Ala Leu Ser Lys Met Ala Ser	
857 862 867 872	
cca gcg aca gtg cat ctg aca gaa aag gag gaa gaa atc gtg gac tgg	2991
Pro Ala Thr Val His Leu Thr Glu Lys Glu Glu Glu Ile Val Asp Trp	
873 878 883 888	
tgg agt aaa ttt tat gct tcc tca ggg gaa cat gaa aaa tgc gga cag	3039
Trp Ser Lys Phe Tyr Ala Ser Ser Gly Glu His Glu Lys Cys Gly Gln	
889 894 899 904	
tat att cag aaa ggc tat tcc aag ctc aag ata tat aat tgt gaa cta	3087
Tyr Ile Gln Lys Gly Tyr Ser Lys Leu Lys Ile Tyr Asn Cys Glu Leu	
905 910 915 920	
gaa aat gta gca gaa ttt gag ggc ctg aca gac ttc tca gat acg ttc	3135
Glu Asn Val Ala Glu Phe Glu Gly Leu Thr Asp Phe Ser Asp Thr Phe	
921 926 931 936	
aag ttg tac cga ggc aag tcg gat gaa aat gaa gat cct tct gtg gtt	3183
Lys Leu Tyr Arg Gly Lys Ser Asp Glu Asn Glu Asp Pro Ser Val Val	
937 942 947 952	
gga gag ttt aag ggc tcc ttt cgg atc tac cct ctg ccg gat gac ccc	3231
Gly Glu Phe Lys Gly Ser Phe Arg Ile Tyr Pro Leu Pro Asp Asp Pro	
953 958 963 968	
agc gtg cca gcc cct ccc aga cag ttt cgg gaa tta cct gac agc gtc	3279
Ser Val Pro Ala Pro Pro Arg Gln Phe Arg Glu Leu Pro Asp Ser Val	
969 974 979 984	
cca cag gaa tgc acg gtt agg att tac att gtt cga ggc tta gag ctc	3327
Pro Gln Glu Cys Thr Val Arg Ile Tyr Ile Val Arg Gly Leu Glu Leu	
985 990 995 1000	
cag ccc cag gac aac aat ggc ctg tgt gac cct tac ata aaa ata aca	3375
Gln Pro Gln Asp Asn Asn Gly Leu Cys Asp Pro Tyr Ile Lys Ile Thr	
1001 1006 1011 1016	

ctg ggc aaa aaa gtc att gaa gac cga gat cac tac att ccc aac act	3423
Leu Gly Lys Lys Val Ile Glu Asp Arg Asp His Tyr Ile Pro Asn Thr	
1017 1022 1027 1032	
ctc aac cca gtc ttt ggc agg atg tac gaa ctg agc tgc tac tta cct	3471
Leu Asn Pro Val Phe Gly Arg Met Tyr Glu Leu Ser Cys Tyr Leu Pro	
1033 1038 1043 1048	
caa gaa aaa gac ctg aaa att tct gtc tat gat tat gac acc ttt acc	3519
Gln Glu Lys Asp Leu Lys Ile Ser Val Tyr Asp Tyr Asp Thr Phe Thr	
1049 1054 1059 1064	
cgg gat gaa aaa gta gga gaa aca att att gat ctg gaa aac cga ttc	3567
Arg Asp Glu Lys Val Gly Glu Thr Ile Ile Asp Leu Glu Asn Arg Phe	
1065 1070 1075 1080	
ctt tcc cgc ttt ggg tcc cac tgc ggc ata cca gag gag tac tgt gtt	3615
Leu Ser Arg Phe Gly Ser His Cys Gly Ile Pro Glu Glu Tyr Cys Val	
1081 1086 1091 1096	
tct gga gtc aat acc tgg cga gat caa ctg aga cca aca cag ctg ctt	3663
Ser Gly Val Asn Thr Trp Arg Asp Gln Leu Arg Pro Thr Gln Leu Leu	
1097 1102 1107 1112	
caa aat gtc gcc aga ttc aaa ggc ttc cca caa ccc atc ctt tcc gaa	3711
Gln Asn Val Ala Arg Phe Lys Gly Phe Pro Gln Pro Ile Leu Ser Glu	
1113 1118 1123 1128	
gat ggg agt aga atc ata tat gga gga cga gac tac agc ttg gat gaa	3759
Asp Gly Ser Arg Ile Ile Tyr Gly Gly Arg Asp Tyr Ser Leu Asp Glu	
1129 1134 1139 1144	
ttt gaa gcc aac aaa atc ctg cac cag cac ctc ggg gcc cct gaa gag	3807
Phe Glu Ala Asn Lys Ile Leu His Gln His Leu Gly Ala Pro Glu Glu	
1145 1150 1155 1160	
cgg ctt gct ctt cac atc ctc agg act cag ggg ctg gtc cct gag cac	3855
Arg Leu Ala Leu His Ile Leu Arg Thr Gln Gly Leu Val Pro Glu His	
1161 1166 1171 1176	
gtg gaa aca agg act ttg cac agc acc ttc cag ccc aac att tcc cag	3903
Val Glu Thr Arg Thr Leu His Ser Thr Phe Gln Pro Asn Ile Ser Gln	
1177 1182 1187 1192	
gga aaa ctt cag atg tgg gtg gat gtt ttc ccc aag agt ttg ggg cca	3951
Gly Lys Leu Gln Met Trp Val Asp Val Phe Pro Lys Ser Leu Gly Pro	
1193 1198 1203 1208	
cca ggc cct cct ttc aac atc aca ccc cgg aaa gcc aag aga tac tac	3999
Pro Gly Pro Pro Phe Asn Ile Thr Pro Arg Lys Ala Lys Arg Tyr Tyr	
1209 1214 1219 1224	
ctg cgt gtg atc atc tgg aac acc aag gac gtt atc ttg gac gag aaa	4047
Leu Arg Val Ile Ile Trp Asn Thr Lys Asp Val Ile Leu Asp Glu Lys	
1225 1230 1235 1240	
agc atc aca gga gag gaa atg agt gac atc tac gtc aaa ggc tgg att	4095

Ser Ile Thr Gly Glu Glu Met Ser Asp Ile Tyr Val Lys Gly Trp Ile
1241 1246 1251 1256

cct ggc aat gaa gaa aac aaa cag aaa aca gat gtc cgt tac aga tct 4143
Pro Gly Asn Glu Glu Asn Lys Gln Lys Thr Asp Val Arg Tyr Arg Ser
1257 1262 1267 1272

ttg gat ggt gaa ggg aat ttt aac tgg cga ttt gtt ttc ccg ttt gac 4191
Leu Asp Gly Glu Gly Asn Phe Asn Trp Arg Phe Val Phe Pro Phe Asp
1273 1278 1283 1288

tac ctt cca gcc gaa caa ctc tgt atc gtt gcg aaa aaa gag cat ttc 4239
Tyr Leu Pro Ala Glu Gln Leu Cys Ile Val Ala Lys Lys Glu His Phe
1289 1294 1299 1304

tgg agt att gac caa acg gaa ttt cga atc cca ccc agg ctg atc att 4287
Trp Ser Ile Asp Gln Thr Glu Phe Arg Ile Pro Pro Arg Leu Ile Ile
1305 1310 1315 1320

cag ata tgg gac aat gac aag ttt tct ctg gat gac tac ttg ggt ttc 4335
Gln Ile Trp Asp Asn Asp Lys Phe Ser Leu Asp Asp Tyr Leu Gly Phe
1321 1326 1331 1336

cta gaa ctt gac ttg cgt cac acg atc att cct gca aaa tca cca gag 4383
Leu Glu Leu Asp Leu Arg His Thr Ile Ile Pro Ala Lys Ser Pro Glu
1337 1342 1347 1352

aaa tgc aga ttg gac atg att ccg gac ctc aaa gcc atg aac ccc ctt 4431
Lys Cys Arg Leu Asp Met Ile Pro Asp Leu Lys Ala Met Asn Pro Leu
1353 1358 1363 1368

aaa gcc aag aca gcc tcc ctc ttt gag cag aag tcc atg aaa gga tgg 4479
Lys Ala Lys Thr Ala Ser Leu Phe Glu Gln Lys Ser Met Lys Gly Trp
1369 1374 1379 1384

tgg cca tgc tac gca gag aaa gat ggc gcc cgc gta atg gct ggg aaa 4527
Trp Pro Cys Tyr Ala Glu Lys Asp Gly Ala Arg Val Met Ala Gly Lys
1385 1390 1395 1400

gtg gag atg aca ttg gaa atc ctc aac gag aag gag gcc gac gag agg 4575
Val Glu Met Thr Leu Glu Ile Leu Asn Glu Lys Glu Ala Asp Glu Arg
1401 1406 1411 1416

cca gcc ggg aag ggg cgg gac gaa ccc aac atg aac ccc aag ctg gac 4623
Pro Ala Gly Lys Gly Arg Asp Glu Pro Asn Met Asn Pro Lys Leu Asp
1417 1422 1427 1432

tta cca aat cga cca gaa acc tcc ttc ctc tgg ttc acc aac cca tgc 4671
Leu Pro Asn Arg Pro Glu Thr Ser Phe Leu Trp Phe Thr Asn Pro Cys
1433 1438 1443 1448

aag acc atg aag ttc atc gtg tgg cgc cgc ttt aag tgg gtc atc atc 4719
Lys Thr Met Lys Phe Ile Val Trp Arg Arg Phe Lys Trp Val Ile Ile
1449 1454 1459 1464

ggc ttg ctg ttc ctg ctt atc ctg ctg ctc ttc gtg gcc gtg ctc ctc 4767
Gly Leu Leu Phe Leu Leu Ile Leu Leu Leu Phe Val Ala Val Leu Leu

1465	1470	1475	1480	
tac tct ttg ccg aac tat ttg tca atg aag att gta aag cca aat gtg				4815
Tyr Ser Leu Pro Asn Tyr Leu Ser Met Lys Ile Val Lys Pro Asn Val				
1481	1486	1491	1496	

taa caaa ggcaaaggct tcatttcaag agtcatccag caatgagaga atcctgcctc	4872
*	
1497	

tgtagaccaa catccagtgt gatttttgtgt ctgagaccac accccagtag cagggttacgc	4932
catgtcaccg agccccattg attcccagag ggtcttagtc ctggaaagtc aggccaacaa	4992
gcaacgtttg catcatgtta tctcttaagt attaaaagtt ttattttcta aagtttaa	5052
catgtttttc aaaatatttt tcaaggtggc tggttccatt taaaaatcat ctttttat	5112
gtgtcttcgg ttctagactt cagcttttgg aaattgctaa atagaattca aaaatctctg	5172
catcctgagg tgatatactt catatttgta atcaactgaa agagctgtgc attataaa	5232
cagttagaat agttagaaca attcttattt atgccacaa ccattgctat attttgtatg	5292
gatgtcataa aagtctattt aacctctgta atgaaactaa ataaaaatgt ttcaccttta	5352
aaaaaaaaaa aa	5364

<210> 346
 <211> 1414
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (175) .. (975)

<400> 346	
gcagattcag ctgcctagcg tttaaactta agcttggtac cgagctcgga tccactagtc	60
cagtgtggtg gaattcgcgc gagccgggct gtcgggtgtg ttttgctctc cagcctccgt	120
cgtctctgca gcactccggg ttctcctcca gagcgctagt cccaggagct cgga atg	177
	Met
	1
ttc gtg gaa ctt aat aac ctg ctt aac acc acc ccc gac agg gcg gag	225
Phe Val Glu Leu Asn Asn Leu Leu Asn Thr Thr Pro Asp Arg Ala Glu	
2 7 12 17	
cag ggg aaa ctg act cta ctc tgt gat gcc aag aca gat ggg agt ttc	273
Gln Gly Lys Leu Thr Leu Leu Cys Asp Ala Lys Thr Asp Gly Ser Phe	
18 23 28 33	

ctt gta cac cac ttt ctc tcc ttc tat ctc aaa gct aat tgt aaa gtc	321
Leu Val His His Phe Leu Ser Phe Tyr Leu Lys Ala Asn Cys Lys Val	
34 39 44 49	
tgC ttt gtg gca ctc atc cag tcc ttc agc cac tac agt atc gtg gga	369
Cys Phe Val Ala Leu Ile Gln Ser Phe Ser His Tyr Ser Ile Val Gly	
50 55 60 65	
cag aag ctg ggt gtc agc ctg acc atg gcg cgg gag cgt ggg cag ctt	417
Gln Lys Leu Gly Val Ser Leu Thr Met Ala Arg Glu Arg Gly Gln Leu	
66 71 76 81	
gtg ttc ctt gag gga ctc aag tct gca gtg gac gtc gtc ttc cag gct	465
Val Phe Leu Glu Gly Leu Lys Ser Ala Val Asp Val Val Phe Gln Ala	
82 87 92 97	
caa aag gag cca cac ccc ctg cag ttt ctc agg gag gct aat gct ggg	513
Gln Lys Glu Pro His Pro Leu Gln Phe Leu Arg Glu Ala Asn Ala Gly	
98 103 108 113	
aac ttg aaa cca ttg ttt gag ttt gta cgg gag gcc ctg aag cca gta	561
Asn Leu Lys Pro Leu Phe Glu Phe Val Arg Glu Ala Leu Lys Pro Val	
114 119 124 129	
gac agt gga gag gct cgg tgg acg tac ccg gtg ctg ttg gtg gac gac	609
Asp Ser Gly Glu Ala Arg Trp Thr Tyr Pro Val Leu Leu Val Asp Asp	
130 135 140 145	
ctc agt gtg ctc ctg agc ctg ggc atg ggg gcg gtg gct gtg cta gac	657
Leu Ser Val Leu Leu Ser Leu Gly Met Gly Ala Val Ala Val Leu Asp	
146 151 156 161	
ttc att cac tac tgc aga gcc acc gtg tgc tgg gaa cta aag gga aac	705
Phe Ile His Tyr Cys Arg Ala Thr Val Cys Trp Glu Leu Lys Gly Asn	
162 167 172 177	
atg gtg gtc ctt gtg cac gac agt gga gat gcg gag gat gag gag aat	753
Met Val Val Leu Val His Asp Ser Gly Asp Ala Glu Asp Glu Glu Asn	
178 183 188 193	
gac atc ctg ctg aat ggc ctc agt cat cag agc cat ctg ata ctg cgg	801
Asp Ile Leu Leu Asn Gly Leu Ser His Gln Ser His Leu Ile Leu Arg	
194 199 204 209	
gct gag ggc ctg gcc act ggc ttc tgc agg gat gtg cac ggg cag ctg	849
Ala Glu Gly Leu Ala Thr Gly Phe Cys Arg Asp Val His Gly Gln Leu	
210 215 220 225	
agg atc ctg tgg agg aga cca tcg cag ccc gca gtc cac cgg gat cag	897
Arg Ile Leu Trp Arg Arg Pro Ser Gln Pro Ala Val His Arg Asp Gln	
226 231 236 241	
agc ttc act tac cag tat aag ata dag gac aaa agc gtg tcc ttt ttt	945
Ser Phe Thr Tyr Gln Tyr Lys Ile Gln Asp Lys Ser Val Ser Phe Phe	
242 247 252 257	
gcc aaa gga atg tct cct gct gtt ctg tga c ctgatttcgg agcagctgaa	996

Ala Lys Gly Met Ser Pro Ala Val Leu *
 258 263

gctacatagg actgtttttg gacgtggaag atagagcaac atagcaagaa tgggtctttc 1056
 tcctctgtag taatatttca ggctggaccg gcgactccac tgtgaccaga gggttgagt 1116
 ctgcagtgat ggcattgcctt ggctgccctg ggccctgttc agaaaacaca agggaccaca 1176
 atcctgcctt tgctgagaga gaggtctgat gctagaccca agtgaaaggg gtcctttgga 1236
 gcctttgttt aaatatgcct tagccccagc tgccattttt tggttgacaa gcctttcaga 1296
 gccagagtgg gtatagatgt gccagccagg agatggcacc ggatggcagg tgtgcaaggt 1356
 gacaactagg ataatcatgg ctggaataaa gtaagtttcc aactggaaa aaaaaaaaa 1414

<210> 347
 <211> 4351
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (13)..(3378)

<400> 347
 cttcgacccc cg atg att gga atg ggc gtg atg tat ata act atc tat 48
 Met Ile Gly Met Gly Val Met Tyr Ile Thr Ile Tyr
 1 5 10
 tcg atg atg aag ata ccc cac caa acc caa aaa aag aga tct ctc gag 96
 Ser Met Met Lys Ile Pro His Gln Thr Gln Lys Lys Arg Ser Leu Glu
 13 18 23 28
 gat ccg aat tcg cgg ccg cgt cga cct ttt cta agc ttt ctg tgt tac 144
 Asp Pro Asn Ser Arg Pro Arg Arg Pro Phe Leu Ser Phe Leu Cys Tyr
 29 34 39 44
 ccc cgg ttc cgc tgt ctt ttc tgt cta cag ttt gcg atc ccc gcg tcc 192
 Pro Arg Phe Arg Cys Leu Phe Cys Leu Gln Phe Ala Ile Pro Ala Ser
 45 50 55 60
 agg atg gag cag ctg aac gaa ctg gag ctg ctg atg gag aag agt ttt 240
 Arg Met Glu Gln Leu Asn Glu Leu Glu Leu Leu Met Glu Lys Ser Phe
 61 66 71 76
 tgg gag gag gcg gag ctg ccg gcg gag cta ttt cag aag aaa gtg gta 288
 Trp Glu Glu Ala Glu Leu Pro Ala Glu Leu Phe Gln Lys Lys Val Val
 77 82 87 92
 gct tcc ttt cca aga aca gtt ctg agc aca gga atg gat aac cgg tac 336
 Ala Ser Phe Pro Arg Thr Val Leu Ser Thr Gly Met Asp Asn Arg Tyr
 93 98 103 108

ctg gtg ttg gca gtc aat act gta cag aac aaa gag gga aac tgt gaa	384
Leu Val Leu Ala Val Asn Thr Val Gln Asn Lys Glu Gly Asn Cys Glu	
109 114 119 124	
aag cgc ctg gtc atc act gct tca cag tca cta gaa aat aaa gaa cta	432
Lys Arg Leu Val Ile Thr Ala Ser Gln Ser Leu Glu Asn Lys Glu Leu	
125 130 135 140	
tgc atc ctt agg aat gac tgg tgt tct gtt cca gta gag cca gga gat	480
Cys Ile Leu Arg Asn Asp Trp Cys Ser Val Pro Val Glu Pro Gly Asp	
141 146 151 156	
atc att cat ttg gag gga gac tgc aca tct gac act tgg ata ata gat	528
Ile Ile His Leu Glu Gly Asp Cys Thr Ser Asp Thr Trp Ile Ile Asp	
157 162 167 172	
aaa gat ttt gga tat ttg att ctg tat cca gac atg ctg att tct ggc	576
Lys Asp Phe Gly Tyr Leu Ile Leu Tyr Pro Asp Met Leu Ile Ser Gly	
173 178 183 188	
acc agc ata gcc agt agt att cga tgt atg aga aga gct gtc ctg agt	624
Thr Ser Ile Ala Ser Ser Ile Arg Cys Met Arg Arg Ala Val Leu Ser	
189 194 199 204	
gaa act ttt agg agc tct gat cca gcc aca cgc caa atg cta att ggt	672
Glu Thr Phe Arg Ser Ser Asp Pro Ala Thr Arg Gln Met Leu Ile Gly	
205 210 215 220	
acg gtt ctc cat gag gtg ttt caa aaa gcc ata aat aat agc ttt gcc	720
Thr Val Leu His Glu Val Phe Gln Lys Ala Ile Asn Asn Ser Phe Ala	
221 226 231 236	
cca gaa aag cta caa gaa ctt gct ttt caa aca att caa gaa ata aga	768
Pro Glu Lys Leu Gln Glu Leu Ala Phe Gln Thr Ile Gln Glu Ile Arg	
237 242 247 252	
cat ttg aag gaa atg tac cgc tta aat cta agt caa gat gaa ata aaa	816
His Leu Lys Glu Met Tyr Arg Leu Asn Leu Ser Gln Asp Glu Ile Lys	
253 258 263 268	
caa gaa gta gag gac tat ctt cct tcg ttt tgt aaa tgg gca gga gat	864
Gln Glu Val Glu Asp Tyr Leu Pro Ser Phe Cys Lys Trp Ala Gly Asp	
269 274 279 284	
ttc atg cat aaa aac act tcg act gac ttc cct cag atg cag ctc tct	912
Phe Met His Lys Asn Thr Ser Thr Asp Phe Pro Gln Met Gln Leu Ser	
285 290 295 300	
ctg cca agt gat aat agt aag gat aat tca aca tgt aac att gaa gtc	960
Leu Pro Ser Asp Asn Ser Lys Asp Asn Ser Thr Cys Asn Ile Glu Val	
301 306 311 316	
gtg aaa cca atg gat att gaa gaa agc att tgg tcc cct agg ttt gga	1008
Val Lys Pro Met Asp Ile Glu Glu Ser Ile Trp Ser Pro Arg Phe Gly	
317 322 327 332	

ttg aaa ggc aaa ata gat gtt aca gtt ggt gtg aaa ata cat cga ggg Leu Lys Gly Lys Ile Asp Val Thr Val Gly Val Lys Ile His Arg Gly 333 338 343 348	1056
tat aaa aca aaa tac aag ata atg ccg ctg gaa ctt aaa act ggc aaa Tyr Lys Thr Lys Tyr Lys Ile Met Pro Leu Glu Leu Lys Thr Gly Lys 349 354 359 364	1104
gaa tca aat tct att gaa cac cgt agt cag gtt gtt ctg tac act cta Glu Ser Asn Ser Ile Glu His Arg Ser Gln Val Val Leu Tyr Thr Leu 365 370 375 380	1152
cta agc caa gag aga aga gct gat cca gag gct ggc ttg ctt ctc tac Leu Ser Gln Glu Arg Arg Ala Asp Pro Glu Ala Gly Leu Leu Leu Tyr 381 386 391 396	1200
ctc aag act ggt cag atg tac cct gtg cct gcc aac cat cta gat aaa Leu Lys Thr Gly Gln Met Tyr Pro Val Pro Ala Asn His Leu Asp Lys 397 402 407 412	1248
aga gaa tta tta aag cta aga aac cag atg gca ttc tca ttg ttt cac Arg Glu Leu Leu Lys Leu Arg Asn Gln Met Ala Phe Ser Leu Phe His 413 418 423 428	1296
cgt att agc aaa tct gct act aga cag aag aca cag ctt gct tct ttg Arg Ile Ser Lys Ser Ala Thr Arg Gln Lys Thr Gln Leu Ala Ser Leu 429 434 439 444	1344
cca caa ata att gag gaa gag aaa act tgt aaa tat tgt tca caa att Pro Gln Ile Ile Glu Glu Glu Lys Thr Cys Lys Tyr Cys Ser Gln Ile 445 450 455 460	1392
ggc aat tgt gct ctt tat agc aga gca gtt gaa caa cag atg gat tgt Gly Asn Cys Ala Leu Tyr Ser Arg Ala Val Glu Gln Gln Met Asp Cys 461 466 471 476	1440
agt tca gtc cca att gtg atg ctg ccc aaa ata gaa gaa gaa acc cag Ser Ser Val Pro Ile Val Met Leu Pro Lys Ile Glu Glu Glu Thr Gln 477 482 487 492	1488
cat ctg aag caa aca cac tta gaa tat ttc agc ctt tgg tgt cta atg His Leu Lys Gln Thr His Leu Glu Tyr Phe Ser Leu Trp Cys Leu Met 493 498 503 508	1536
tta acc ctg gag tca caa tcg aag gat aat aaa aag aat cac caa aat Leu Thr Leu Glu Ser Gln Ser Lys Asp Asn Lys Lys Asn His Gln Asn 509 514 519 524	1584
atc tgg cta atg cct gct tcg gaa atg gag aag agt ggc agt tgc att Ile Trp Leu Met Pro Ala Ser Glu Met Glu Lys Ser Gly Ser Cys Ile 525 530 535 540	1632
gga aac ctg att aga atg gaa cat gta aag ata gtt tgt gat ggg caa Gly Asn Leu Ile Arg Met Glu His Val Lys Ile Val Cys Asp Gly Gln 541 546 551 556	1680
tat tta cat aat ttc caa tgt aaa cat ggt gcc ata cct gtc aca aat	1728

Tyr	Leu	His	Asn	Phe	Gln	Cys	Lys	His	Gly	Ala	Ile	Pro	Val	Thr	Asn	
557					562					567					572	
cta	atg	gca	ggg	gac	aga	gtt	att	gta	agt	gga	gaa	gaa	agg	tca	ctg	1776
Leu	Met	Ala	Gly	Asp	Arg	Val	Ile	Val	Ser	Gly	Glu	Glu	Arg	Ser	Leu	
573					578					583					588	
ttt	gct	ttg	tct	aga	gga	tat	gtg	aag	gag	att	aac	atg	aca	aca	gta	1824
Phe	Ala	Leu	Ser	Arg	Gly	Tyr	Val	Lys	Glu	Ile	Asn	Met	Thr	Thr	Val	
589					594					599					604	
act	tgt	tta	tta	gac	aga	aac	ttg	tcg	gtc	ctt	cca	gaa	tca	act	ttg	1872
Thr	Cys	Leu	Leu	Asp	Arg	Asn	Leu	Ser	Val	Leu	Pro	Glu	Ser	Thr	Leu	
605					610					615					620	
ttc	aga	tta	gac	caa	gaa	gaa	aaa	aat	tgt	gat	ata	gat	acc	cca	tta	1920
Phe	Arg	Leu	Asp	Gln	Glu	Glu	Lys	Asn	Cys	Asp	Ile	Asp	Thr	Pro	Leu	
621					626					631					636	
gga	aat	ctt	tcc	aaa	ttg	atg	gaa	aac	acg	ttt	gtc	agc	aaa	aaa	ctt	1968
Gly	Asn	Leu	Ser	Lys	Leu	Met	Glu	Asn	Thr	Phe	Val	Ser	Lys	Lys	Leu	
637					642					647					652	
cga	gat	tta	att	att	gac	ttt	cgt	gaa	cct	cag	ttt	ata	tcc	tac	ctt	2016
Arg	Asp	Leu	Ile	Ile	Asp	Phe	Arg	Glu	Pro	Gln	Phe	Ile	Ser	Tyr	Leu	
653					658					663					668	
agt	tct	gtt	ctt	cca	cat	gat	gca	aag	gat	aca	gtt	gcc	tgc	att	cta	2064
Ser	Ser	Val	Leu	Pro	His	Asp	Ala	Lys	Asp	Thr	Val	Ala	Cys	Ile	Leu	
669					674					679					684	
aag	ggg	ttg	aat	aag	cct	cag	agg	caa	gcg	atg	aaa	aag	gta	ctt	ctt	2112
Lys	Gly	Leu	Asn	Lys	Pro	Gln	Arg	Gln	Ala	Met	Lys	Lys	Val	Leu	Leu	
685					690					695					700	
tca	aaa	gac	tac	aca	ctc	atc	gtg	ggg	atg	cct	ggg	aca	gga	aaa	aca	2160
Ser	Lys	Asp	Tyr	Thr	Leu	Ile	Val	Gly	Met	Pro	Gly	Thr	Gly	Lys	Thr	
701					706					711					716	
act	acg	ata	tgt	act	ctc	gta	aga	att	ctc	tac	gcc	tgt	ggg	ttt	agc	2208
Thr	Thr	Ile	Cys	Thr	Leu	Val	Arg	Ile	Leu	Tyr	Ala	Cys	Gly	Phe	Ser	
717					722					727					732	
gtt	ttg	ttg	acc	agc	tat	aca	cac	tct	gct	gtt	gac	aat	att	ctt	ttg	2256
Val	Leu	Leu	Thr	Ser	Tyr	Thr	His	Ser	Ala	Val	Asp	Asn	Ile	Leu	Leu	
733					738					743					748	
aag	tta	gcc	aag	ttt	aaa	ata	gga	ttt	ttg	cgt	ttg	ggg	cag	att	cag	2304
Lys	Leu	Ala	Lys	Phe	Lys	Ile	Gly	Phe	Leu	Arg	Leu	Gly	Gln	Ile	Gln	
749					754					759					764	
aag	gtt	cat	cca	gct	atc	cag	caa	ttt	aca	gag	caa	gaa	att	tgc	aga	2352
Lys	Val	His	Pro	Ala	Ile	Gln	Gln	Phe	Thr	Glu	Gln	Glu	Ile	Cys	Arg	
765					770					775					780	
tca	aag	tcc	att	aaa	tcc	tta	gct	ctt	cta	gaa	gaa	ctc	tac	aat	agt	2400
Ser	Lys	Ser	Ile	Lys	Ser	Leu	Ala	Leu	Leu	Glu	Glu	Leu	Tyr	Asn	Ser	

781	786	791	796	
caa ctt ata gtt gca	aca aca tgt atg gga	ata aac cat cca	ata ttt	2448
Gln Leu Ile Val Ala	Thr Thr Cys Met Gly	Ile Asn His Pro Ile	Phe	
797	802	807	812	
tcc cgt aaa att ttt	gat ttt tgt att gtg	gat gaa gcc tct caa	att	2496
Ser Arg Lys Ile Phe	Asp Phe Cys Ile Val	Asp Glu Ala Ser Gln	Ile	
813	818	823	828	
agc caa cca att tgt	ctg ggc ccc ctt ttt	ttt tca cgg aga ttt	gtg	2544
Ser Gln Pro Ile Cys	Leu Gly Pro Leu Phe	Phe Ser Arg Arg Phe	Val	
829	834	839	844	
tta gtg ggg gac cat	cag cag ctt cct ccc	ctg gtg cta aac cgt	gaa	2592
Leu Val Gly Asp His	Gln Gln Leu Pro Pro	Leu Val Leu Asn Arg	Glu	
845	850	855	860	
gca aga gct ctt ggc	atg agt gaa agc tta	ttc aag agg ctg gag	cag	2640
Ala Arg Ala Leu Gly	Met Ser Glu Ser Leu	Phe Lys Arg Leu Glu	Gln	
861	866	871	876	
aat aag agt gct gtt	gta cag tta acc gtg	cag tac aga atg aac	agt	2688
Asn Lys Ser Ala Val	Val Gln Leu Thr Val	Gln Tyr Arg Met Asn	Ser	
877	882	887	892	
aaa att atg tcc tta	agt aat aag ctg acc	tat gag ggc aag ctg	gag	2736
Lys Ile Met Ser Leu	Ser Asn Lys Leu Thr	Tyr Glu Gly Lys Leu	Glu	
893	898	903	908	
tgt gga tca gac aaa	gtg gcc aat gca gtg	ata aac cta cgt cac	ttt	2784
Cys Gly Ser Asp Lys	Val Ala Asn Ala Val	Ile Asn Leu Arg His	Phe	
909	914	919	924	
aaa gat gtg aag ctg	gaa ctg gaa ttt tat	gct gac tat tct gat	aat	2832
Lys Asp Val Lys Leu	Glu Leu Glu Phe Tyr	Ala Asp Tyr Ser Asp	Asn	
925	930	935	940	
cct tgg ttg atg gga	gta ttt gaa ccc aac	aat cct gtt tgt ttc	ctt	2880
Pro Trp Leu Met Gly	Val Phe Glu Pro Asn	Asn Pro Val Cys Phe	Leu	
941	946	951	956	
aat aca gac aag gtt	cca gcg cca gaa caa	gtt gaa aaa ggt ggt	gtg	2928
Asn Thr Asp Lys Val	Pro Ala Pro Glu Gln	Val Glu Lys Gly Gly	Val	
957	962	967	972	
agc aat gta aca gaa	gcc aaa ctc ata gtt	ttc cta acc tcc att	ttt	2976
Ser Asn Val Thr Glu	Ala Lys Leu Ile Val	Phe Leu Thr Ser Ile	Phe	
973	978	983	988	
gtt aag gct gga tgc	agt ccc tct gat att	ggt att att gca ccg	tac	3024
Val Lys Ala Gly Cys	Ser Pro Ser Asp Ile	Gly Ile Ile Ala Pro	Tyr	
989	994	999	1004	
agg cag caa tta aag	atc atc aat gat tta	ttg gca cgt tct att	ggg	3072
Arg Gln Gln Leu Lys	Ile Ile Asn Asp Leu	Leu Ala Arg Ser Ile	Gly	
1005	1010	1015	1020	

tgagtgttaa atatgttaaa atttttatctt ctacctcatg tgttttttta aattattact 4314
tgaagttttt tatttaataa attttttcta ctaatgg 4351

<210> 348
<211> 4062
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (25) .. (2976)

<400> 348
tcactccaac ggctgccggg actg atg cac aac tta cag aca ttt ttg ttg 51
Met His Asn Leu Gln Thr Phe Leu Leu
1 5

gat gga aac ttt ctc caa tcc ctt cct gct gag ttg gag aac atg aag 99
Asp Gly Asn Phe Leu Gln Ser Leu Pro Ala Glu Leu Glu Asn Met Lys
10 15 20 25

cag ctt agt tat ctg ggt ctt tct ttc aat gaa ttt act gac att ccc 147
Gln Leu Ser Tyr Leu Gly Leu Ser Phe Asn Glu Phe Thr Asp Ile Pro
26 31 36 41

gaa gta ttg gag aaa ttg act gct gtg gat aaa ctt tgt atg tct gga 195
Glu Val Leu Glu Lys Leu Thr Ala Val Asp Lys Leu Cys Met Ser Gly
42 47 52 57

aac tgt gtg gag acc ctt agg cta cag gct tta aga aaa atg cct cac 243
Asn Cys Val Glu Thr Leu Arg Leu Gln Ala Leu Arg Lys Met Pro His
58 63 68 73

att aaa cat gtg gat cta agg ttg aac gta att agg aag ctg ata gca 291
Ile Lys His Val Asp Leu Arg Leu Asn Val Ile Arg Lys Leu Ile Ala
74 79 84 89

gat gaa gtg gac ttt cta cag cat gtt act cag ctt gac cta cga gac 339
Asp Glu Val Asp Phe Leu Gln His Val Thr Gln Leu Asp Leu Arg Asp
90 95 100 105

aat aag ctt ggt gat cta gat gct atg att ttc aac aac att gaa gtt 387
Asn Lys Leu Gly Asp Leu Asp Ala Met Ile Phe Asn Asn Ile Glu Val
106 111 116 121

tta cac tgt gaa agg aat caa ctg gtc aca tta gac atc tgt ggc tat 435
Leu His Cys Glu Arg Asn Gln Leu Val Thr Leu Asp Ile Cys Gly Tyr
122 127 132 137

ttc cta aaa gcg ctc tat gcc tct tct aat gaa ctt gtt caa ctt gat 483
Phe Leu Lys Ala Leu Tyr Ala Ser Ser Asn Glu Leu Val Gln Leu Asp
138 143 148 153

gtt tac cca gtt cca aat tat ctg tcc tac atg gat gtt tca agg aac	531
Val Tyr Pro Val Pro Asn Tyr Leu Ser Tyr Met Asp Val Ser Arg Asn	
154 159 164 169	
cgc tta gaa aat gtg cct gag tgg gta tgt gaa agc cga aag cta gaa	579
Arg Leu Glu Asn Val Pro Glu Trp Val Cys Glu Ser Arg Lys Leu Glu	
170 175 180 185	
gtt ttg gat att ggc cat aat caa ata tgt gaa ctt cct gcc cgc tta	627
Val Leu Asp Ile Gly His Asn Gln Ile Cys Glu Leu Pro Ala Arg Leu	
186 191 196 201	
ttt tgt aat agc agt ctc cgg aaa cta ctg gca gga cac aac cag ttg	675
Phe Cys Asn Ser Ser Leu Arg Lys Leu Leu Ala Gly His Asn Gln Leu	
202 207 212 217	
gca agg ctg cct gaa agg cta gaa aga acc tcg gtg gag gtc ttg gat	723
Ala Arg Leu Pro Glu Arg Leu Glu Arg Thr Ser Val Glu Val Leu Asp	
218 223 228 233	
gtg caa cac aac cag ctc ctt gag ctc cca cct aac ctt ctg atg aag	771
Val Gln His Asn Gln Leu Leu Glu Leu Pro Pro Asn Leu Leu Met Lys	
234 239 244 249	
gct gac agc ctg aga ttc ctg aac gcc tct gcg aac aaa ctg gaa agc	819
Ala Asp Ser Leu Arg Phe Leu Asn Ala Ser Ala Asn Lys Leu Glu Ser	
250 255 260 265	
ctt cct cca gcc acg ctt tcc gaa gag aca aac agt atc tta caa gag	867
Leu Pro Pro Ala Thr Leu Ser Glu Glu Thr Asn Ser Ile Leu Gln Glu	
266 271 276 281	
ttg tat ttg aca aat aac agc ctc aca gac aaa tgt gtg ccc ttg tta	915
Leu Tyr Leu Thr Asn Asn Ser Leu Thr Asp Lys Cys Val Pro Leu Leu	
282 287 292 297	
acg gga cac ccc cat ttg aag atc ctt cac atg gcc tat aac cga ctt	963
Thr Gly His Pro His Leu Lys Ile Leu His Met Ala Tyr Asn Arg Leu	
298 303 308 313	
cag agt ttt cca gca agt aaa atg gcg aaa ctg gag gaa ctt gaa gaa	1011
Gln Ser Phe Pro Ala Ser Lys Met Ala Lys Leu Glu Glu Leu Glu Glu	
314 319 324 329	
att gat ctc agt ggg aat aag ctg aaa gcc atc cca aca acg atc atg	1059
Ile Asp Leu Ser Gly Asn Lys Leu Lys Ala Ile Pro Thr Thr Ile Met	
330 335 340 345	
aat tgc agg cgc atg cac acc gtg att gct cac tcc aac tgc atc gag	1107
Asn Cys Arg Arg Met His Thr Val Ile Ala His Ser Asn Cys Ile Glu	
346 351 356 361	
gtc ttt ccc gaa gtt atg cag ctc cca gag atc aag tgt gtg gac ctg	1155
Val Phe Pro Glu Val Met Gln Leu Pro Glu Ile Lys Cys Val Asp Leu	
362 367 372 377	
agc tgt aat gag cta agt gaa gtc aca tta cca gaa aac ctg cct ccc	1203

Ser Cys Asn Glu Leu Ser Glu Val Thr Leu Pro Glu Asn Leu Pro Pro	
378 383 388 393	
aaa ctg cag gag cta gac ctg act gga aac ccg cgc ctt gtc ctt gat	1251
Lys Leu Gln Glu Leu Asp Leu Thr Gly Asn Pro Arg Leu Val Leu Asp	
394 399 404 409	
cac aaa acc ctg gaa cta ctg aat aat atc cgc tgt ttc aag att gat	1299
His Lys Thr Leu Glu Leu Leu Asn Asn Ile Arg Cys Phe Lys Ile Asp	
410 415 420 425	
cag cct tct aca gga gac gct tcc gga gcc cca gct gta tgg agt cat	1347
Gln Pro Ser Thr Gly Asp Ala Ser Gly Ala Pro Ala Val Trp Ser His	
426 431 436 441	
ggt tac act gaa gct tcg ggg gta aaa aac aag ttg tgt gtc gca gcc	1395
Gly Tyr Thr Glu Ala Ser Gly Val Lys Asn Lys Leu Cys Val Ala Ala	
442 447 452 457	
ctg tcg gtg aat aac ttc tgt gac aac cgc gaa gcc ctg tat ggt gtg	1443
Leu Ser Val Asn Asn Phe Cys Asp Asn Arg Glu Ala Leu Tyr Gly Val	
458 463 468 473	
ttt gac gga gac cgg aat gtg gag gtg ccc tac ctt ctc cag tgc act	1491
Phe Asp Gly Asp Arg Asn Val Glu Val Pro Tyr Leu Leu Gln Cys Thr	
474 479 484 489	
atg agt gac att ttg gct gaa gag ctg caa aaa aaa aca aaa aac gaa	1539
Met Ser Asp Ile Leu Ala Glu Glu Leu Gln Lys Lys Thr Lys Asn Glu	
490 495 500 505	
gaa gaa tac atg gtc aat aca ttc att gtc atg caa agg aaa ctt gga	1587
Glu Glu Tyr Met Val Asn Thr Phe Ile Val Met Gln Arg Lys Leu Gly	
506 511 516 521	
act gct ggg cag aag ctt ggt ggt gcc gct gtc ctt tgt cat atc aag	1635
Thr Ala Gly Gln Lys Leu Gly Gly Ala Ala Val Leu Cys His Ile Lys	
522 527 532 537	
cat gac cct gtg gat cca gga gga tcc ttc acc ttg acc tct gct aat	1683
His Asp Pro Val Asp Pro Gly Gly Ser Phe Thr Leu Thr Ser Ala Asn	
538 543 548 553	
gtg ggc aag tgc caa aca gtt ctc tgt cga aat gga aag ccg ctg cct	1731
Val Gly Lys Cys Gln Thr Val Leu Cys Arg Asn Gly Lys Pro Leu Pro	
554 559 564 569	
ctg tcc aga tct tac atc atg agc tgt gaa gaa gag ctg aag agg att	1779
Leu Ser Arg Ser Tyr Ile Met Ser Cys Glu Glu Leu Lys Arg Ile	
570 575 580 585	
aaa cag cac aag gcc att atc act gag gat ggc aag gtg aac gga gtg	1827
Lys Gln His Lys Ala Ile Ile Thr Glu Asp Gly Lys Val Asn Gly Val	
586 591 596 601	
act gag tcc acg cgc atc ctg ggc tac acc ttc ctc cat ccc agt gtg	1875
Thr Glu Ser Thr Arg Ile Leu Gly Tyr Thr Phe Leu His Pro Ser Val	

602	607	612	617	
gtg cct cgc ccc cac	gtg cag tcc gtg ctc	ctg act ccc cag gat	gag	1923
Val Pro Arg Pro His	Val Gln Ser Val Leu	Leu Thr Pro Gln Asp	Glu	
618	623	628	633	
ttc ttc atc cta ggc	agt aag ggg ttg tgg	gac agc ctg tcc gtc	gag	1971
Phe Phe Ile Leu Gly	Ser Lys Gly Leu Trp	Asp Ser Leu Ser Val	Glu	
634	639	644	649	
gag gcc gtg gaa gcc	gtg cgc aac gtg ccc	gat gcc ctg gct gct	gcc	2019
Glu Ala Val Glu Ala	Val Arg Asn Val Pro	Asp Ala Leu Ala Ala	Ala	
650	655	660	665	
aag aag ctg tgt acc	ctg gcc cag agc tac	ggc tgc cac gac agc	atc	2067
Lys Lys Leu Cys Thr	Leu Ala Gln Ser Tyr	Gly Cys His Asp Ser	Ile	
666	671	676	681	
agc gct gtg gtg gtg	cag ctc agt gtc act	gag gac agc ttc tgc	tgc	2115
Ser Ala Val Val Val	Gln Leu Ser Val Thr	Glu Asp Ser Phe Cys	Cys	
682	687	692	697	
tgc gag ctc agc gcc	ggg ggt gct gtg cca	cca ccc agt cct ggc	atc	2163
Cys Glu Leu Ser Ala	Gly Gly Ala Val Pro	Pro Pro Ser Pro Gly	Ile	
698	703	708	713	
ttt cct ccc tca gtg	aac atg gtg atc aag	gat cgg ccc tca gat	ggg	2211
Phe Pro Pro Ser Val	Asn Met Val Ile Lys	Asp Arg Pro Ser Asp	Gly	
714	719	724	729	
ctg ggc gtg ccg tcc	tcc agc agc ggc atg	gct tcc gag att agc	agt	2259
Leu Gly Val Pro Ser	Ser Ser Ser Gly Met	Ala Ser Glu Ile Ser	Ser	
730	735	740	745	
gag ctc tcc act tct	gag atg agc agc gag	gtg ggg tca aca gcc	tcc	2307
Glu Leu Ser Thr Ser	Glu Met Ser Ser Glu	Val Gly Ser Thr Ala	Ser	
746	751	756	761	
gat gag ccc ccg ccc	gga gcc cta agc gag	aac agc cct gcc tac	ccc	2355
Asp Glu Pro Pro Pro	Gly Ala Leu Ser Glu	Asn Ser Pro Ala Tyr	Pro	
762	767	772	777	
agt gag cag cgc tgc	atg ctc cac ccc atc	tgt ctg tcc aac tcc	ttc	2403
Ser Glu Gln Arg Cys	Met Leu His Pro Ile	Cys Leu Ser Asn Ser	Phe	
778	783	788	793	
cag cgc cag cta tcc	agc gcc acg ttc tct	agc gcc ttc tcc gac	aac	2451
Gln Arg Gln Leu Ser	Ser Ala Thr Phe Ser	Ser Ala Phe Ser Asp	Asn	
794	799	804	809	
ggc ctt gac agt gac	gat gag gag ccc atc	gag ggc gtc ttc acc	aac	2499
Gly Leu Asp Ser Asp	Asp Glu Glu Pro Ile	Glu Gly Val Phe Thr	Asn	
810	815	820	825	
ggc agc cgg gtg gag	gtg gag gtg gac atc	cac tgc agc cgg gcc	aag	2547
Gly Ser Arg Val Glu	Val Glu Val Asp Ile	His Cys Ser Arg Ala	Lys	
826	831	836	841	

gag aag gag aaa cag cag cac ctg ctt cag gtg cca gca gag gcc agt	2595
Glu Lys Glu Lys Gln Gln His Leu Leu Gln Val Pro Ala Glu Ala Ser	
842 847 852 857	
gat gag ggc att gtc atc agc gcc aac gag gat gag cca ggt ctg ccc	2643
Asp Glu Gly Ile Val Ile Ser Ala Asn Glu Asp Glu Pro Gly Leu Pro	
858 863 868 873	
agg aag gca gac ttc tct gcc gtt ggg acc att ggg cgc cgg agg gcc	2691
Arg Lys Ala Asp Phe Ser Ala Val Gly Thr Ile Gly Arg Arg Arg Ala	
874 879 884 889	
aat ggc tct gtt gcg ccc cag gaa agg agc cac aat ^h gtg ata gag gtg	2739
Asn Gly Ser Val Ala Pro Gln Glu Arg Ser His Asn Val Ile Glu Val	
890 895 900 905	
gct aca gac gca cct ctt cga aag cct gga ggc tat ttt gct gcc ccg	2787
Ala Thr Asp Ala Pro Leu Arg Lys Pro Gly Gly Tyr Phe Ala Ala Pro	
906 911 916 921	
gct cag ccg gat cct gat gat cag ttt atc ata ccc ccg gag ctg gaa	2835
Ala Gln Pro Asp Pro Asp Asp Gln Phe Ile Ile Pro Pro Glu Leu Glu	
922 927 932 937	
gag gag gtc aaa gaa atc atg aag cat cac cag gag caa cag cag cag	2883
Glu Glu Val Lys Glu Ile Met Lys His His Gln Glu Gln Gln Gln	
938 943 948 953	
cag cag ccg cca cca ccc cct cag ctc cag ccg cag ctg ccg cgg cac	2931
Gln Gln Pro Pro Pro Pro Pro Gln Leu Gln Pro Gln Leu Pro Arg His	
954 959 964 969	
tac cag ctg gac cag ctg cca gat tat tac gac acg cca cta tga ccc	2979
Tyr Gln Leu Asp Gln Leu Pro Asp Tyr Tyr Asp Thr Pro Leu *	
970 975 980	
agccgagctg tttaacaaat aaactaacca caaaagactg agttgcaaga gtctcccagg	3039
ctcacattaa accagggggtt ttactccaca tccttcccc agacactgtt cccaacctgt	3099
catcgagct aatctgtagg ttctctttct ttgggttatt tttttaagta atcaccactt	3159
tcttctagtg atgctttacc aatatgattt acatttgta acttctcccc ctaacatatc	3219
agatatgtaa agacaaagaa caaaagggtt aatatattac agagaaacag ttaatgataa	3279
tgtaatatatt tttaaaatgg ctttttggtt tttggttgga aggcagggca ggctgccgtt	3339
gctaaatgat ttaataatat tgtaattctg tatttctttg gggggaaaag gcttttggtt	3399
tgttttggtt tgttttggtt tgttttgtc ttgaaaataa tagacatttg tagaatatgg	3459
agactaactc ctaggagttg ctttactctg tcagggtgact taagtcactg ggattcacta	3519
atcttctctg agagaacagc tgattgagaa tttccattgt aaatagctca gtgttgtata	3579

gtgaggctta cgatgttttg tagtcttggc gtaaggacac agcccaagta actgacgttt 3639
 cccctcccc tccctctga ggagcctgcc tgcctcacia ctcaccctca cttcactgaa 3699
 tgaggaggct gagcagctgc agtgtttctg tccggaggaa atggatctta ggccactgga 3759
 caagaacctg cacccaaggg ccttgaaccc attttcctcc cctgtcccag ccttcccact 3819
 ttgacagaca cttttaactg tgttccttac tgctgccaca atcagcatgg ttgtatagtg 3879
 cccattagg ccatttacat acccagagtt atactcaagc agaatgcaca aatggacatg 3939
 tcataatttt tggtacaata aatatgaaat ttacaagtaa aaaaaaaaaa aaagggcggc 3999
 cgctctagag tatccctcga ggggcccag cttacgcgta ccagctttc ttgtacaaag 4059
 tgg 4062

<210> 349
 <211> 4139
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (260) .. (2164)

<400> 349
 ccatgcggtta ccgggtccgga attcccgggt cgacccaagc gtccgagggg ggaacacgtg 60
 ggcgccggct gccggggcgg cgatcttagg gaactagggt cacctggaga gccgcccacc 120
 gtctctgccc gctcgactcc tccgcccggg ccgctcggcc ggtccagccg cggccggcgc 180
 ctggctgtga ggtggattcc cggcccagtc tgaccatctc cctccagttt ttccacttcg 240
 ttcggacctt ctcataact atg tcc acc ctc tac gtc tcc cct cac cca gat 292
 Met Ser Thr Leu Tyr Val Ser Pro His Pro Asp
 1 5
 gcc ttc ccc agc ctc cga gcc ctc ata gcc gct cgc tat ggg gag gct 340
 Ala Phe Pro Ser Leu Arg Ala Leu Ile Ala Ala Arg Tyr Gly Glu Ala
 12 17 22 27
 ggg gag ggt ccc gga tgg gga gga gcc cac ccc cgc atc tgt ctc cag 388
 Gly Glu Gly Pro Gly Trp Gly Gly Ala His Pro Arg Ile Cys Leu Gln
 28 33 38 43
 cca ccc ccg act agc agg act agc ttt ccc cca ccc cgc ctg ccg gcc 436
 Pro Pro Pro Thr Ser Arg Thr Ser Phe Pro Pro Pro Arg Leu Pro Ala
 44 49 54 59
 ctg gag cag ggg ccc ggt ggg ctc tgg gtg tgg ggg gcc acg gct gtg 484
 Leu Glu Gln Gly Pro Gly Gly Leu Trp Val Trp Gly Ala Thr Ala Val

60	65	70	75	
gcc cag ctg ctg tgg cca gca ggc ctg ggg ggc cca ggg ggc agc cgg				532
Ala Gln Leu Leu Trp Pro Ala Gly Leu Gly Gly Pro Gly Gly Ser Arg				
76	81	86	91	
gcg gct gtc ctt gtc caa cag tgg gtc agt tac gcc gac acg gag tta				580
Ala Ala Val Leu Val Gln Gln Trp Val Ser Tyr Ala Asp Thr Glu Leu				
92	97	102	107	
ata cca gct gcc tgt gga gca acg ctg ccg gcc ctg gga ctc cga agc				628
Ile Pro Ala Ala Cys Gly Ala Thr Leu Pro Ala Leu Gly Leu Arg Ser				
108	113	118	123	
tcg gcc cag gac ccc cag gct gtg ctg ggg gcc ctg ggc agg gcc ctg				676
Ser Ala Gln Asp Pro Gln Ala Val Leu Gly Ala Leu Gly Arg Ala Leu				
124	129	134	139	
agc ccc ttg gag gag tgg ctt cgg ctg cac acc tac ttg gcc ggg gag				724
Ser Pro Leu Glu Glu Trp Leu Arg Leu His Thr Tyr Leu Ala Gly Glu				
140	145	150	155	
gcc ccc act ctg gct gac ctg gcg gct gtc aca gcc ttg ctg ctg cct				772
Ala Pro Thr Leu Ala Asp Leu Ala Ala Val Thr Ala Leu Leu Leu Pro				
156	161	166	171	
ttc cga tac gtc cta gac cca cct gcc cgc cgg atc tgg aat aat gtg				820
Phe Arg Tyr Val Leu Asp Pro Pro Ala Arg Arg Ile Trp Asn Asn Val				
172	177	182	187	
act cgc tgg ttt gtc acg tgt gtc cgg cag cca gaa ttc cga gcc gtg				868
Thr Arg Trp Phe Val Thr Cys Val Arg Gln Pro Glu Phe Arg Ala Val				
188	193	198	203	
cta gga gaa gtg gtt cta tac tca gga gcc agg cct ctc tct cat cag				916
Leu Gly Glu Val Val Leu Tyr Ser Gly Ala Arg Pro Leu Ser His Gln				
204	209	214	219	
cca ggc ccc gag gct cct gcc ctc cca aag aca gct gct cag ctc aag				964
Pro Gly Pro Glu Ala Pro Ala Leu Pro Lys Thr Ala Ala Gln Leu Lys				
220	225	230	235	
aaa gag gca aag aaa cgg gag aag cta gag aaa ttc caa cag aag cag				1012
Lys Glu Ala Lys Lys Arg Glu Lys Leu Glu Lys Phe Gln Gln Lys Gln				
236	241	246	251	
aag atc caa cag cag cag cca cct cca ggg gag aag aaa cca aaa cca				1060
Lys Ile Gln Gln Gln Gln Pro Pro Pro Gly Glu Lys Lys Pro Lys Pro				
252	257	262	267	
gag aag agg gag aaa cgg gat cct ggg gtc att acc tat gac ctc cca				1108
Glu Lys Arg Glu Lys Arg Asp Pro Gly Val Ile Thr Tyr Asp Leu Pro				
268	273	278	283	
acc cca ccc ggg gaa aag aaa gat gtc agt ggc ccc atg ccc gac tcc				1156
Thr Pro Pro Gly Glu Lys Lys Asp Val Ser Gly Pro Met Pro Asp Ser				
284	289	294	299	

tac agc cct cgg tat gtg gag gct gcc tgg tac cct tgg tgg gag cag	1204
Tyr Ser Pro Arg Tyr Val Glu Ala Ala Trp Tyr Pro Trp Trp Glu Gln	
300 305 310 315	
cag ggc ttc ttc aag cca gag tat ggg cgt cct aat gtg tca gca gca	1252
Gln Gly Phe Phe Lys Pro Glu Tyr Gly Arg Pro Asn Val Ser Ala Ala	
316 321 326 331	
aat ccc cga ggt gtc ttc atg atg tgc atc cca ccc ccc aat gtg aca	1300
Asn Pro Arg Gly Val Phe Met Met Cys Ile Pro Pro Pro Asn Val Thr	
332 337 342 347	
ggc tcc ctg cac ctg ggc cat gca ctc acc aac gcc atc cag gac tcc	1348
Gly Ser Leu His Leu Gly His Ala Leu Thr Asn Ala Ile Gln Asp Ser	
348 353 358 363	
ctg act cga tgg cac cgc atg cgt ggg gag acc acc ctg tgg aac cct	1396
Leu Thr Arg Trp His Arg Met Arg Gly Glu Thr Thr Leu Trp Asn Pro	
364 369 374 379	
ggc tgt gac cat gca ggt att gcc acc cag gtg gtg gtg gag aag aag	1444
Gly Cys Asp His Ala Gly Ile Ala Thr Gln Val Val Val Glu Lys Lys	
380 385 390 395	
cta tgg cgt gag cag gga ctg agc cgg cac cag ctg ggc cgc gag gcc	1492
Leu Trp Arg Glu Gln Gly Leu Ser Arg His Gln Leu Gly Arg Glu Ala	
396 401 406 411	
ttt cta cag gaa gtc tgg aag tgg aag gag gag aaa ggt gac cgg att	1540
Phe Leu Gln Glu Val Trp Lys Trp Lys Glu Glu Lys Gly Asp Arg Ile	
412 417 422 427	
tac cac cag ttg aag aag ctt ggc agc tcc ttg gac tgg gat cga gcc	1588
Tyr His Gln Leu Lys Lys Leu Gly Ser Ser Leu Asp Trp Asp Arg Ala	
428 433 438 443	
tgt ttc acc atg gac cct aaa ctc tca gca gct gtg aca gag gcc ttt	1636
Cys Phe Thr Met Asp Pro Lys Leu Ser Ala Ala Val Thr Glu Ala Phe	
444 449 454 459	
gtc cgg ctt cac gag gaa ggc atc atc tat cgc agt acc cgc ctt gtt	1684
Val Arg Leu His Glu Glu Gly Ile Ile Tyr Arg Ser Thr Arg Leu Val	
460 465 470 475	
aac tgg tcc tgc acc ctc aac tcc gcc atc tct gac att gag gtg gat	1732
Asn Trp Ser Cys Thr Leu Asn Ser Ala Ile Ser Asp Ile Glu Val Asp	
476 481 486 491	
aag aag gag ctg aca ggt cgc acc ctg ctc tcc gtg cct ggc tac aag	1780
Lys Lys Glu Leu Thr Gly Arg Thr Leu Leu Ser Val Pro Gly Tyr Lys	
492 497 502 507	
gag aag gtg gag ttc ggg gtc ctc gtg tcc ttt gcc tat aag gtc caa	1828
Glu Lys Val Glu Phe Gly Val Leu Val Ser Phe Ala Tyr Lys Val Gln	
508 513 518 523	

ggc tca gat agc gac gag gag gtg gtg gtg gca aca act cgg atc gag	1876
Gly Ser Asp Ser Asp Glu Glu Val Val Val Ala Thr Thr Arg Ile Glu	
524 529 534 539	
aca atg ctg gga gat gtg gct gta gct gtg cac ccc aaa gat acc aga	1924
Thr Met Leu Gly Asp Val Ala Val Ala Val His Pro Lys Asp Thr Arg	
540 545 550 555	
tac cag cac ctg aag ggg aag aac gtg atc cac cca ttc ctg tct cgg	1972
Tyr Gln His Leu Lys Gly Lys Asn Val Ile His Pro Phe Leu Ser Arg	
556 561 566 571	
agc ctt ccc att gtc ttc gat gaa ttt gtg gac atg gac ttt ggc aca	2020
Ser Leu Pro Ile Val Phe Asp Glu Phe Val Asp Met Asp Phe Gly Thr	
572 577 582 587	
ggg gct gtg aag atc acc ccc gca cat gac caa aat gac tat gaa gtt	2068
Gly Ala Val Lys Ile Thr Pro Ala His Asp Gln Asn Asp Tyr Glu Val	
588 593 598 603	
ggg cag cgg cac ggg ctg gag gcc atc agc atc atg gac tcc cgg ggg	2116
Gly Gln Arg His Gly Leu Glu Ala Ile Ser Ile Met Asp Ser Arg Gly	
604 609 614 619	
ggc cct cat caa tgt gcc tcc gcc ttt cct ggg cct gcc cag gtt tga	2164
Gly Pro His Gln Cys Ala Ser Ala Phe Pro Gly Pro Ala Gln Val *	
620 625 630 635	
ggccaggaaa gcggtgctgg tggcgctgaa ggagcgggga ctgttccgtg gcattgagga	2224
caaccccatg gtggtgccac tttgcaaccg gtcgaaggac gtggtagagc ctctgctgcg	2284
gccgcagtgg tacgttcgct gcggggagat ggcccaggct gccagcgccg ctgtgactcg	2344
gggtgacctc cgcatacctgc ctgaggccca tcagcgacata tggcatgcct ggatggacaa	2404
catccgggag tgggtgcatct ccaggcagct gtggtggggc catcgcatcc cagcctactt	2464
tgtcactgtc agtgaccag cgggtgcccc tggggaggac cctgatgggc ggtactgggt	2524
gagtggacgc aatgaggcgg agggccggga gaaggcagcc aaggagtctg gagtgtcccc	2584
tgacaagatc agtctccagc aagatgagga tgtattggat acctggttct cctctggcct	2644
cttcccccta tccatttttg gctggcccaa ccagtcagaa gacctgagtg tgttctaccc	2704
cgggacactg ctggagaccg gtcatacat cctcttcttc tgggtggccc ggatgggcat	2764
gctgggcctg aagctcacgg gcaggctgcc ctttagagag gtctacctcc atgccatcgt	2824
gcgagatgct cacggccgga agatgagcaa gtctctaggg aatgtcatcg atccccctgga	2884
cgtcatctat ggaatctccc tgcagggcct ccacaaccag ctgctgaaca gcaacctgga	2944
tcccagcgag gtggagaagg ccaaagaagg gcagaaagct gacttcccag cggggattcc	3004
tgaatgtggc accgatgctc tccggttttg attatgtgcc tacatgtccc agggtcgtga	3064

catcaacctg gatgtgaacc ggatactggg ttaccgccac ttctgcaaca agctctggaa	3124
tgccaccaag tttgcccttc gtggccttgg gaagggtttt gtgccctcac ccacctcca	3184
gcccggaggc catgagagcc tgggtggaccg ctggatccgc agccgcctga cagaggctgt	3244
gaggctcagc aatcaaggct tccaggccta cgacttcccg gccgtcacca ctgcccagta	3304
cagcttctgg ctctatgagc tctgtgatgt ctacttggag tgcctgaaac ctgtactgaa	3364
tggggtggac cagggtggcag ctgagtgtgc ccgccagacc ctgtacactt gcctggacgt	3424
tggcctgagg ctgctctcac ccttcatgcc cttcgtgacg gaggagctgt tccagaggct	3484
gcccggagg atgccgcaag ctccccctag cctctgtgtt accccctacc cggagccctc	3544
agagtgtccc tggaaggacc ccgaggcaga agccgcctt gagctggcgc taagcatcac	3604
gcgagccgtg cgctccctgc gggccgacta caacctcacc cggatccggc ctgactgttt	3664
cctggaagtg gcggatgagg ccacgggcgc cctggcatcg gcggtgtcgg gctacgtgca	3724
ggccctggcc agcgcagggt tgggtggctgt tctggccctg ggggctcccg cccccagg	3784
ttgcgctgtg gctctggctt ctgatecgtg ctccatccac ctgcagcttc aggggctgg	3844
ggacctgca cgggagctgg gcaagctgca agccaagcga gttgaggccc agcggcaggc	3904
ccagcgtctg cgggaacgcc gtgctgcctc gggctatcct gtcaagggtgc cgctcgaagt	3964
ccaggaggca gatgaagcca agctccaaca gacagaagca gagctcagga aggtggatga	4024
ggccatcgcc ctattccaga agatgctgtg atccaccacc cagcttcacc cctcaccccc	4084
agcggctcac catggggatg gcagcaataa aatattttcc cacaaaaaaa aaaaa	4139

<210> 350

<211> 2461

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232) .. (2358)

<400> 350

ataggggaatt tggccctcga gcagtagctt cggcacgagg gcatgacatt tttggcacia	60
tgcaactgtg gactggcac ttatttcagt gaagaaaaac tttgtggttc tatggcattc	120
atcatttgac aaatgcaagc atcttcctta tcaatcagct cctattgaac ttactagcac	180
tgactgtgga atccttaagg gccattaca tttctgaaga agaaagctaa g atg aag	237

Met Lys
1

gac atg cca ctc cga att cat gtg cta ctt ggc cta gct atc act aca	285
Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile Thr Thr	
3 8 13 18	
cta gta caa gct gta gat aaa aaa gtg gat tgt cca cgg tta tgt acg	333
Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu Cys Thr	
19 24 29 34	
tgt gaa atc agg cct tgg ttt aca ccc aga tcc att tat atg gaa gca	381
Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met Glu Ala	
35 40 45 50	
tct aca gtg gat tgt aat gat tta ggt ctt tta act ttc cca gcc aga	429
Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro Ala Arg	
51 56 61 66	
ttg cca gct aac aca cag att ctt ctc cta cag act aac aat att gca	477
Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn Ile Ala	
67 72 77 82	
aaa att gaa tac tcc aca gac ttt cca gta aac ctt act ggc ctg gat	525
Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly Leu Asp	
83 88 93 98	
tta tct caa aac aat tta tct tca gtc acc aat att aat gta aaa aag	573
Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val Lys Lys	
99 104 109 114	
atg cct cag ctc ctt tct gtg tac cta gag gaa aac aaa ctt act gaa	621
Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu Thr Glu	
115 120 125 130	
ctg cct gaa aaa tgt ctg tcc gaa ctg agc aac tta caa gaa ctc tat	669
Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu Leu Tyr	
131 136 141 146	
att aat cac aac ttg ctt tct aca att tca cct gga gcc ttt att ggc	717
Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe Ile Gly	
147 152 157 162	
cta cat aat ctt ctt cga ctt cat ctc aat tca aat aga ttg cag atg	765
Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu Gln Met	
163 168 173 178	
atc aac agt aag tgg ttt gat gct ctt cca aat cta gag att ctg atg	813
Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile Leu Met	
179 184 189 194	
att ggg gaa aat cca att atc aga atc aaa gac atg aac ttt aag cct	861
Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe Lys Pro	
195 200 205 210	
ctt atc aat ctt cgc agc ctg gtt ata gct ggt ata aac ctc aca gaa	909
Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu Thr Glu	

211	216	221	226	
ata cca gat aac gcc ttg gtt gga ctg gaa aac tta gaa agc atc tct				957
Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser Ile Ser				
227	232	237	242	
ttt tac gat aac agg ctt att aaa gta ccc cat gtt gct ctt caa aaa				1005
Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu Gln Lys				
243	248	253	258	
gtt gta aat ctc aaa ttt ttg gat cta aat aaa aat cct att aat aga				1053
Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile Asn Arg				
259	264	269	274	
ata cga agg ggt gat ttt agc aat atg cta cac tta aaa gag ttg ggg				1101
Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu Leu Gly				
275	280	285	290	
ata aat aat atg cct gag ctg att tcc atc gat agt ctt gct gtg gat				1149
Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala Val Asp				
291	296	301	306	
aac ctg cca gat tta aga aaa ata gaa gct act aac aac cct aga ttg				1197
Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro Arg Leu				
307	312	317	322	
tct tac att cac ccc aat gca ttt ttc aga ctc ccc aag ctg gaa tca				1245
Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu Glu Ser				
323	328	333	338	
ctc atg ctg aac agc aat gct ctc agt gcc ctg tac cat ggt acc att				1293
Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly Thr Ile				
339	344	349	354	
gag tct ctg cca aac ctc aag gaa atc agc ata cac agt aac ccc atc				1341
Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn Pro Ile				
355	360	365	370	
agg tgt gac tgt gtc atc cgt tgg atg aac atg aac aaa acc aac att				1389
Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr Asn Ile				
371	376	381	386	
cga ttc atg gag cca gat tca ctg ttt tgc gtg gac cca cct gaa ttc				1437
Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro Glu Phe				
387	392	397	402	
caa ggt cag aat gtt cgg caa gtg cat ttc agg gac atg atg gaa att				1485
Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met Glu Ile				
403	408	413	418	
tgt ctc cct ctt ata gct cct gag agc ttt cct tct aat cta aat gta				1533
Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu Asn Val				
419	424	429	434	
gaa gct ggg agc tat gtt tcc ttt cac tgt aga gct act gca gaa cca				1581
Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala Glu Pro				
435	440	445	450	

cag cct gaa atc tac tgg ata aca cct tct ggt caa aaa ctc ttg cct	1629
Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu Leu Pro	
451 456 461 466	
aat acc ctg aca gac aag ttc tat gtc cat tct gag gga aca cta gat	1677
Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr Leu Asp	
467 472 477 482	
ata aat ggc gta act ccc aaa gaa ggg ggt tta tat act tgt ata gca	1725
Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys Ile Ala	
483 488 493 498	
act aac cta gtt ggc gct gac ttg aag tct gtt atg atc aaa gtg gat	1773
Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys Val Asp	
499 504 509 514	
gga tct ttt cca caa gat aac aat ggc tct ttg aat att aaa ata aga	1821
Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys Ile Arg	
515 520 525 530	
gat att cag gcc aat tca gtt ttg gtg tcc tgg aaa gca agt tct aaa	1869
Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser Ser Lys	
531 536 541 546	
att ctc aaa tct agt gtt aaa tgg aca gcc ttt gtc aag act gaa aat	1917
Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr Glu Asn	
547 552 557 562	
tct cat gct gcg caa agt gct cga ata cca tct gat gtc aag gta tat	1965
Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys Val Tyr	
563 568 573 578	
aat ctt act cat ctg aat cca tca act gag tat aaa att tgt att gat	2013
Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys Ile Asp	
579 584 589 594	
att ccc acc atc tat cag aaa aac aga aaa aaa tgt gta aat gtc acc	2061
Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn Val Thr	
595 600 605 610	
acc aaa ggt ttg cac cct gat caa aaa gag tat gaa aag aat aat acc	2109
Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn Asn Thr	
611 616 621 626	
aca aca ctt atg gcc tgt ctt gga ggc ctt ctg ggg att att ggt gtg	2157
Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile Gly Val	
627 632 637 642	
ata tgt ctt atc agc tgc ctc tct cca gaa atg aac tgt gat ggt gga	2205
Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp Gly Gly	
643 648 653 658	
cac agc tat gtg agg aat tac tta cag aaa cca acc ttt gca tta ggt	2253
His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala Leu Gly	
659 664 669 674	

gag ctt tat cct cct ctg ata aat ctc tgg gaa gca gga aaa gaa aaa	2301
Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys Glu Lys	
675 680 685 690	
agt aca tca ctg aaa gta aaa gca act gtt ata ggt tta cca aca aat	2349
Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro Thr Asn	
691 696 701 706	
atg tcc taa aaaccac caaggaaacc tactccaaaa atgaacaaaa aaaaaaaaaag	2405
Met Ser *	
707	
cgaaagactg cagttgtgct aaaaacaaaa caaaacaaac aaacaaaaaa aaaaaa	2461

<210> 351
 <211> 5238
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (278) .. (1108)

<400> 351	
taagcttgcg gccgcggcgg cggcggccgg gaaggagcat caaagatgaa gaagaagaga	60
cagtctttcg agaggtggtc agtttttccc cggaccccct gccagatatt atgacaagga	120
caccacaaaa ccaatcagct ttacttgtc ttcgctggag gagctcttgg cgtggaagcc	180
cgccttggag gatggcttta atgtggccct ggagcccctg gcgtgtcgcc agccccctct	240
gagcagccag aggccccgga ctttgttgtg tcatgac atg atg ggc ggg tac ctg	295
Met Met Gly Gly Tyr Leu	
1	
gat gac agg ttc att cag ggc tgc gtg gtg cag act ccc tat gct ttc	343
Asp Asp Arg Phe Ile Gln Gly Ser Val Val Gln Thr Pro Tyr Ala Phe	
7 12 17 22	
tac cac tgg cag tgc atc gac gtc ttt gtg tac ttc agc cac cac acc	391
Tyr His Trp Gln Cys Ile Asp Val Phe Val Tyr Phe Ser His His Thr	
23 28 33 38	
gtc acc att ccc cca gtg ggc tgg acc aac act gcc cac agg cat ggg	439
Val Thr Ile Pro Pro Val Gly Trp Thr Asn Thr Ala His Arg His Gly	
39 44 49 54	
gtc tgc gtg ctg ggg act ttc atc acg gag tgg aat gaa ggg gga agg	487
Val Cys Val Leu Gly Thr Phe Ile Thr Glu Trp Asn Glu Gly Gly Arg	
55 60 65 70	
ctc tgt gaa gcc ttc ctg gcc ggg gat gag cgc tgc tac cag gca gtg	535
Leu Cys Glu Ala Phe Leu Ala Gly Asp Glu Arg Ser Tyr Gln Ala Val	

71	76	81	86	
gct gac cgg ctg gtc	cag atc act cag ttt	ttt cgt ttt gat ggc tgg		583
Ala Asp Arg Leu Val	Gln Ile Thr Gln Phe	Phe Arg Phe Asp Gly Trp		
87	92	97	102	
ctg atc aac atc gag	aac tgc ctg agt ctg	gcc gct gtg ggg aac atg		631
Leu Ile Asn Ile Glu	Asn Ser Leu Ser Leu	Ala Ala Val Gly Asn Met		
103	108	113	118	
cct cct ttc ctg cgg	tac ctc acc aca cag	ctg cac cgg cag gtc cca		679
Pro Pro Phe Leu Arg	Tyr Leu Thr Thr Gln	Leu His Arg Gln Val Pro		
119	124	129	134	
ggg ggc ctg gtg ctc	tgg tat gac agc gtg	gtg caa agt ggg cag ctc		727
Gly Gly Leu Val Leu	Trp Tyr Asp Ser Val	Val Gln Ser Gly Gln Leu		
135	140	145	150	
aaa tgg caa gac gaa	ctc aac cag cac aac	agg gtc ttc ttt gat tcc		775
Lys Trp Gln Asp Glu	Leu Asn Gln His Asn	Arg Val Phe Phe Asp Ser		
151	156	161	166	
tgc gac ggc ttc ttc	act aac tat aac tgg	cgg gag gag cac ttg gag		823
Cys Asp Gly Phe Phe	Thr Asn Tyr Asn Trp	Arg Glu Glu His Leu Glu		
167	172	177	182	
cgg atg ctg ggg cag	gct ggg gag cgc cgg	gct gat gtg tac gtg ggc		871
Arg Met Leu Gly Gln	Ala Gly Glu Arg Arg	Ala Asp Val Tyr Val Gly		
183	188	193	198	
gtg gat gtg ttt gct	cga ggg aac gtg gtc	gga ggc cga ttc gac aca		919
Val Asp Val Phe Ala	Arg Gly Asn Val Val	Gly Gly Arg Phe Asp Thr		
199	204	209	214	
gac aag gtg ggt ggt	ggc ttt cgt cca agg	gcc agc ggc cca gtg cct		967
Asp Lys Val Gly Gly	Gly Phe Arg Pro Arg	Ala Ser Gly Pro Val Pro		
215	220	225	230	
ccc ctg gga cct cat	ttc ctc atg gac ctt	cca ttc ccg tct gca cct		1015
Pro Leu Gly Pro His	Phe Leu Met Asp Leu	Pro Phe Pro Ser Ala Pro		
231	236	241	246	
caa agg aat gac agc	agc tgt tct tcc cag	agt ggg gat ccc gtg gca		1063
Gln Arg Asn Asp Ser	Ser Cys Ser Ser Gln	Ser Gly Asp Pro Val Ala		
247	252	257	262	
ctg aga aac agg tgt	cct gcc ccg gcc aag	cta tgt ccc cac tga aac		1111
Leu Arg Asn Arg Cys	Pro Ala Pro Ala Lys	Leu Cys Pro His *		
263	268	273		
ccctttcccg gctattttcta	caatcagata atgtattttt	gtgtgggtgt taccagacag		1171
aggcgcgtcg ttcccccgct	gtccggtcct cggcgggcct	gggcctcctg tcccagctgc		1231
gttccttgat cttccccgtg	agggaaagcct gcggggacgc	acaggggcct gcagcgcctc		1291
tcactgcggc tcagggggcga	ggacggggga ggtgccagg	gtttggggat cggtaggtgt		1351

catgacgagg gagcattttc tggcaaggca ggtcacacca gcacagagga aggagcgggg	1411
ccaggccggt gcccctggcg tgggatgcmc agggctctgc ctgcctctgg tctatcagtc	1471
ctgccogttc ccagagcccc agggatgttc tcagccctta atttagcttt aaatgagtaa	1531
attaatccaa taactaaaga gcctctttac tgccogtgat tctgataatc gaatgagagg	1591
tgtgccagag gacaatggga ccgcgcagcc acagccagtt ggggcccagc cctgcccc	1651
ctgcccttgc agcagcgtg accgcctctc ccgcgcctc ttctggcggg cttgtggaac	1711
gacgggggtg atgccagca gcctccagtc gttggagctg atccgaaagc atggcttctc	1771
cgtggctttg tttgccccg gctgggtgta tgagtgtctg gagaagaagg atttcttcca	1831
gaaccaggac aagttctggg gccgactgga gcgttatctg cccacacata gcatctgctc	1891
cttgcccttc gtacgtctt tctgcctggg catgggtgca cggagggtct gctatggcca	1951
ggaagaggcg gtagggccct ggtaccacct gagcgcccag gagatccagc ccttgtttg	2011
agaacacagg ctgggagggg atggccgggg ctgggtgagg acgactgct gcctggagga	2071
tgccctggcag ggaggcagct cctgctcgt ccgggggtgt atcccaccg aggttggaaa	2131
tgtggctgtg aggttatctt cccgcaggc cccagtgcc cccaagattt acctgtccat	2191
ggtgtataag cttgaggggc ccacggacgt cacagttgct ttggagctga ccacagggga	2251
tgccggcagc tgccacatcg gtggcatctc agtgttgaac gcagaaacaa gctcaagaca	2311
cagcctccga cccctccggg tgccccccac caagctggcc agatgggtgg gccgctgcgg	2371
ccggcagctg agtgggggct ggggtccagca ctgctacgag gtgagcctgc gtgggtgcct	2431
gctgctagac ctccctgctt gcttctcacg gccgccgggt agtcgggagg aggagagctt	2491
cacctgtcgg cttggagaga tccaggtggt ggacgctgcc agcctgctgg cccctctgcc	2551
ccaggtgcag gccgtcacca tctctcact ccgctggcag ccatccgcct ctgagcggga	2611
ggggccccct gctctgctcc agctcagctg caccctgcac tggctcctcc tctctcaca	2671
agtccgttgc ttccgaatcc actgctgggg agggatgagt gatgactctc cgggcaggga	2731
gctgccgagg ccagagatgc ccatgttctt ggggttggt tttgccacc agtaccggat	2791
agtggacctg ctggtggaag ccgccgggcc cggccaggat cgtcgcatgg aatttctggt	2851
ggagcctgtc cccaaggaag ggttccgggt acctcaggcc gagtggggca gggcagttct	2911
gctttattca gccctgcat gagcggatgc taaggccggg tggctctctg gcctcgggct	2971
gaggcctctt cccggctgtc tgccccctggc ctgcgctgga cctgctaagt gccacagtg	3031

gcagcgaggt cccggtcccc gggctggggg gggagacccc gggctgagtg ctgtggcttt	3091
ctggtggggg gcgatggaaa caggaaacca agcagtggga tcgcagcggt ggtcactgcg	3151
aggcgagtgg cgggctttct gtttctgcct tgtccctccc cacggtaoct ggttcccagg	3211
tgaaaatgaa aggaggggag aagttgagaa cagaacattc cataaaggat atttcctaata	3271
aggctgcaag atgctgatgc cgagaatgat gattttcttt cctgcagatg aaactattag	3331
aaagggctct agattgtggc aggtaggctt tggagcaggc gccgagacat ttctgagcat	3391
gaggacgagc tacagcagct cctgggggtg ggctgcctgc gggatggcgg gagaggatgc	3451
cctggagaac cgtcctccca gtgtggaagg cccttttccc tgaggagtgg gcattctggg	3511
ccagccggcg ctggcttcgt gcctccacgt gggccagccc cagctgctcc gtgtttcctg	3571
gcgttggaac tttactgtgc tgctgagtgt gaggtcatct ccggagcggt ttccagcagcc	3631
cctggctctg cggcgtctct tccgggctgt gggcatgcag ggaagtggct gtgaggcagt	3691
ctgcgctgtg gccctgcctc tgcccagcga gaggccgtgg gctctggaca agccgccctt	3751
caggctgggg tagcaggcca gtccaggcag gaagcagcac ctgccccccg cggcagccca	3811
gccccagcct gagtgcagga gctgcaggac ccgcgggggc ttttccagct actctgttcc	3871
ttcacgtcct cccttctcag cctcgtccaa gcaccgggaa gacctccagg ctgaacctt	3931
gagcagcagt cagcacaggt gcgtgggggc gtgaggaggc cagggtcttc accacaggcg	3991
ccttctctg tcttctctgc tctttcttct ctgcccaggc cgctgcagct gcacagcctc	4051
tgctacacct gggctgcctg ggaggcttcc tgggtgtggtg tctggacccc acggccttgg	4111
gtcatcctgc ggetggctg ggggtggggc tgttgtggtc cttccacggg gtcagtggcc	4171
tgaagtccct cgcttttggg ggggggggtc ctcacccca ggccacatag ggccagtggg	4231
aggggttccc tctatgtcgg gcagtgctga gggctgggat gctctgtgac ccagctgga	4291
gcccacacct aagggtggc atccacatca tttcacctg cagtgaggga agaggccacc	4351
agggtggcagc acagccacac ccgttcccac gtcagaggag ggcaaggctg ggtactcagc	4411
agccactctg agccggggct ccttccagga gctgaaatcc acctgtctct atcttctt	4471
cctgcctggg tactcatgcc aagcagagac tgggattagg ggttctgtgc tottgccata	4531
ttaggaacat tctcccatgt ctcttgtgtg gtcccagaag gagaagtgag tttgccaagg	4591
atatggggca ggaggctccc tctgctgacc ccctgcagcc tggagccagc ccggggactg	4651
tcctgggtgg agggcagggtg aacacaagct gctgccgggg actgtcctgg gtggagggca	4711
ggtgaacaca agctgctgcc ggggactgtc ctgggtggac ggcaggtgaa cacaagcggc	4771

tgccgcatgt agccactcac tcgacttttt ttcagctgtg accattcctg ggagctcttt 4831
 gagcctttct gtctcatttg gaaccagggg gaaccaggaa ggggctcctg gcctctctgt 4891
 gtcctctgca gtgggggttg tggggggcgc agcatccacg ccttgctgcc cttctttcat 4951
 gaagtctgtt ttttaagtgc tgggtccccc gaatatttta tgcagaggag ggaaaattta 5011
 tagtggcaat tattttctca cagtctggtg agcaggcaat taattaggag taagggggcc 5071
 tagtagagcg tggcgtgtgg cagaatcgca ccgccccggc tccccagccc accgccatgc 5131
 agggctcgcg tgcgggaaaa ctaatatgcc ggcgtttaag cctgtgcccc tctgctgggt 5191
 gtaactgcgc tgaaataaat gatctgacaa tgtgaaaaaa aaaaaaa 5238

<210> 352
 <211> 4495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (307)..(3006)

<400> 352
 tgccgtaccg gtcttgaatt cccggttcga cccacgcgtc cggaaaggca aatctaattgg 60
 tacctggctg ttcttaagaa tgcatagaga ggcttagcag gctgggattg attgaagctt 120
 atttctctgct tgaaactgac agtggtttatg gccccaaactt aaaactgcct attacttcag 180
 gccaaagggt tccatggcga aattgaggat ttgcagcagt ggctgactga cacggagcgt 240
 catctgttgg catctaaacc gctgggaggt ttaccggaaa cagccaagga gcagcttaat 300
 gtccat atg gaa gtc tgt gct gcc ttt gaa gct aaa gaa gaa aca tat 348
 Met Glu Val Cys Ala Ala Phe Glu Ala Lys Glu Glu Thr Tyr
 1 5 10
 aag agt ctg atg cag aaa ggc cag cag atg ctt gca aga tgc cca aaa 396
 Lys Ser Leu Met Gln Lys Gly Gln Gln Met Leu Ala Arg Cys Pro Lys
 15 20 25 30
 tct gca gag aca aat att gac caa gac ata aat aac ttg aaa gaa aaa 444
 Ser Ala Glu Thr Asn Ile Asp Gln Asp Ile Asn Asn Leu Lys Glu Lys
 31 36 41 46
 tgg gaa tcg gtg gaa acc aaa ctc aat gaa agg aaa act aaa ctg gaa 492
 Trp Glu Ser Val Glu Thr Lys Leu Asn Glu Arg Lys Thr Lys Leu Glu
 47 52 57 62
 gag gct ctc aac ttg gca atg gag ttc cac aat tct ctc caa gac ttc 540

Glu	Ala	Leu	Asn	Leu	Ala	Met	Glu	Phe	His	Asn	Ser	Leu	Gln	Asp	Phe	
63					68					73					78	
atc	aac	tgg	ctt	act	cag	gct	gaa	cag	acc	cta	aat	gta	gct	tct	cgg	588
Ile	Asn	Trp	Leu	Thr	Gln	Ala	Glu	Gln	Thr	Leu	Asn	Val	Ala	Ser	Arg	
79					84					89					94	
cca	agt	ctc	atc	ttg	gac	aca	gtc	tta	ttt	caa	att	gac	gaa	cac	aag	636
Pro	Ser	Leu	Ile	Leu	Asp	Thr	Val	Leu	Phe	Gln	Ile	Asp	Glu	His	Lys	
95					100					105					110	
gtt	ttt	gcc	aat	gaa	gta	aat	tct	cat	cgt	gag	cag	ata	ata	gag	ctg	684
Val	Phe	Ala	Asn	Glu	Val	Asn	Ser	His	Arg	Glu	Gln	Ile	Ile	Glu	Leu	
111					116					121					126	
gac	aaa	act	gga	acc	cac	cta	aaa	tat	ttt	agt	cag	aaa	caa	gat	gtt	732
Asp	Lys	Thr	Gly	Thr	His	Leu	Lys	Tyr	Phe	Ser	Gln	Lys	Gln	Asp	Val	
127					132					137					142	
gtt	cta	atc	aag	aat	cta	ctt	atc	agt	gta	caa	agt	cga	tgg	gaa	aaa	780
Val	Leu	Ile	Lys	Asn	Leu	Leu	Ile	Ser	Val	Gln	Ser	Arg	Trp	Glu	Lys	
143					148					153					158	
gtg	gtt	caa	cgg	ttg	gta	gag	aga	gga	aga	tct	ttg	gat	gat	gca	agg	828
Val	Val	Gln	Arg	Leu	Val	Glu	Arg	Gly	Arg	Ser	Leu	Asp	Asp	Ala	Arg	
159					164					169					174	
aag	aga	gcc	aag	cag	ttc	cat	gaa	gct	tgg	agt	aaa	ctt	atg	gag	tgg	876
Lys	Arg	Ala	Lys	Gln	Phe	His	Glu	Ala	Trp	Ser	Lys	Leu	Met	Glu	Trp	
175					180					185					190	
cta	gaa	gag	tca	gaa	aag	tct	ttg	gat	tct	gaa	ctg	gaa	atc	gca	aat	924
Leu	Glu	Glu	Ser	Glu	Lys	Ser	Leu	Asp	Ser	Glu	Leu	Glu	Ile	Ala	Asn	
191					196					201					206	
gat	cca	gac	aaa	ata	aaa	aca	caa	ctt	gca	caa	cat	aag	gag	ttt	cag	972
Asp	Pro	Asp	Lys	Ile	Lys	Thr	Gln	Leu	Ala	Gln	His	Lys	Glu	Phe	Gln	
207					212					217					222	
aaa	tca	ctc	gga	gcc	aag	cat	tct	gtc	tac	gac	acc	acc	aac	agg	act	1020
Lys	Ser	Leu	Gly	Ala	Lys	His	Ser	Val	Tyr	Asp	Thr	Thr	Asn	Arg	Thr	
223					228					233					238	
gga	cgt	tct	ctg	aag	gag	aaa	acc	tcc	ctg	gct	gat	gac	aac	ctg	aaa	1068
Gly	Arg	Ser	Leu	Lys	Glu	Lys	Thr	Ser	Leu	Ala	Asp	Asp	Asn	Leu	Lys	
239					244					249					254	
ctg	gat	gac	atg	ctg	agt	gaa	ctc	aga	gac	aaa	tgg	gat	acc	ata	tgt	1116
Leu	Asp	Asp	Met	Leu	Ser	Glu	Leu	Arg	Asp	Lys	Trp	Asp	Thr	Ile	Cys	
255					260					265					270	
gga	aaa	tct	gtg	gaa	aga	caa	aac	aaa	ttg	gag	gaa	gcc	ctg	tta	ttt	1164
Gly	Lys	Ser	Val	Glu	Arg	Gln	Asn	Lys	Leu	Glu	Glu	Ala	Leu	Leu	Phe	
271					276					281					286	
tct	gga	caa	ttc	aca	gat	gcc	cta	cag	gct	ctc	att	gat	tgg	tta	tat	1212
Ser	Gly	Gln	Phe	Thr	Asp	Ala	Leu	Gln	Ala	Leu	Ile	Asp	Trp	Leu	Tyr	

287	292	297	302	
aga gtt gaa ccc cag ctg gca gaa gac cag cct gtt cat gga gac att				1260
Arg Val Glu Pro Gln Leu Ala Glu Asp Gln Pro Val His Gly Asp Ile				
303	308	313	318	
gat ttg gtg atg aat ctg atc gat aat cac aag gcc ttc caa aaa gag				1308
Asp Leu Val Met Asn Leu Ile Asp Asn His Lys Ala Phe Gln Lys Glu				
319	324	329	334	
ttg ggg aag agg acc agc agt gtg cag gcc ctg aag cgc tca gcc cga				1356
Leu Gly Lys Arg Thr Ser Ser Val Gln Ala Leu Lys Arg Ser Ala Arg				
335	340	345	350	
gaa ctc ata gaa ggc agt cgg gat gac tcc tcc tgg gtc aag gtc cag				1404
Glu Leu Ile Glu Gly Ser Arg Asp Asp Ser Ser Trp Val Lys Val Gln				
351	356	361	366	
atg cag gaa tta agc aca cgc tgg gag acc gtg tgt gca ctt tct ata				1452
Met Gln Glu Leu Ser Thr Arg Trp Glu Thr Val Cys Ala Leu Ser Ile				
367	372	377	382	
tca aag caa aca cgg tta gaa gca gcc ctg cgt cag gca gag gaa ttc				1500
Ser Lys Gln Thr Arg Leu Glu Ala Ala Leu Arg Gln Ala Glu Glu Phe				
383	388	393	398	
cac tcg gtg gta cat gcc ctc ttg gag tgg ctg gct gag gcg gag caa				1548
His Ser Val Val His Ala Leu Leu Glu Trp Leu Ala Glu Ala Glu Gln				
399	404	409	414	
acc ctg cgt ttc cat ggt gtc ctc cca gat gat gag gat gct ctc cgg				1596
Thr Leu Arg Phe His Gly Val Leu Pro Asp Asp Glu Asp Ala Leu Arg				
415	420	425	430	
act ctc att gat cag cat aaa gaa ttc atg aag aaa ctg gaa gaa aag				1644
Thr Leu Ile Asp Gln His Lys Glu Phe Met Lys Lys Leu Glu Glu Lys				
431	436	441	446	
aga gct gaa cta aat aaa gcc acc act atg ggc gac acc gtt ttg gct				1692
Arg Ala Glu Leu Asn Lys Ala Thr Thr Met Gly Asp Thr Val Leu Ala				
447	452	457	462	
atc tgc cac ccc gac tcc atc act acc att aag cac tgg ata aca atc				1740
Ile Cys His Pro Asp Ser Ile Thr Thr Ile Lys His Trp Ile Thr Ile				
463	468	473	478	
atc cgg gcg agg ttt gag gag gtg ctg gcc tgg gca aag caa cat cag				1788
Ile Arg Ala Arg Phe Glu Glu Val Leu Ala Trp Ala Lys Gln His Gln				
479	484	489	494	
cag aga tta gca agt gct ctg gct ggg ctt att gcc aaa cag gaa ttg				1836
Gln Arg Leu Ala Ser Ala Leu Ala Gly Leu Ile Ala Lys Gln Glu Leu				
495	500	505	510	
ttg gaa gct ttg ctg gct tgg ttg caa tgg gct gaa act aca ctt act				1884
Leu Glu Ala Leu Leu Ala Trp Leu Gln Trp Ala Glu Thr Thr Leu Thr				
511	516	521	526	

gat aag gat aaa gaa gtc atc ccc cag gag atc gaa gag gtg aaa gca	1932
Asp Lys Asp Lys Glu Val Ile Pro Gln Glu Ile Glu Glu Val Lys Ala	
527 532 537 542	
ctc att gca gaa cac cag acc ttc atg gag gaa atg acc aga aaa cag	1980
Leu Ile Ala Glu His Gln Thr Phe Met Glu Glu Met Thr Arg Lys Gln	
543 548 553 558	
cct gat gtt gat aaa gta acg aag acc tat aag agg aga gct gct gat	2028
Pro Asp Val Asp Lys Val Thr Lys Thr Tyr Lys Arg Arg Ala Ala Asp	
559 564 569 574	
cct tcc tca tta caa tcc cat att cca gtc ttg gat aag gga cga gca	2076
Pro Ser Ser Leu Gln Ser His Ile Pro Val Leu Asp Lys Gly Arg Ala	
575 580 585 590	
gga aga aaa cgc ttt cca gca tca agc ttg tat ccc tct ggg tca cag	2124
Gly Arg Lys Arg Phe Pro Ala Ser Ser Leu Tyr Pro Ser Gly Ser Gln	
591 596 601 606	
aca caa att gaa acc aaa aat cct agg gta aac tta ctg gtg agc aaa	2172
Thr Gln Ile Glu Thr Lys Asn Pro Arg Val Asn Leu Leu Val Ser Lys	
607 612 617 622	
tgg cag caa gtc tgg ctc ctg gcg ttg gaa aga agg agg aaa ctc aat	2220
Trp Gln Gln Val Trp Leu Leu Ala Leu Glu Arg Arg Arg Lys Leu Asn	
623 628 633 638	
gat gcc ttg gac aga cta gag gag ctg agg gaa ttt gct aac ttt gat	2268
Asp Ala Leu Asp Arg Leu Glu Glu Leu Arg Glu Phe Ala Asn Phe Asp	
639 644 649 654	
ttt gat atc tgg cgc aaa aaa tac atg cga tgg atg aat cac aag aaa	2316
Phe Asp Ile Trp Arg Lys Lys Tyr Met Arg Trp Met Asn His Lys Lys	
655 660 665 670	
tct cga gtg atg gac ttc ttc agg aga att gat aaa gac cag gat ggg	2364
Ser Arg Val Met Asp Phe Phe Arg Arg Ile Asp Lys Asp Gln Asp Gly	
671 676 681 686	
aaa ata acg cgg cag gaa ttt att gat gga att ctt tcc tca aag ttt	2412
Lys Ile Thr Arg Gln Glu Phe Ile Asp Gly Ile Leu Ser Ser Lys Phe	
687 692 697 702	
cca acc agt cgc ttg gag atg agc gca gtt gca gac atc ttt gac aga	2460
Pro Thr Ser Arg Leu Glu Met Ser Ala Val Ala Asp Ile Phe Asp Arg	
703 708 713 718	
gat ggc gat gga tat att gac tac tat gaa ttt gta gca gcc ctt cac	2508
Asp Gly Asp Gly Tyr Ile Asp Tyr Tyr Glu Phe Val Ala Ala Leu His	
719 724 729 734	
cca aat aaa gat gca tat aaa cct atc aca gat gcc gac aaa atc gaa	2556
Pro Asn Lys Asp Ala Tyr Lys Pro Ile Thr Asp Ala Asp Lys Ile Glu	
735 740 745 750	

gat gag gtg aca agg cag gta gct aag tgt aaa tgt gca aag cga ttt	2604
Asp Glu Val Thr Arg Gln Val Ala Lys Cys Lys Cys Ala Lys Arg Phe	
751 756 761 766	
caa gtt gag cag att ggt gat aat aaa tac agg ttc ttc ctg gga aat	2652
Gln Val Glu Gln Ile Gly Asp Asn Lys Tyr Arg Phe Phe Leu Gly Asn	
767 772 777 782	
cag ttt gga gac tcc cag caa ctg cga ctg gtc cgg atc ctg cgg agt	2700
Gln Phe Gly Asp Ser Gln Gln Leu Arg Leu Val Arg Ile Leu Arg Ser	
783 788 793 798	
act gtg atg gtt cgt gtt gga ggt gga tgg atg gca ctt gat gag ttc	2748
Thr Val Met Val Arg Val Gly Gly Gly Trp Met Ala Leu Asp Glu Phe	
799 804 809 814	
tta gtg aaa aat gat cct tgc agg gcc aaa gga agg aca aac atg gaa	2796
Leu Val Lys Asn Asp Pro Cys Arg Ala Lys Gly Arg Thr Asn Met Glu	
815 820 825 830	
ctg cgt gag aag ttc att tta ggc aga tgg tgc cag cca ggg tat ggc	2844
Leu Arg Glu Lys Phe Ile Leu Gly Arg Trp Cys Gln Pro Gly Tyr Gly	
831 836 841 846	
tgc ttt ccg acc ccg agg ccg aag atc ccg gcc atc atc acg agg cgc	2892
Cys Phe Pro Thr Pro Arg Pro Lys Ile Pro Ala Ile Ile Thr Arg Arg	
847 852 857 862	
ttc acc caa cag atc cac ttc tgt gtc cag tca ggc tgc gca ggc ggc	2940
Phe Thr Gln Gln Ile His Phe Cys Val Gln Ser Gly Cys Ala Gly Gly	
863 868 873 878	
ctc ccc aca ggt ccc tgc cac cac cac acc caa gat tct cca tcc ttt	2988
Leu Pro Thr Gly Pro Cys His His His Thr Gln Asp Ser Pro Ser Phe	
879 884 889 894	
aac acg caa tta tgg taa accatg gttgacaaac agcaaaatgt caactccttg	3042
Asn Thr Gln Leu Trp *	
895 900	
taaagcagca gagtgtcag actttcccggt gccatctgca gagggaaacgc caatacaagg	3102
aagcaagctt cgacttccag gatatttatc agggaaaggc ttccactctg gggaggacag	3162
tggcttgata acaactgcag ctgccagagt ccgaacacag tttgctgatt ccaagaagac	3222
tcccagccga ccaggaagtc gagctggaag caaagctggc agcagggcca gcagccgccg	3282
aggcagtgat gcatcagact ttgacatttc agaaatccag tccgtgtgct cagatgtgga	3342
aactgtcccc cagacacaca gacctacacc ccgagcaggt tctcggccat ccacagcgaa	3402
gccttcaaaa atccccacgc cccagaggaa atcacctgcc agcaaattgg acaagtcctc	3462
aaagagatag tgcaattgggt tctaccaagg cccttccttg agcatttatt atttaagttt	3522
gaacgatgta aaatatgggtg tagaaattct tgtgaaatat tgcaagaggc gagtttaaaa	3582

ttotgcagat ggccttattt gtgtatttgt ctttttattt tatctgtata attttttttg	3642
tcagatattc tgggggttaaa gtcacatcat atgtgaggag gaaaagttta acatgaacta	3702
acattttctgc actgtaacgt gccgggcaca cactaaactc agttaactgta cctacaggta	3762
agtcctacatc ctctctgaca gccacagcac tacatcaatc cctgacgtta gggatacctc	3822
atgacatttt cctgttttta tggaaactct gagaagctga atgatacatg caggggatat	3882
tttttgagat gatttaaagt taaaccaaaa gatggaagac aaaaagacaa acacaccac	3942
acgcagtctt tgcagtatct gacagagaac tcacaggaag ttacttcaag cacttgccca	4002
gtactatgat attcaagtac cttgcagcat ttctctgccca ttgctttcaa tgaggccaga	4062
ggcatcctgg atattagacc tattatactg taagaatata agtataaagt gcgttcatat	4122
acatgtgagg ttttcttttg cttgagtgga cagtagcacc tgtatcattg aactcatttt	4182
gtatcagagc aattttgctt gcagaaagct atgaaataaa acacgtccct taactgcatt	4242
gctatggaat taattttttt tccccaggga aaactagtgt atttttttat gagcaatatc	4302
aatttggagt gaccaaaga tacttaaaaa tgggtttatt ttgattttctc atctgaaata	4362
atcatgttct ggtattatat ctatctatat ttaataaata tatacatttt aatttattat	4422
gtgtactcac atactataga aagatattag tatgcattta ataaaacata ttcacttgaa	4482
aaaaaaaaa aaa	4495

<210> 353
 <211> 7657
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (132)..(3629)

<400> 353	
aaaatctcct ggctgcagct gcaagagctg tgacagagag catcaatcaa ctcatcactc	60
tggtgaccca acaagctccg ggccagaaaag agtgcgataa tgccctgcgg gagctcgaga	120
ctgtgaaggg g atg ttg gac aat cct aat gaa cct gtt agt gac ctc tct	170
Met Leu Asp Asn Pro Asn Glu Pro Val Ser Asp Leu Ser	
1 5 10	
tac ttt gac tgc att gag agt gtg atg gaa aac tcc aag gtt ctg ggt	218
Tyr Phe Asp Cys Ile Glu Ser Val Met Glu Ser Lys Val Leu Gly	
14 19 24 29	

gaa tgc atg gca ggg att tca cag aat gcc aag acc gga gac ctc cct	266
Glu Ser Met Ala Gly Ile Ser Gln Asn Ala Lys Thr Gly Asp Leu Pro	
30 35 40 45	
gcc ttt ggg gaa tgt gtg ggg att gca tcc aag gct ctc tgt ggg ctg	314
Ala Phe Gly Glu Cys Val Gly Ile Ala Ser Lys Ala Leu Cys Gly Leu	
46 51 56 61	
aca gag gct gca gcc cag gct gca tac ttg gtt ggc atc ttt gat cca	362
Thr Glu Ala Ala Ala Gln Ala Ala Tyr Leu Val Gly Ile Phe Asp Pro	
62 67 72 77	
aac agc cag gca ggc cac cag ggc ctg gtg gac ccc ^{at} atc cag ttt gcc	410
Asn Ser Gln Ala Gly His Gln Gly Leu Val Asp Pro Ile Gln Phe Ala	
78 83 88 93	
agg gct aac cag gcc atc cag atg gca tgc cag aac ttg gtg gac cct	458
Arg Ala Asn Gln Ala Ile Gln Met Ala Cys Gln Asn Leu Val Asp Pro	
94 99 104 109	
ggc agc agc cca tca cag gtc ctg tca gcc gcc aca att gtt gcc aag	506
Gly Ser Ser Pro Ser Gln Val Leu Ser Ala Ala Thr Ile Val Ala Lys	
110 115 120 125	
cac acg tca gcc ttg tgt aat gcc tgc cgc atc gcc tca tcc aag acg	554
His Thr Ser Ala Leu Cys Asn Ala Cys Arg Ile Ala Ser Ser Lys Thr	
126 131 136 141	
gcc aac cca gta gcc aag agg cac ttc gtc cag tgc gcc aag gaa gtc	602
Ala Asn Pro Val Ala Lys Arg His Phe Val Gln Ser Ala Lys Glu Val	
142 147 152 157	
gcc aac agc act gcc aac ctg gtg aag acc atc aag gcc ctg gat ggg	650
Ala Asn Ser Thr Ala Asn Leu Val Lys Thr Ile Lys Ala Leu Asp Gly	
158 163 168 173	
gat ttc tct gaa gac aac cgc aat aag tgt cgc atc gcc acc gca ccc	698
Asp Phe Ser Glu Asp Asn Arg Asn Lys Cys Arg Ile Ala Thr Ala Pro	
174 179 184 189	
ttg att gaa gct gtg gag aac ctg aca gcg ttc gcc tca aac cct gag	746
Leu Ile Glu Ala Val Glu Asn Leu Thr Ala Phe Ala Ser Asn Pro Glu	
190 195 200 205	
ttt gtc agc att cct gcc cag atc agc tcc gag ggt tcc cag gca cag	794
Phe Val Ser Ile Pro Ala Gln Ile Ser Ser Glu Gly Ser Gln Ala Gln	
206 211 216 221	
gaa cca atc ctg gtc tca gcc aag acc atg ctg gag agt tca tgc tac	842
Glu Pro Ile Leu Val Ser Ala Lys Thr Met Leu Glu Ser Ser Ser Tyr	
222 227 232 237	
ctc att cgc act gca cgc tct ctg gcc atc aac ccc aaa gac cca ccc	890
Leu Ile Arg Thr Ala Arg Ser Leu Ala Ile Asn Pro Lys Asp Pro Pro	
238 243 248 253	

acc tgg tct gta ctg gct gga cat tcc cat aca gtg tcc gac tcc atc	938
Thr Trp Ser Val Leu Ala Gly His Ser His Thr Val Ser Asp Ser Ile	
254 259 264 269	
aag agt ctc atc act tct atc agg gac aag gcc cct gga cag agg gag	986
Lys Ser Leu Ile Thr Ser Ile Arg Asp Lys Ala Pro Gly Gln Arg Glu	
270 275 280 285	
tgt gat tac tcc atc gat ggc atc aac cgg tgc atc cgg gac atc gag	1034
Cys Asp Tyr Ser Ile Asp Gly Ile Asn Arg Cys Ile Arg Asp Ile Glu	
286 291 296 301	
cag gcc tcg ctg gcc gcc gtc agc cag agc ctg gcc acg agg gac gac	1082
Gln Ala Ser Leu Ala Ala Val Ser Gln Ser Leu Ala Thr Arg Asp Asp	
302 307 312 317	
atc tct gtg gag gcc ctg cag gag cag ctg act tcg gtg gtc cag gaa	1130
Ile Ser Val Glu Ala Leu Gln Glu Gln Leu Thr Ser Val Val Gln Glu	
318 323 328 333	
atc gga cac ctt atc gat ccc atc gcc aca gcg gct cgg gga gaa gca	1178
Ile Gly His Leu Ile Asp Pro Ile Ala Thr Ala Ala Arg Gly Glu Ala	
334 339 344 349	
gct cag ctg gga cat aag gtg aca caa ctg gca agc tat ttt gag ccc	1226
Ala Gln Leu Gly His Lys Val Thr Gln Leu Ala Ser Tyr Phe Glu Pro	
350 355 360 365	
ttg atc tta gcc gca gtt ggt gtg gcc tcc aag att ctt gat cat cag	1274
Leu Ile Leu Ala Ala Val Gly Val Ala Ser Lys Ile Leu Asp His Gln	
366 371 376 381	
cag cag atg acg gtg ctg gac cag acc aag act ctc gca gag tct gcc	1322
Gln Gln Met Thr Val Leu Asp Gln Thr Lys Thr Leu Ala Glu Ser Ala	
382 387 392 397	
ttg cag atg ttg tat gca gcc aaa gaa ggt ggc gga aac ccc aag gca	1370
Leu Gln Met Leu Tyr Ala Ala Lys Glu Gly Gly Gly Asn Pro Lys Ala	
398 403 408 413	
caa cac acc cat gac gcc atc aca gag gcc gcc cag ttg atg aag gaa	1418
Gln His Thr His Asp Ala Ile Thr Glu Ala Ala Gln Leu Met Lys Glu	
414 419 424 429	
gcc gtg gat gac atc atg gtg acg ctg aac gaa gct gcc agt gaa gtg	1466
Ala Val Asp Asp Ile Met Val Thr Leu Asn Glu Ala Ala Ser Glu Val	
430 435 440 445	
ggg ctg gtt ggg ggc atg gtg gac gcc att gca gaa gcc atg agc aag	1514
Gly Leu Val Gly Gly Met Val Asp Ala Ile Ala Glu Ala Met Ser Lys	
446 451 456 461	
ctg gat gaa ggc act cct cca gaa cca aag gga aca ttt gtc gac tat	1562
Leu Asp Glu Gly Thr Pro Pro Glu Pro Lys Gly Thr Phe Val Asp Tyr	
462 467 472 477	
cag acg act gtg gtt aaa tac tcc aaa agc att gcg gtg aca gct cag	1610

Gln Thr Thr Val Val Lys Tyr Ser Lys Ser Ile Ala Val Thr Ala Gln	
478 483 488 493	
gaa atg atg act aag tcg gtt act aac ccg gag gag ttg gga gga ctg	1658
Glu Met Met Thr Lys Ser Val Thr Asn Pro Glu Glu Leu Gly Gly Leu	
494 499 504 509	
gct tca caa atg acc agt gac tat ggg cac ctg gct ttc cag ggc cag	1706
Ala Ser Gln Met Thr Ser Asp Tyr Gly His Leu Ala Phe Gln Gly Gln	
510 515 520 525	
atg gca gca gcc acg gcg gaa cca gag gag atc gga ttc cag att cgc	1754
Met Ala Ala Ala Thr Ala Glu Pro Glu Glu Ile Gly Phe Gln Ile Arg	
526 531 536 541	
act cgt gtg cag gac ctg ggc cac ggc tgt atc ttc ctg gtg cag aag	1802
Thr Arg Val Gln Asp Leu Gly His Gly Cys Ile Phe Leu Val Gln Lys	
542 547 552 557	
gca ggg gcc ctc cag gtc tgc ccc aca gac agc tac acc aag agg gag	1850
Ala Gly Ala Leu Gln Val Cys Pro Thr Asp Ser Tyr Thr Lys Arg Glu	
558 563 568 573	
ctg atc gaa tgc gcc cgt gcc gtc acg gaa aag gtc tcc ttg gtg ctc	1898
Leu Ile Glu Cys Ala Arg Ala Val Thr Glu Lys Val Ser Leu Val Leu	
574 579 584 589	
tcg gct ctc cag gcc ggg aac aaa gga acc cag gca tgc att aca gcc	1946
Ser Ala Leu Gln Ala Gly Asn Lys Gly Thr Gln Ala Cys Ile Thr Ala	
590 595 600 605	
gcc acc gct gtg tct ggg atc att gcc gac ctg gac acc acc att atg	1994
Ala Thr Ala Val Ser Gly Ile Ile Ala Asp Leu Asp Thr Thr Ile Met	
606 611 616 621	
ttt gca aca gcg ggg acg ctg aat gca gag aac agt gag acc ttc gca	2042
Phe Ala Thr Ala Gly Thr Leu Asn Ala Glu Asn Ser Glu Thr Phe Ala	
622 627 632 637	
gac cac agg gag aac att ctc aag acg gcc aag gcc ttg gta gaa gac	2090
Asp His Arg Glu Asn Ile Leu Lys Thr Ala Lys Ala Leu Val Glu Asp	
638 643 648 653	
acg aaa cta ctt gtg tca gga gct gcg tcc act cct gac aag ctg gcc	2138
Thr Lys Leu Leu Val Ser Gly Ala Ala Ser Thr Pro Asp Lys Leu Ala	
654 659 664 669	
cag gcg gcc cag tcc tca gca gcc acc atc acc cag ctc gca gaa gtg	2186
Gln Ala Ala Gln Ser Ser Ala Ala Thr Ile Thr Gln Leu Ala Glu Val	
670 675 680 685	
gtc aag ctg ggg gca gcc agc ctg ggc tcc gac gac ccc gag acc cag	2234
Val Lys Leu Gly Ala Ala Ser Leu Gly Ser Asp Asp Pro Glu Thr Gln	
686 691 696 701	
gtg gtt ttg atc aat gcc atc aaa gat gtg gcc aag gcc ctt tct gat	2282
Val Val Leu Ile Asn Ala Ile Lys Asp Val Ala Lys Ala Leu Ser Asp	

702	707	712	717	
ctc atc agt gct acc aag gga gct gcc agc aag cca gtg gac gac cct				2330
Leu Ile Ser Ala Thr Lys Gly Ala Ala Ser Lys Pro Val Asp Asp Pro				
718	723	728	733	
tcc atg tac cag ctc aag ggg gct gcc aag gtg atg gtg acc aat gtc				2378
Ser Met Tyr Gln Leu Lys Gly Ala Ala Lys Val Met Val Thr Asn Val				
734	739	744	749	
acc tcg ctc ctc aag act gta aag gca gtg gag gat gag gcc acc cgg				2426
Thr Ser Leu Leu Lys Thr Val Lys Ala Val Glu Asp Glu Ala Thr Arg				
750	755	760	765	
ggc acc agg gcg ctt gag gcc aca att gaa tgc ata aag cag gag ctt				2474
Gly Thr Arg Ala Leu Glu Ala Thr Ile Glu Cys Ile Lys Gln Glu Leu				
766	771	776	781	
acg gtg ttc cag tca aaa gac gta cct gaa aag aca tca tca cct gaa				2522
Thr Val Phe Gln Ser Lys Asp Val Pro Glu Lys Thr Ser Ser Pro Glu				
782	787	792	797	
gaa tcc ata agg atg acg aaa ggc atc acc atg gca aca gcc aaa gcc				2570
Glu Ser Ile Arg Met Thr Lys Gly Ile Thr Met Ala Thr Ala Lys Ala				
798	803	808	813	
gtg gca gct ggg aac tca tgt aga cag gag gac gtg att gct act gcc				2618
Val Ala Ala Gly Asn Ser Cys Arg Gln Glu Asp Val Ile Ala Thr Ala				
814	819	824	829	
aac ctg agc cgg aaa gcc gtg tca gat atg ttg acg gct tgc aag caa				2666
Asn Leu Ser Arg Lys Ala Val Ser Asp Met Leu Thr Ala Cys Lys Gln				
830	835	840	845	
gca tcc ttc cac ccc gat gtc agt gac gag gtg aga acc aga gcc ttg				2714
Ala Ser Phe His Pro Asp Val Ser Asp Glu Val Arg Thr Arg Ala Leu				
846	851	856	861	
cgt ttc ggg acg gag tgc acc ctt ggc tac ttg gac ctc ctg gag cac				2762
Arg Phe Gly Thr Glu Cys Thr Leu Gly Tyr Leu Asp Leu Leu Glu His				
862	867	872	877	
gtc ttg gtg att ctt cag aaa cca acc cca gaa ttc aag cag cag ctg				2810
Val Leu Val Ile Leu Gln Lys Pro Thr Pro Glu Phe Lys Gln Gln Leu				
878	883	888	893	
gcc gct ttc tcc aag cga gtc gcc ggc gct gtg aca gag ctc atc cag				2858
Ala Ala Phe Ser Lys Arg Val Ala Gly Ala Val Thr Glu Leu Ile Gln				
894	899	904	909	
gcg gcg gaa gcc atg aaa gga aca gag tgg gtg gat cca gaa gac cca				2906
Ala Ala Glu Ala Met Lys Gly Thr Glu Trp Val Asp Pro Glu Asp Pro				
910	915	920	925	
act gtc att gca gaa aca gag tta ctg ggg gct gca gca tcc atc gaa				2954
Thr Val Ile Ala Glu Thr Glu Leu Leu Gly Ala Ala Ala Ser Ile Glu				
926	931	936	941	

gct gct gct aag aag tta gag caa ctg aag cca aga gca aaa cca aaa	3002
Ala Ala Ala Lys Lys Leu Glu Gln Leu Lys Pro Arg Ala Lys Pro Lys	
942 947 952 957	
caa gcg gat gag acc ctg gac ttt gag gaa cag atc ttg gaa gct gct	3050
Gln Ala Asp Glu Thr Leu Asp Phe Glu Glu Gln Ile Leu Glu Ala Ala	
958 963 968 973	
aaa tcc att gct gct gcc aca agc gcc ctg gtc aaa tcg gcc tca gca	3098
Lys Ser Ile Ala Ala Ala Thr Ser Ala Leu Val Lys Ser Ala Ser Ala	
974 979 984 989	
gcc cag agg gag ctg gtg gcc caa gga aag gtg ggc tcc atc cct gcc	3146
Ala Gln Arg Glu Leu Val Ala Gln Gly Lys Val Gly Ser Ile Pro Ala	
990 995 1000 1005	
aat gct gca gac gac gga cag tgg tca cag ggg ctg att tct gct gcc	3194
Asn Ala Ala Asp Asp Gly Gln Trp Ser Gln Gly Leu Ile Ser Ala Ala	
1006 1011 1016 1021	
cgg atg gtg gcg gct gcg acc agc agt ctc tgt gag gcg gcc aat gcc	3242
Arg Met Val Ala Ala Ala Thr Ser Ser Leu Cys Glu Ala Ala Asn Ala	
1022 1027 1032 1037	
tcc gtt cag gga cac gcc agc gag gag aag ctc atc tca tct gcc aag	3290
Ser Val Gln Gly His Ala Ser Glu Glu Lys Leu Ile Ser Ser Ala Lys	
1038 1043 1048 1053	
cag gtc gcc gct tcc acg gct cag ctg ctg gtg gcc tgc aag gtg aag	3338
Gln Val Ala Ala Ser Thr Ala Gln Leu Leu Val Ala Cys Lys Val Lys	
1054 1059 1064 1069	
gcc gac cag gat tca gag gcc atg agg cgg cta cag gcg gca gga aat	3386
Ala Asp Gln Asp Ser Glu Ala Met Arg Arg Leu Gln Ala Ala Gly Asn	
1070 1075 1080 1085	
gct gtg aaa aga gcc tca gac aat ctt gtc cgt gca gcc cag aag gca	3434
Ala Val Lys Arg Ala Ser Asp Asn Leu Val Arg Ala Ala Gln Lys Ala	
1086 1091 1096 1101	
gct ttt ggc aaa gct gat gac gac gat gtt gta gtg aaa acc aag ttt	3482
Ala Phe Gly Lys Ala Asp Asp Asp Val Val Val Lys Thr Lys Phe	
1102 1107 1112 1117	
gtg ggg ggc att gct cag atc atc gcc gcc cag gaa gaa atg cta aag	3530
Val Gly Gly Ile Ala Gln Ile Ile Ala Ala Gln Glu Glu Met Leu Lys	
1118 1123 1128 1133	
aaa gag cga gaa ctg gaa gaa gca agg aaa aaa ctg gcc caa atc cgc	3578
Lys Glu Arg Glu Leu Glu Glu Ala Arg Lys Lys Leu Ala Gln Ile Arg	
1134 1139 1144 1149	
cag cag cag tat aag ttt tta ccc acc gag ctg agg gaa gat gag ggc	3626
Gln Gln Gln Tyr Lys Phe Leu Pro Thr Glu Leu Arg Glu Asp Glu Gly	
1150 1155 1160 1165	

taa aggt gcgagcccag atggcgagcc ccaggggatg gccctggctg aactggacag 3683

*

1166

acagtgttcc tgagaggctg ggcacttagc tggaaacogc ccacctccct cccgggtgag 3743

cctggagccc tgcgtgcttg ttctcacatc tctgtcccgt cggcactggc tgcattgatc 3803

tgatgtcaca cggtagaatg tcctaccac aactcctctg ccgcctcccc tcatgcctca 3863

ccgtgtctca ggagagaggg gtgcacgttt catggactgt taccaacaaa gaaaagtcag 3923

tattatgttg ttctcagaca ctttggcttt tgttggtoct totcttaggc ctgctcctgg 3983

acctctttat gatattgtga tagggaaaaa aatcattgac gtcatagaat attcttcttc 4043

ctctcaggag aagacggaag ctggagtgg acatggttca taaaagccag aaacacaaac 4103

ccgtgtggac tccgggaggg tgactcaggt cctccttcca tgtcttgagc actggctcac 4163

ccaggggggtg aaaaattccc gccctgttt gcacgctttc ttgcctccgt gtgtaagctc 4223

cttgtagaac ccagacccat cttgtatttt gtggccaga aaactgaacg attattttgt 4283

tcctccgtag tccaaagggc agagtgcgg aaggccgtcg gggcttggtg agcaggggct 4343

gtaatacagt ctgtgggctc cttaccctgc agaggctgtt tcagctcaca cagagtcac 4403

cacacaaacc cacggctccc agttgacagt cagtggaatg ctcgtctcct tagcgtccag 4463

gggtggggatt ctgctggaat aaagagcttc ctcagtgcact catctttagg tcccacgctg 4523

gtttctgtgc cttcagaatg gtcacaagcc cggattggaa aggatctgct taaaaacctg 4583

tcccctgtcc tccaaccaa aacgcctttt tttctgtctt aatatccaga aaatctaaat 4643

gcacctaata atcaatgtga acctttaaca agatagtttt acttattatc acataagaca 4703

taagatgttt tcatcttctg gatgtcacac ttccagaatt tcatattttt cccctctttt 4763

ctttccctt tttagagccc tcccatagga aggaagggc ttgaatttac ccttaatctg 4823

cacctttagc caaggcagt catggaagat gaatggctcg tggggccaga atctaagcc 4883

aggagcagg agtgtttgaa agaattcata gtggggaagg taaaagttaa tggaagtaca 4943

tgattttcaa aactggtaac agttaaggc actcaccctc cgctctctc tctctctctc 5003

tctctggtgt gctatcatgt cttggactcc atccacacta tagtttcaaa gttccactga 5063

cgggggaaag ttggtgcttt ggtcctccga agatgtcacc tttagacctt gccgatctt 5123

gtttcaccag actctagccc atgtcatggt tttaaaatac ataaacttct gacagcttcc 5183

catatttata agttacttat aagtgtgca cgtattagaa tttttttttt tcagaccagt 5243

aaagttagag aaaagacgct gtaaaggaaa agcaagtgag agtatgtgta ggacactgac 5303

agtgtgtggg caccagttct gaagaggagg ggagctgctg gagccctagc ctgttgggga 5363
 aaagetggca cactcttggc tcgccctctt tgagtggagc tgatccaaca cctcatgcct 5423
 gccttggccg gacactgaga ggaggggcac acgtgcttcc agagacactc aggagtcaga 5483
 cccaatgct cagagtcaca atgtgttcat ggctcctgt aacaggactc tggggatccc 5543
 ctctgtggcc cagcccaccc caccctctgc tcttctatgc tgtgcccagg gcagctgccc 5603
 tcttctgcct gtgccccatc ccatcctgaa aaccaggac caaggcaggg gcaggcagcc 5663
 agttcttcca ccttgccctca gagtcattha aaacctttac tgcatttgat accagaaaag 5723
 cctccagaga caaaccaaat gcaaaggcct ttcctttata actctaaaga acaggcatcg 5783
 aaagtttatt tttgtaggag ctatataaat actcaccttt ctggagtcgt ccagtgcctg 5843
 gagctttggg gagtttgggt ctcagttatc acctgggatg gtcccagttt ctcatctgtc 5903
 ctttctcat ccaccctgca catgtgtatg tgaacggctt cgtggccgggt gtggtgggtt 5963
 ctcatctcat aagatagttg aaggggccatg ccttgtctgg atgttattta ataggcacta 6023
 ctgcggtgtc ctcagatggt actgaggggg ccttctggtc cttcaaagga aaataacaca 6083
 ggcattgagtt catttgggag tgtgaacttt cagaacacct aataagagag tgggtgtcaga 6143
 gtaaaaacgg cccaggtct ggagcataga agtgtatctc tgtgaagaga gagccgggtg 6203
 gttgacatgt ggttcttctc acaccctctc actcctcgag ggctttgaat ccttgggctg 6263
 atttttgtgc cagaaattgc tgttcccgat ggccaaaagg ggaacctgaa ctggatttca 6323
 gaactgcccga gtgatttgaa aatttagatt ttacttgggc ctttcaggag tctttagata 6383
 gggatgctga ggtcatattt agttcaatga acagcccttg ttttaagtttt gccagtgtcc 6443
 agccagctgt ggccctggcc atctgtgcag gcaggttcct caattcctgg ttggccctgc 6503
 agtcggtcaa cacagtccct ccaggtcggc tgcagaggca gctgcccagc ctgcagtcta 6563
 tgcacgggccc ttaagaaatg agctgcctgt agcctcacgg catatgcttt tatcaggga 6623
 aacccttcga gcttcttctg attctcacct gcttgctttc tggctgtctt agtcagtgtg 6683
 ttacaggca actaaagcct gttcctaatt tatcaaaaaa ttataaccaa aattcaccat 6743
 agcctaagag agtaaaccct acctccaaag tgatgccaaag gccaaaacct catcaaggaa 6803
 ccagacacag gtcaaaagtgt gtgagcaagc catgggtctct gctcctgggg aactcacacg 6863
 ctgacccccg aggagccttg gtttctctcc tggcagatag tccccagaat cttctctccc 6923
 agctttgagg ttctgggctc tggaaaggcc tctgggatgc tggccttaag atctcagcac 6983

agactatcag catgttccat tctcagattc ctggaggaaa ggtaccctct gttgaccaag 7043
 gggctggctg cttctgagac ttaccaaccc aagaaatttg gagacattcc cctcaggcta 7103
 aaaggcagcg gtccccagag ttcagaaagc aaaagatctt gacaactgtg ccagtagtgg 7163
 ctctggtcct atctctccac agtgctggcc tctgctgggg aaggcatctt tcccaaaggt 7223
 atccccaggt accatgttga aaatgtctc agtctgttgc tccatctttc tgagcctctg 7283
 cttggtatgt catgtttatg gtcactacgg atgagtgtgt gcagagtttg ggttgattct 7343
 tttaaatgct acaaacaaga gctatttctt ttcaataaaa aagggttgga ttcggcctct 7403
 tcctctgagc ccacctccca gccctccagg gagcatcagt gtacctgagt cactttgtct 7463
 gcatctcttc atcccacaaa acacgaggct gggctctcatt cagcggcctc tcaccaacct 7523
 tcaagatcca gaagaaaaca ggaacgttca gctctgccct gtgtcgtatc taatcacata 7583
 cattaattta tctaaccaca taagttattt ttttttattt gccagaaata aacctttaaa 7643
 ggaaaaaaaa aaaa 7657

<210> 354
 <211> 1958
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (60)..(1775)

<400> 354
 aattccggg togaggaggt ccagctctgc agctggaggt gctcatctgc ctggggctc 59
 atg ggt ttg gaa cgg gca ctc aat gtg ttg gcg cct ata ttc tat agg 107
 Met Gly Leu Glu Arg Ala Leu Asn Val Leu Ala Pro Ile Phe Tyr Arg
 1 5 10 15

 aac att gtg aac ttg ctg act gaa aat gca cct tgg aac tct ctg gcc 155
 Asn Ile Val Asn Leu Leu Thr Glu Asn Ala Pro Trp Asn Ser Leu Ala
 17 22 27 32

 tgg act gtt acc agt tac gtc ttc ctc aag ttc ctc cag ggg ggt ggc 203
 Trp Thr Val Thr Ser Tyr Val Phe Leu Lys Phe Leu Gln Gly Gly Gly
 33 38 43 48

 act ggc agt aca ggc ttc gtg agc aac ctg cgc acc ttc ctg tgg atc 251
 Thr Gly Ser Thr Gly Phe Val Ser Asn Leu Arg Thr Phe Leu Trp Ile
 49 54 59 64

 cgg gtg cag cag ttc acg tct cgg cgg gtg gag ctg ctc atc ttc tcc 299
 Arg Val Gln Gln Phe Thr Ser Arg Arg Val Glu Leu Leu Ile Phe Ser
 65 70 75 80

cac ctg cac gag ctc tca ctg cgc tgg cac ctg ggg cgc cgc aca ggg	347
His Leu His Glu Leu Ser Leu Arg Trp His Leu Gly Arg Arg Thr Gly	
81 86 91 96	
gag gtg ctg cgg atc gcg gat cgg ggc aca tcc agt gtc aca ggg ctg	395
Glu Val Leu Arg Ile Ala Asp Arg Gly Thr Ser Ser Val Thr Gly Leu	
97 102 107 112	
ctc agc tac ctg gtg ttc aat gtc atc ccc acg ctg gcc gac atc atc	443
Leu Ser Tyr Leu Val Phe Asn Val Ile Pro Thr Leu Ala Asp Ile Ile	
113 118 123 128	
att ggc atc atc tac ttc agc atg ttc ttc aac gcc tgg ttt ggc ctc	491
Ile Gly Ile Ile Tyr Phe Ser Met Phe Phe Asn Ala Trp Phe Gly Leu	
129 134 139 144	
att gtg ttc ctg tgc atg agt ctt tac ctc acc ctg acc att gtg gtc	539
Ile Val Phe Leu Cys Met Ser Leu Tyr Leu Thr Leu Thr Ile Val Val	
145 150 155 160	
act gag tgg aga acc aag ttt cgt cgt gct atg aac aca cag gag aac	587
Thr Glu Trp Arg Thr Lys Phe Arg Arg Ala Met Asn Thr Gln Glu Asn	
161 166 171 176	
gct acc cgg gca cga gca gtg gac tct ctg cta aac ttc gag acg gtg	635
Ala Thr Arg Ala Arg Ala Val Asp Ser Leu Leu Asn Phe Glu Thr Val	
177 182 187 192	
aag tat tac aac gcc gag agt tac gaa gtg gaa cgc tat cga gag gcc	683
Lys Tyr Tyr Asn Ala Glu Ser Tyr Glu Val Glu Arg Tyr Arg Glu Ala	
193 198 203 208	
atc atc aaa tat cag ggt ttg gag tgg aag tgc agc gct tca ctg gtt	731
Ile Ile Lys Tyr Gln Gly Leu Glu Trp Lys Ser Ser Ala Ser Leu Val	
209 214 219 224	
tta cta aat cag acc cag aac ctg gtg att ggg ctc ggg ctc ctc gcc	779
Leu Leu Asn Gln Thr Gln Asn Leu Val Ile Gly Leu Gly Leu Leu Ala	
225 230 235 240	
ggc tcc ctg ctt tgc gca tac ttt gtc act gag cag aag cta cag gtt	827
Gly Ser Leu Leu Cys Ala Tyr Phe Val Thr Glu Gln Lys Leu Gln Val	
241 246 251 256	
ggg gac tat gtg ctc ttt ggc acc tac att atc cag ctg tac atg ccc	875
Gly Asp Tyr Val Leu Phe Gly Thr Tyr Ile Ile Gln Leu Tyr Met Pro	
257 262 267 272	
ctc aat tgg ttt ggc acc tac tac agg atg atc cag acc aac ttc att	923
Leu Asn Trp Phe Gly Thr Tyr Tyr Arg Met Ile Gln Thr Asn Phe Ile	
273 278 283 288	
gac atg gag aac atg ttt gac ttg ctg aaa gag gag aca gaa gtg aag	971
Asp Met Glu Asn Met Phe Asp Leu Leu Lys Glu Glu Thr Glu Val Lys	
289 294 299 304	

gac ctt cct gga gca ggg ccc ctt cgc ttt cag aag ggc cgt att gag Asp Leu Pro Gly Ala Gly Pro Leu Arg Phe Gln Lys Gly Arg Ile Glu 305 310 315 320	1019
ttt gag aac gtg cac ttc agc tat gcc gat ggg cgg gag act ctg cag Phe Glu Asn Val His Phe Ser Tyr Ala Asp Gly Arg Glu Thr Leu Gln 321 326 331 336	1067
gac gtg tct ttc act gtg atg cct gga cag aca ctt gcc ctg gtg ggc Asp Val Ser Phe Thr Val Met Pro Gly Gln Thr Leu Ala Leu Val Gly 337 342 347 352	1115
cca tct ggg gca ggg aag agc aca att ttg cgc ctg ctg ttt cgc ttc Pro Ser Gly Ala Gly Lys Ser Thr Ile Leu Arg Leu ³ Leu Phe Arg Phe 353 358 363 368	1163
tac gac atc agc tct ggc tgc atc cga ata gat ggg cag gac att tca Tyr Asp Ile Ser Ser Gly Cys Ile Arg Ile Asp Gly Gln Asp Ile Ser 369 374 379 384	1211
cag gtg acc cag gcc tct ctc cgg tct cac att gga gtt gtg ccc caa Gln Val Thr Gln Ala Ser Leu Arg Ser His Ile Gly Val Val Pro Gln 385 390 395 400	1259
gac act gtc ctc ttt aat gac acc atc gcc gac aat atc cgt tac ggc Asp Thr Val Leu Phe Asn Asp Thr Ile Ala Asp Asn Ile Arg Tyr Gly 401 406 411 416	1307
cgt gtc aca gct ggg aat gat gag gtg gag gct gct gct cag gct gca Arg Val Thr Ala Gly Asn Asp Glu Val Glu Ala Ala Ala Gln Ala Ala 417 422 427 432	1355
ggc atc cat gat gcc att atg gct ttc cct gaa ggg tac agg aca cag Gly Ile His Asp Ala Ile Met Ala Phe Pro Glu Gly Tyr Arg Thr Gln 433 438 443 448	1403
gtg ggc gag cgg gga ctg aag ctg agc ggc ggg gag aag cag cgc gtc Val Gly Glu Arg Gly Leu Lys Leu Ser Gly Gly Glu Lys Gln Arg Val 449 454 459 464	1451
gcc att gcc cgc acc atc ctc aag gct ccg ggc atc att ctg ctg gat Ala Ile Ala Arg Thr Ile Leu Lys Ala Pro Gly Ile Ile Leu Leu Asp 465 470 475 480	1499
gag gca acg tca gcg ctg gat aca tct aat gag agg gcc atc cag gct Glu Ala Thr Ser Ala Leu Asp Thr Ser Asn Glu Arg Ala Ile Gln Ala 481 486 491 496	1547
tct ctg gcc aaa gtc tgt gcc aac cgc acc acc atc gta gtg gca cac Ser Leu Ala Lys Val Cys Ala Asn Arg Thr Thr Ile Val Val Ala His 497 502 507 512	1595
agg ctc tca act gtg gtc aat gct gac cag atc ctc gtc atc aag gat Arg Leu Ser Thr Val Val Asn Ala Asp Gln Ile Leu Val Ile Lys Asp 513 518 523 528	1643
ggc tgc atc gtg gag agg gga cga cac gag gct ctg ttg tcc cga ggt	1691

Gly Cys Ile Val Glu Arg Gly Arg His Glu Ala Leu Leu Ser Arg Gly	
529	534 539 544
ggg gtg tat gct gac atg tgg cag ctg cag cag gga cag gaa gaa acc	1739
Gly Val Tyr Ala Asp Met Trp Gln Leu Gln Gln Gly Gln Glu Glu Thr	
545	550 555 560
tct gaa gac act aag cct cag acc atg gaa cgg tga caaa agtttggcca	1789
Ser Glu Asp Thr Lys Pro Gln Thr Met Glu Arg *	
561	566 571
cttcctctc aaagactaac ccagaaggga ataagatgtg tctcctttcc ctggcttatt	1849
tcctcctggt cttgggggtat ggtgctagct atggtaaggg aaagggacct ttccgaaaaa	1909
catcttttgg ggaaataaaa atgtggactg tgcgagcaaa aaaaaaaaaa	1958

```
<210> 355 .
<211> 1864
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (167)..(1696)
```

<400>	355								
cgggtcgcagc	atttcgtcct	cggaggggca	gaggctgaac	cgccoctacc	tgccgcgcac				60
ccctccggct	tccgccgcgg	cgccagcccg	cgccctgatto	gcggcgggag	cggcaggagg				120
gagaacgccc	actccgtggc	aggaaagtga	ataaaacttaa	ttgaga	atg tct gaa				175
					Met Ser Glu				
					1				

aac ctt gac aag tcc aat gta aat gaa gca gga aaa tca aaa tcc aat 223
Asn Leu Asp Lys Ser Asn Val Asn Glu Ala Gly Lys Ser Lys Ser Asn
4 9 14 19

gat tct gag gaa ggc ctt gaa gat gct gtg gaa ggt gct gat gaa gcc 271
Asp Ser Glu Glu Gly Leu Glu Asp Ala Val Glu Gly Ala Asp Glu Ala
20 25 30 35

tta caa aaa gca ata aag tca gac tcc tcc agc ccc caa aga gtg cag 319
Leu Gln Lys Ala Ile Lys Ser Asp Ser Ser Ser Pro Gln Arg Val Gln
36 41 46 51

aga cct cac tct agt cct cct cgc ttt gtg aca gta gaa gaa ctt cta 367
Arg Pro His Ser Ser Pro Pro Arg Phe Val Thr Val Glu Glu Leu Leu
52 57 62 67

gag aca gcg aga ggc gtc acc aac atg gct cta gcc cat gaa att gta 415
Glu Thr Ala Arg Gly Val Thr Asn Met Ala Leu Ala His Glu Ile Val
68 73 78 83

gta aat gga gac ttt cag att aaa cca gtt gaa tta cca gaa aac agc	463
Val Asn Gly Asp Phe Gln Ile Lys Pro Val Glu Leu Pro Glu Asn Ser	
84 89 94 99	
ttg aag aag aga gta aag gag att gta cat aaa gcg ttt tgg gat tgc	511
Leu Lys Lys Arg Val Lys Glu Ile Val His Lys Ala Phe Trp Asp Cys	
100 105 110 115	
ttg agt gtg cag cta agt gaa gat ccc cca gca tat gac cat gct atc	559
Leu Ser Val Gln Leu Ser Glu Asp Pro Pro Ala Tyr Asp His Ala Ile	
116 121 126 131	
aaa ctt gta gga gaa atc aaa gag act ctc tta tct ttc ttg ctg cct	607
Lys Leu Val Gly Glu Ile Lys Glu Thr Leu Leu Ser Phe Leu Leu Pro	
132 137 142 147	
ggt cat act aga ctg aga aac cag ata aca gaa gtc ttg gat ctg gat	655
Gly His Thr Arg Leu Arg Asn Gln Ile Thr Glu Val Leu Asp Leu Asp	
148 153 158 163	
ctg ata aag cag gaa gca gag aat ggg gcg cta gac att tcc aag ctg	703
Leu Ile Lys Gln Glu Ala Glu Asn Gly Ala Leu Asp Ile Ser Lys Leu	
164 169 174 179	
gca gaa ttc att att ggc atg atg ggg aca ctg tgt gca cct gct cga	751
Ala Glu Phe Ile Ile Gly Met Met Gly Thr Leu Cys Ala Pro Ala Arg	
180 185 190 195	
gat gag gaa gtt aag aaa cta aag gac att aag gaa ata gtg ccc ctt	799
Asp Glu Glu Val Lys Lys Leu Lys Asp Ile Lys Glu Ile Val Pro Leu	
196 201 206 211	
ttc aga gaa att ttt tct gtg ttg gac cta atg aaa gtg gac atg gcc	847
Phe Arg Glu Ile Phe Ser Val Leu Asp Leu Met Lys Val Asp Met Ala	
212 217 222 227	
aac ttt gct atc agt agc atc agg cct cat ctc atg cag cag tca gtt	895
Asn Phe Ala Ile Ser Ser Ile Arg Pro His Leu Met Gln Gln Ser Val	
228 233 238 243	
gaa tac gaa agg aag aag ttt caa gag att ttg gag agg caa cca aat	943
Glu Tyr Glu Arg Lys Lys Phe Gln Glu Ile Leu Glu Arg Gln Pro Asn	
244 249 254 259	
tcc ctg gac ttt gtc acc cag tgg ctg gaa gaa gcc tca gag gac ctt	991
Ser Leu Asp Phe Val Thr Gln Trp Leu Glu Glu Ala Ser Glu Asp Leu	
260 265 270 275	
atg act cag aag tat aaa cac gcc ctg cca gtg ggg gga atg gct gct	1039
Met Thr Gln Lys Tyr Lys His Ala Leu Pro Val Gly Gly Met Ala Ala	
276 281 286 291	
ggc tct ggg gac atg ccc agg ctg agc cct gtt gct gtc cag aat tac	1087
Gly Ser Gly Asp Met Pro Arg Leu Ser Pro Val Ala Val Gln Asn Tyr	
292 297 302 307	

gct tac ctg aag ctt ctg aag tgg gac cac ctc cag agg ccg ttc ccc	1135
Ala Tyr Leu Lys Leu Leu Lys Trp Asp His Leu Gln Arg Pro Phe Pro	
308 313 318 323	
gaa aca gtt tta atg gac cag tct cgc ttc cac gag ctc cag ttg cag	1183
Glu Thr Val Leu Met Asp Gln Ser Arg Phe His Glu Leu Gln Leu Gln	
324 329 334 339	
ctg gaa caa ctg acc atc ctg ggg gct gtg ttg ctg gtc acc ttc agc	1231
Leu Glu Gln Leu Thr Ile Leu Gly Ala Val Leu Leu Val Thr Phe Ser	
340 345 350 355	
atg gca gcg cca gga att tcc agc cag gcc gac ttt gct gag aaa ctc	1279
Met Ala Ala Pro Gly Ile Ser Ser Gln Ala Asp Phe Ala Glu Lys Leu	
356 361 366 371	
aag atg att gtg aag att ttg cta aca gat atg cac ctg ccc tcc ttc	1327
Lys Met Ile Val Lys Ile Leu Leu Thr Asp Met His Leu Pro Ser Phe	
372 377 382 387	
cat ctg aag gac gtc ctc act acc atc ggg gag aag gtg tgc ctg gag	1375
His Leu Lys Asp Val Leu Thr Thr Ile Gly Glu Lys Val Cys Leu Glu	
388 393 398 403	
gtg agc agc tgc ctc tcc ctg tgt ggg tcc tct ccc ttc acc acg gac	1423
Val Ser Ser Cys Leu Ser Leu Cys Gly Ser Ser Pro Phe Thr Thr Asp	
404 409 414 419	
aag gag acc gtg ctc aag ggc cag atc cag gcc gtg gcc agt ccc gat	1471
Lys Glu Thr Val Leu Lys Gly Gln Ile Gln Ala Val Ala Ser Pro Asp	
420 425 430 435	
gac ccc att cgc agg atc atg gaa tct cga atc ctg acc ttc tta gaa	1519
Asp Pro Ile Arg Arg Ile Met Glu Ser Arg Ile Leu Thr Phe Leu Glu	
436 441 446 451	
acc tac ctt gcc tcg ggt cat cag aag cca ttg ccc aca gtc cct ggg	1567
Thr Tyr Leu Ala Ser Gly His Gln Lys Pro Leu Pro Thr Val Pro Gly	
452 457 462 467	
gga ctc agt cca gtt cag aga gag ctg gag gaa gtt gct att aaa ttt	1615
Gly Leu Ser Pro Val Gln Arg Glu Leu Glu Val Ala Ile Lys Phe	
468 473 478 483	
gct cgc ctg gtc aac tat aac aag atg gtc ttc tgt ccc tac tac gat	1663
Ala Arg Leu Val Asn Tyr Asn Lys Met Val Phe Cys Pro Tyr Tyr Asp	
484 489 494 499	
gca atc ctg agt aag atc ctc gtc caa tcc taa cgtgtatg caccctacag	1714
Ala Ile Leu Ser Lys Ile Leu Val Gln Ser *	
500 505 510	
cagcagtatt actcactagc cacagaatac ctgttctgta ctctaattgtt gcattggaaa	1774
atggctatat agtacatgtc tatttaacag caccgattcc aaagggaaga atattgtgta	1834
tcactgttga aaagacttgt tgagaaatcc	1864

<210> 356
 <211> 2850
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (81)..(2405)

<220>
 <221> misc_feature
 <222> (1)...(2850)
 <223> n = a,t,c or g

<400> 356

tgcggccgcc	tcctcttcgg	ggtcattaaa	gccaatgagc	cgcgcgccctc	tgccgagcgc	60
agccaactaa	atcggttgg	atg att cgc gac ctg agc aag atg tac ccg				110
		Met Ile Arg Asp Leu Ser Lys Met Tyr Pro				
		1 5				
cag acc aga cac ccg gca ccg cat cag cct gct caa ccc ttt aaa ttt						158
Gln Thr Arg His Pro Ala Pro His Gln Pro Ala Gln Pro Phe Lys Phe						
11 16 21 26						
aca att tcc gaa tcc tgt gat cgg att aag gaa gag ttt cag ttt tta						206
Thr Ile Ser Glu Ser Cys Asp Arg Ile Lys Glu Glu Phe Gln Phe Leu						
27 32 37 42						
cag gct caa tac cac agt ctg aag ctg gaa tgt gag aaa ctc gcc agt						254
Gln Ala Gln Tyr His Ser Leu Lys Leu Glu Cys Glu Lys Leu Ala Ser						
43 48 53 58						
gag aag aca gag atg cag cgg cat tat gtc atg tat tat gaa atg tcc						302
Glu Lys Thr Glu Met Gln Arg His Tyr Val Met Tyr Tyr Glu Met Ser						
59 64 69 74						
tat ggg ttg aat ata gaa atg cac aag cag gca gag att gtc aag agg						350
Tyr Gly Leu Asn Ile Glu Met His Lys Gln Ala Glu Ile Val Lys Arg						
75 80 85 90						
ctg aat gct atc tgt gca caa gtc att cct ttc ctg tcc caa gag cac						398
Leu Asn Ala Ile Cys Ala Gln Val Ile Pro Phe Leu Ser Gln Glu His						
91 96 101 106						
cag caa caa gtg gtg cag gct gtg gaa cgg gcc aag cag gtg acc atg						446
Gln Gln Gln Val Val Gln Ala Val Glu Arg Ala Lys Gln Val Thr Met						
107 112 117 122						
gca gaa ctg aac gcc atc att ggg cag caa caa ctc cag gcc cag cat						494
Ala Glu Leu Asn Ala Ile Ile Gly Gln Gln Gln Leu Gln Ala Gln His						
123 128 133 138						

tta tca cat gga cat ggt ctc ccc gta cct ctg act cca cac cct tca	542
Leu Ser His Gly His Gly Leu Pro Val Pro Leu Thr Pro His Pro Ser	
139 144 149 154	
ggg ctc cag ccc cct gcc att cca ccc atc ggt agc agt gcc ggg ctt	590
Gly Leu Gln Pro Pro Ala Ile Pro Pro Ile Gly Ser Ser Ala Gly Leu	
155 160 165 170	
ctg gcc ctc tcc agt gct cta gga ggt cag tcc cat ctt cca att aaa	638
Leu Ala Leu Ser Ser Ala Leu Gly Gly Gln Ser His Leu Pro Ile Lys	
171 176 181 186	
gat gag aag aag cac cat gac aat gat cac caa aga gac aga gac tcc	686
Asp Glu Lys Lys His His Asp Asn Asp His Gln Arg Asp Arg Asp Ser	
187 192 197 202	
atc aag agc tct tca gta tcc cca tca gcc agt ttc cga ggt gct gag	734
Ile Lys Ser Ser Ser Val Ser Pro Ser Ala Ser Phe Arg Gly Ala Glu	
203 208 213 218	
aag cac aga aac tcc gca gac tac tcc tca gag agc aaa aag cag aaa	782
Lys His Arg Asn Ser Ala Asp Tyr Ser Ser Glu Ser Lys Lys Gln Lys	
219 224 229 234	
act gaa gaa aag gaa att gca gct cgt tat gac agc gat ggt gag aaa	830
Thr Glu Glu Lys Glu Ile Ala Ala Arg Tyr Asp Ser Asp Gly Glu Lys	
235 240 245 250	
agt gat gac aac ttg gtg gtt gac gtt tcc aat gag gat cca tct tcc	878
Ser Asp Asp Asn Leu Val Val Asp Val Ser Asn Glu Asp Pro Ser Ser	
251 256 261 266	
cct cga ggg agc cca gca cat tcc ccc aga gag aat ggc cta gac aag	926
Pro Arg Gly Ser Pro Ala His Ser Pro Arg Glu Asn Gly Leu Asp Lys	
267 272 277 282	
aca cgc ctg ctc aag aaa gat gcc ccg att agt cca gcc tct att gca	974
Thr Arg Leu Leu Lys Lys Asp Ala Pro Ile Ser Pro Ala Ser Ile Ala	
283 288 293 298	
tct tcc agc agt act ccc tcc tcc aaa tcc aaa gaa ctt agc ctt aat	1022
Ser Ser Ser Ser Thr Pro Ser Ser Lys Ser Lys Glu Leu Ser Leu Asn	
299 304 309 314	
gaa aaa tct act act ccc gtc tca aag tcc aat acc cct act cca cga	1070
Glu Lys Ser Thr Thr Pro Val Ser Lys Ser Asn Thr Pro Thr Pro Arg	
315 320 325 330	
act gat gcg ccc acc cca ggc agt aac tct act ccc gga ttg agg cct	1118
Thr Asp Ala Pro Thr Pro Gly Ser Asn Ser Thr Pro Gly Leu Arg Pro	
331 336 341 346	
gta cct gga aaa cca cca gga gtt gac cct ttg gcc tca agc cta agg	1166
Val Pro Gly Lys Pro Pro Gly Val Asp Pro Leu Ala Ser Ser Leu Arg	
347 352 357 362	
acc cca atg gca gta cct tgt cca tat cca act cca ttt ggg att gtg	1214

Thr Pro Met Ala Val Pro Cys Pro Tyr Pro Thr Pro Phe Gly Ile Val
363 368 373 378

ccc cat gct gga atg aac gga gag ctg acc agc ccc gga gcg gcc tac 1262
Pro His Ala Gly Met Asn Gly Glu Leu Thr Ser Pro Gly Ala Ala Tyr
379 384 389 394

gct ggg ctc cac aac atc tcc cct cag atg agc gca gct gct gcc gcc 1310
Ala Gly Leu His Asn Ile Ser Pro Gln Met Ser Ala Ala Ala Ala Ala
395 400 405 410

gcc gct gct gct gct gcc tat ggg aga tca cca gtg gtg gga ttt gat 1358
Ala Ala Ala Ala Ala Ala Tyr Gly Arg Ser Pro Val Val Gly Phe Asp
411 416 421 426

cca cac cat cac atg cgt gtg cca gca ata cct cca aac ctg aca ggc 1406
Pro His His His Met Arg Val Pro Ala Ile Pro Pro Asn Leu Thr Gly
427 432 437 442

att cca gga gga aaa cca gca tac tcc ttc cat gtt agc gca gat ggt 1454
Ile Pro Gly Gly Lys Pro Ala Tyr Ser Phe His Val Ser Ala Asp Gly
443 448 453 458

cag atg cag cct gtc cct ttt cca ccc gac gcc ctc atc gga cct gga 1502
Gln Met Gln Pro Val Pro Phe Pro Pro Asp Ala Leu Ile Gly Pro Gly
459 464 469 474

atc ccc cgg cat gct cgc cag atc aac acc ctc aac cac ggg gag gtg 1550
Ile Pro Arg His Ala Arg Gln Ile Asn Thr Leu Asn His Gly Glu Val
475 480 485 490

gtg tgc gcg gtg acc atc agc aac ccc acg aga cac gtg tac acg ggt 1598
Val Cys Ala Val Thr Ile Ser Asn Pro Thr Arg His Val Tyr Thr Gly
491 496 501 506

ggg aag ggc tgc gtc aag gtc tgg gac atc agc cac cca ggc aat aag 1646
Gly Lys Gly Cys Val Lys Val Trp Asp Ile Ser His Pro Gly Asn Lys
507 512 517 522

agt cct gtc tcc cag ctc gac tgt ctg aac agg gat aac tac atc cgt 1694
Ser Pro Val Ser Gln Leu Asp Cys Leu Asn Arg Asp Asn Tyr Ile Arg
523 528 533 538

tcc tgc aga ttg ctc cct gat ggt cgc acc cta att gtt gga ggg gaa 1742
Ser Cys Arg Leu Leu Pro Asp Gly Arg Thr Leu Ile Val Gly Gly Glu
539 544 549 554

gcc agt act ttg tcc att tgg gac ctg gcg gct cca acc cca cgc atc 1790
Ala Ser Thr Leu Ser Ile Trp Asp Leu Ala Ala Pro Thr Pro Arg Ile
555 560 565 570

aag gca gag ctg aca tcc tcg gcc ccc gcc tgc tat gcc ctg gcc atc 1838
Lys Ala Glu Leu Thr Ser Ser Ala Pro Ala Cys Tyr Ala Leu Ala Ile
571 576 581 586

agc ccc gat tcc aag gtc tgc ttc tca tgc tgc agc gac ggc aac atc 1886
Ser Pro Asp Ser Lys Val Cys Phe Ser Cys Cys Ser Asp Gly Asn Ile

587	592	597	602	
gct gtg tgg gat ctg cac aac cag acc ttg gtg agg caa ttc cag ggc				1934
Ala Val Trp Asp Leu His Asn Gln Thr Leu Val Arg Gln Phe Gln Gly				
603	608	613	618	
cac aca gat gga gcc agc tgt att gac att tct aat gat ggc acc aag				1982
His Thr Asp Gly Ala Ser Cys Ile Asp Ile Ser Asn Asp Gly Thr Lys				
619	624	629	634	
ctc tgg aca ggt ggt ttg gac aac acg gtc agg tcc tgg gac ctg cgc				2030
Leu Trp Thr Gly Gly Leu Asp Asn Thr Val Arg Ser Trp Asp Leu Arg				
635	640	645	650	
gag ggg cgg cag ctg cag cag cac gac ttc acc tcc cag atc ttt tct				2078
Glu Gly Arg Gln Leu Gln Gln His Asp Phe Thr Ser Gln Ile Phe Ser				
651	656	661	666	
ctg ggc tac tgc cca act gga gag tgg ctt gca gtg ggg atg gag aac				2126
Leu Gly Tyr Cys Pro Thr Gly Glu Trp Leu Ala Val Gly Met Glu Asn				
667	672	677	682	
agc aat gtg gaa gtt ttg cat gtc acc aag cca gac aaa tac caa cta				2174
Ser Asn Val Glu Val Leu His Val Thr Lys Pro Asp Lys Tyr Gln Leu				
683	688	693	698	
cat ctt cat gag agc tgt gtg ctg tgc ctc aag ttt gcc cat tgt ggc				2222
His Leu His Glu Ser Cys Val Leu Ser Leu Lys Phe Ala His Cys Gly				
699	704	709	714	
aaa tgg ttt gta agc act gga aag gac aac ctt ctg aat gcc tgg aga				2270
Lys Trp Phe Val Ser Thr Gly Lys Asp Asn Leu Leu Asn Ala Trp Arg				
715	720	725	730	
aca cct tat ggg gcc agt ata ttc cag tcc aaa gaa tcc tca tgc gtg				2318
Thr Pro Tyr Gly Ala Ser Ile Phe Gln Ser Lys Glu Ser Ser Ser Val				
731	736	741	746	
ctt agc tgt gac atc tcc gtg gac gac aaa tac att gtc act ggc tct				2366
Leu Ser Cys Asp Ile Ser Val Asp Asp Lys Tyr Ile Val Thr Gly Ser				
747	752	757	762	
ggg gat aag aag gcc aca gtt tat gaa gtt att tat taa agacaaatct				2415
Gly Asp Lys Lys Ala Thr Val Tyr Glu Val Ile Tyr *				
763	768	773		
tcatgcagac tggacttctc ctccctggtag cactttgctc tgtcatcctt tttgttcacc				2475
cccatccccg catctaaaac caaggatttc agatactcat tgcagttgtg gagtttaatc				2535
ccctttctta acctcacttc ccacttgcta ttgaattgtg aatagtcatt aaaaacctgt				2595
gataccaaat ctccagctgt ctacttgga gaacatggaa taagcatact taacagtga				2655
aagaatcttt aattatgtat tatatctgta atatatttat tttgtttaaa gaaggctttc				2715
taacaatgac tgactaaata aagctgtctg ctccctggcat tggataatgg aggggtgcggt				2775

tgtatttggga taccctncc cccctttttt tgggcaaggg ngggggnagg gaggggtttt 2835
 aaaatnattg gnttt 2850

<210> 357
 <211> 2787
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (81) .. (2342)

<220>
 <221> misc_feature
 <222> (1) ... (2787)
 <223> n = a,t,c or g

<400> 357
 tgcggccgcc tcctcttcgg ggtcattaaa gccaatgagc cgcgcgcctc tgccgagcgc 60

agccaactaa atcggcttgg atg att cgc gac ctg agc aag atg tac ccg 110
 Met Ile Arg Asp Leu Ser Lys Met Tyr Pro
 1 5

cag acc aga cac ccg gca ccg cat cag cct gct caa ccc ttt aaa ttt 158
 Gln Thr Arg His Pro Ala Pro His Gln Pro Ala Gln Pro Phe Lys Phe
 11 16 21 26

aca att tcc gaa tcc tgt gat cgg att aag gaa gag ttt cag ttt tta 206
 Thr Ile Ser Glu Ser Cys Asp Arg Ile Lys Glu Glu Phe Gln Phe Leu
 27 32 37 42

cag gct caa tac cac agt ctg aag ctg gaa tgt gag aaa ctc gcc agt 254
 Gln Ala Gln Tyr His Ser Leu Lys Leu Glu Cys Glu Lys Leu Ala Ser
 43 48 53 58

gag aag aca gag atg cag cgg cat tat gtc atg tat tat gaa atg tcc 302
 Glu Lys Thr Glu Met Gln Arg His Tyr Val Met Tyr Tyr Glu Met Ser
 59 64 69 74

tat ggg ttg aat ata gaa atg cac aag cag cac cag caa caa gtg gtg 350
 Tyr Gly Leu Asn Ile Glu Met His Lys Gln His Gln Gln Gln Val Val
 75 80 85 90

cag gct gtg gaa ccg gcc aag cag gtg acc atg gca gaa ctg aac gcc 398
 Gln Ala Val Glu Arg Ala Lys Gln Val Thr Met Ala Glu Leu Asn Ala
 91 96 101 106

atc att ggg cag caa caa ctc cag gcc cag cat tta tca cat gga cat 446
 Ile Ile Gly Gln Gln Leu Gln Ala Gln His Leu Ser His Gly His
 107 112 117 122

ggt ctc ccc gta cct ctg act cca cac cct tca ggg ctc cag ccc cct	494
Gly Leu Pro Val Pro Leu Thr Pro His Pro Ser Gly Leu Gln Pro Pro	
123 128 133 138	
gcc att cca ccc atc ggt agc agt gcc ggg ctt ctg gcc ctc tcc agt	542
Ala Ile Pro Pro Ile Gly Ser Ser Ala Gly Leu Leu Ala Leu Ser Ser	
139 144 149 154	
gct cta gga ggt cag tcc cat ctt cca att aaa gat gag aag aag cac	590
Ala Leu Gly Gly Gln Ser His Leu Pro Ile Lys Asp Glu Lys Lys His	
155 160 165 170	
cat gac aat gat cac caa aga gac aga gac tcc atc aag agc tct tca	638
His Asp Asn Asp His Gln Arg Asp Arg Asp Ser Ile Lys Ser Ser Ser	
171 176 181 186	
gta tcc cca tca gcc agt ttc cga ggt gct gag aag cac aga aac tcc	686
Val Ser Pro Ser Ala Ser Phe Arg Gly Ala Glu Lys His Arg Asn Ser	
187 192 197 202	
gca gac tac tcc tca gag agc aaa aag cag aaa act gaa gaa aag gaa	734
Ala Asp Tyr Ser Ser Glu Ser Lys Lys Gln Lys Thr Glu Glu Lys Glu	
203 208 213 218	
att gca gct cgt tat gac agc gat ggt gag aaa agt gat gac aac ttg	782
Ile Ala Ala Arg Tyr Asp Ser Asp Gly Glu Lys Ser Asp Asp Asn Leu	
219 224 229 234	
gtg gtt gac gtt tcc aat gag gat cca tct tcc cct cga ggg agc cca	830
Val Val Asp Val Ser Asn Glu Asp Pro Ser Ser Pro Arg Gly Ser Pro	
235 240 245 250	
gca cat tcc ccc aga gag aat ggc cta gac aag aca cgc ctg ctc aag	878
Ala His Ser Pro Arg Glu Asn Gly Leu Asp Lys Thr Arg Leu Leu Lys	
251 256 261 266	
aaa gat gcc ccg att agt cca gcc tct att gca tct tcc agc agt act	926
Lys Asp Ala Pro Ile Ser Pro Ala Ser Ile Ala Ser Ser Ser Ser Thr	
267 272 277 282	
ccc tcc tcc aaa tcc aaa gaa ctt agc ctt aat gaa aaa tct act act	974
Pro Ser Ser Lys Ser Lys Glu Leu Ser Leu Asn Glu Lys Ser Thr Thr	
283 288 293 298	
ccc gtc tca aag tcc aat acc cct act cca cga act gat gcg ccc acc	1022
Pro Val Ser Lys Ser Asn Thr Pro Thr Pro Arg Thr Asp Ala Pro Thr	
299 304 309 314	
cca ggc agt aac tct act ccc gga ttg agg cct gta cct gga aaa cca	1070
Pro Gly Ser Asn Ser Thr Pro Gly Leu Arg Pro Val Pro Gly Lys Pro	
315 320 325 330	
cca gga gtt gac cct ttg gcc tca agc cta agg acc cca atg gca gta	1118
Pro Gly Val Asp Pro Leu Ala Ser Ser Leu Arg Thr Pro Met Ala Val	
331 336 341 346	
cct tgt cca tat cca act cca ttt ggg att gtg ccc cat gct gga atg	1166

Pro Cys Pro Tyr Pro Thr Pro Phe Gly Ile Val Pro His Ala Gly Met	
347 352 357 362	
aac gga gag ctg acc agc ccc gga gcg gcc tac gct ggg ctc cac aac	1214
Asn Gly Glu Leu Thr Ser Pro Gly Ala Ala Tyr Ala Gly Leu His Asn	
363 368 373 378	
atc tcc cct cag atg agc gca gct gct gcc gcc gcc gct gct gct gct	1262
Ile Ser Pro Gln Met Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala	
379 384 389 394	
gcc tat ggg aga tca cca gtg gtg gga ttt gat cca cac cat cac atg	1310
Ala Tyr Gly Arg Ser Pro Val Val Gly Phe Asp Pro His His His Met	
395 400 405 410	
cgt gtg cca gca ata cct cca aac ctg aca ggc att cca gga gga aaa	1358
Arg Val Pro Ala Ile Pro Pro Asn Leu Thr Gly Ile Pro Gly Gly Lys	
411 416 421 426	
cca gca tac tcc ttc cat gtt agc gca gat ggt cag atg cag cct gtc	1406
Pro Ala Tyr Ser Phe His Val Ser Ala Asp Gly Gln Met Gln Pro Val	
427 432 437 442	
cct ttt cca ccc gac gcc ctc atc gga cct gga atc ccc cgg cat gct	1454
Pro Phe Pro Pro Asp Ala Leu Ile Gly Pro Gly Ile Pro Arg His Ala	
443 448 453 458	
cgc cag atc aac acc ctc aac cac ggg gag gtg gtg tgc gcg gtg acc	1502
Arg Gln Ile Asn Thr Leu Asn His Gly Glu Val Val Cys Ala Val Thr	
459 464 469 474	
atc agc aac ccc acg aga cac gtg tac acg ggt ggg aag ggc tgc gtc	1550
Ile Ser Asn Pro Thr Arg His Val Tyr Thr Gly Gly Lys Gly Cys Val	
475 480 485 490	
aag gtc tgg gac atc agc cac cca ggc aat aag agt cct gtc tcc cag	1598
Lys Val Trp Asp Ile Ser His Pro Gly Asn Lys Ser Pro Val Ser Gln	
491 496 501 506	
ctc gac tgt ctg aac agg gat aac tac atc cgt tcc tgc aga ttg ctc	1646
Leu Asp Cys Leu Asn Arg Asp Asn Tyr Ile Arg Ser Cys Arg Leu Leu	
507 512 517 522	
cct gat ggt cgc acc cta att gtt gga ggg gaa gcc agt act ttg tcc	1694
Pro Asp Gly Arg Thr Leu Ile Val Gly Gly Glu Ala Ser Thr Leu Ser	
523 528 533 538	
att tgg gac ctg gcg gct cca acc cca cgc atc aag gca gag ctg aca	1742
Ile Trp Asp Leu Ala Ala Pro Thr Pro Arg Ile Lys Ala Glu Leu Thr	
539 544 549 554	
tcc tcg gcc ccc gcc tgc tat gcc ctg gcc atc agc ccc gat tcc aag	1790
Ser Ser Ala Pro Ala Cys Tyr Ala Leu Ala Ile Ser Pro Asp Ser Lys	
555 560 565 570	
gtc tgc ttc tca tgc tgc agc gac gcc aac atc gct gtg tgg gat ctg	1838
Val Cys Phe Ser Cys Cys Ser Asp Gly Asn Ile Ala Val Trp Asp Leu	

571	576	581	586	
cac aac cag acc ttg gtg agg caa ttc cag ggc cac aca gat gga gcc				1886
His Asn Gln Thr Leu Val Arg Gln Phe Gln Gly His Thr Asp Gly Ala				
587	592	597	602	
agc tgt att gac att tct aat gat ggc acc aag ctc tgg aca ggt ggt				1934
Ser Cys Ile Asp Ile Ser Asn Asp Gly Thr Lys Leu Trp Thr Gly Gly				
603	608	613	618	
ttg gac aac acg gtc agg tcc tgg gac ctg cgc gag ggg cgg cag ctg				1982
Leu Asp Asn Thr Val Arg Ser Trp Asp Leu Arg Glu Gly Arg Gln Leu				
619	624	629	634	
cag cag cac gac ttc acc tcc cag atc ttt tct ctg ggc tac tgc cca				2030
Gln Gln His Asp Phe Thr Ser Gln Ile Phe Ser Leu Gly Tyr Cys Pro				
635	640	645	650	
act gga gag tgg ctt gca gtg ggg atg gag aac agc aat gtg gaa gtt				2078
Thr Gly Glu Trp Leu Ala Val Gly Met Glu Asn Ser Asn Val Glu Val				
651	656	661	666	
ttg cat gtc acc aag cca gac aaa tac caa cta cat ctt cat gag agc				2126
Leu His Val Thr Lys Pro Asp Lys Tyr Gln Leu His Leu His Glu Ser				
667	672	677	682	
tgt gtg ctg tgc ctc aag ttt gcc cat tgt ggc aaa tgg ttt gta agc				2174
Cys Val Leu Ser Leu Lys Phe Ala His Cys Gly Lys Trp Phe Val Ser				
683	688	693	698	
act gga aag gac aac ctt ctg aat gcc tgg aga aca cct tat ggg gcc				2222
Thr Gly Lys Asp Asn Leu Leu Asn Ala Trp Arg Thr Pro Tyr Gly Ala				
699	704	709	714	
agt ata ttc cag tcc aaa gaa tcc tca tgc gtg ctt agc tgt gac atc				2270
Ser Ile Phe Gln Ser Lys Glu Ser Ser Ser Val Leu Ser Cys Asp Ile				
715	720	725	730	
tcc gtg gac gac aaa tac att gtc act ggc tct ggg gat aag aag gcc				2318
Ser Val Asp Asp Lys Tyr Ile Val Thr Gly Ser Gly Asp Lys Lys Ala				
731	736	741	746	
aca gtt tat gaa gtt att tat taa agacaaatct tcatgcagac tggacttctc				2372
Thr Val Tyr Glu Val Ile Tyr *				
747	752			
ctcctggtag cactttgctc tgtcatcctt tttgttcacc cccatccccg catctaaaac				2432
caaggatttc agatactcat tgcagttgtg gagtttaatc ccctttotta acctcacttc				2492
ccacttgcta ttgaattgtg aatagtcatt aaaaacctgt gataccaaat cttcagctgt				2552
ctacttgga gaacatggaa taagcatact taacagtga aagaatcttt aattatgtat				2612
tatatctgta atatatttat tttgtttaaa gaaggctttc taacaatgac tgactaaata				2672
aagctgtctg ctcctggcat tggataatgg aggggtgcggt tgtatttgga taccctncc				2732

ccccctttttt tgggcaaggg nggggggnagg gaggggtttt aaaatnattg gntttt

2787

<210> 358
<211> 2780
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (219)..(2045)

<220>
<221> misc_feature
<222> (1)...(2780)
<223> n = a,t,c or g

<400> 358

gtagaagtcc ttgcntgagg acttgtagct cttegctgc ggtaccggtc cggaattccc	60
gggccgggcgg cgacgactac gaccactagg agagcggacg gaggcggcgc ctgaagcggc	120
ggcggagccc atgccccggg acggcgggcg gacccggaga gacaaatccg gggccccggg	180
catgtccccg gggcccccggt gaggaggcgg cggcggct	233
atg gag atc gcg ccg	
Met Glu Ile Ala Pro	
1	
cag gag gcg ccg ccc gtg ccg ggc gcg gac ggc gac att gaa gag gcc	281
Gln Glu Ala Pro Pro Val Pro Gly Ala Asp Gly Asp Ile Glu Glu Ala	
6 11 16 21	
cca gct gag gcc ggg tct ccc agc ccc gcg tcg ccc ccc gcc gat ggg	329
Pro Ala Glu Ala Gly Ser Pro Ser Pro Ala Ser Pro Pro Ala Asp Gly	
22 27 32 37	
cgc ctc aag gct gca gcc aag cgc gtc aca ttc ccg tcc gac gag gat	377
Arg Leu Lys Ala Ala Ala Lys Arg Val Thr Phe Pro Ser Asp Glu Asp	
38 43 48 53	
atc gtg tct gga gca gtg gag ccc aaa gac ccc tgg aga cat gcc cag	425
Ile Val Ser Gly Ala Val Glu Pro Lys Asp Pro Trp Arg His Ala Gln	
54 59 64 69	
aat gtg acc gtg gac gag gtc atc ggc gcc tac aag cag gcc tgc cag	473
Asn Val Thr Val Asp Glu Val Ile Gly Ala Tyr Lys Gln Ala Cys Gln	
70 75 80 85	
aag ctg aac tgc agg cag atc ccc aag ctc ctc agg cag ctg cag gaa	521
Lys Leu Asn Cys Arg Gln Ile Pro Lys Leu Leu Arg Gln Leu Gln Glu	
86 91 96 101	
ttc aca gac ctc ggg cac cgc ctc gac tgt ctg gac ctg aaa ggt gag	569
Phe Thr Asp Leu Gly His Arg Leu Asp Cys Leu Asp Leu Lys Gly Glu	

102	107	112	117	
aag ctt gac tac aag acc tgt gag gcc ctg gaa gag gtc ttc aag agg				617
Lys Leu Asp Tyr Lys Thr Cys Glu Ala Leu Glu Glu Val Phe Lys Arg				
118	123	128	133	
ctg cag ttc aag gtc gtg gac ctg gag cag aca aac ctg gat gaa gat				665
Leu Gln Phe Lys Val Val Asp Leu Glu Gln Thr Asn Leu Asp Glu Asp				
134	139	144	149	
ggg gcc tcg gcc ctc ttc gac atg atc gag tac tac gag tcg gcc acc				713
Gly Ala Ser Ala Leu Phe Asp Met Ile Glu Tyr Tyr Glu Ser Ala Thr				
150	155	160	165	
cac ctc aac atc tcc ttc aac aag cac atc ggc acc cgg ggc tgg cag				761
His Leu Asn Ile Ser Phe Asn Lys His Ile Gly Thr Arg Gly Trp Gln				
166	171	176	181	
gcg gcc gcc cac atg atg cgc aag acg agc tgc ctg cag tat ctg gac				809
Ala Ala Ala His Met Met Arg Lys Thr Ser Cys Leu Gln Tyr Leu Asp				
182	187	192	197	
gcc cgc aac acg ccc ctg ctg gac cac tcg gcg ccc ttc gtg gcc cgt				857
Ala Arg Asn Thr Pro Leu Leu Asp His Ser Ala Pro Phe Val Ala Arg				
198	203	208	213	
gcc ctg cgc atc cgc agc agc ctg gca gtg ctg cac ttg gag aac gcc				905
Ala Leu Arg Ile Arg Ser Ser Leu Ala Val Leu His Leu Glu Asn Ala				
214	219	224	229	
agc ctg tcg ggg cgg ccc ctc atg ctg ctc gcc acg gcc ctg aag atg				953
Ser Leu Ser Gly Arg Pro Leu Met Leu Leu Ala Thr Ala Leu Lys Met				
230	235	240	245	
aac atg aac ctg cgg gag ctg tac ctg gcg gac aac aag ctc aac ggc				1001
Asn Met Asn Leu Arg Glu Leu Tyr Leu Ala Asp Asn Lys Leu Asn Gly				
246	251	256	261	
ctg cag gac tcg gcc cag ctg ggt aac ctg ctc aag ttc aac tgc tcc				1049
Leu Gln Asp Ser Ala Gln Leu Gly Asn Leu Leu Lys Phe Asn Cys Ser				
262	267	272	277	
ctg cag atc ctg gac ctc cgg aac aac cac gtg cta gac tcg ggt ctg				1097
Leu Gln Ile Leu Asp Leu Arg Asn Asn His Val Leu Asp Ser Gly Leu				
278	283	288	293	
gcc tac atc tgc gag ggc ctc aag gag cag agg aag ggg ctg gtg acc				1145
Ala Tyr Ile Cys Glu Gly Leu Lys Glu Gln Arg Lys Gly Leu Val Thr				
294	299	304	309	
ctg gtg ctg tgg aac aac cag ctc acg cac aca ggc atg gcc ttc ctg				1193
Leu Val Leu Trp Asn Asn Gln Leu Thr His Thr Gly Met Ala Phe Leu				
310	315	320	325	
ggc atg aca ctg agc ctg gag acg ctg aac ctg ggc cac aac ccc atc				1241
Gly Met Thr Leu Ser Leu Glu Thr Leu Asn Leu Gly His Asn Pro Ile				
326	331	336	341	

ggg aac gag ggt gtg cgg cac ctc aag aac ggg ctc atc agc aac cgc	1289
Gly Asn Glu Gly Val Arg His Leu Lys Asn Gly Leu Ile Ser Asn Arg	
342 347 352 357	
agc gtg ctg cgc ctc ggg ctg gcc tcc acc aag ctc acg tgc gag ggc	1337
Ser Val Leu Arg Leu Gly Leu Ala Ser Thr Lys Leu Thr Cys Glu Gly	
358 363 368 373	
gcg gtg gcg gtg gcg gag ttc atc gct gag agc ccc cgc ctc ctg aga	1385
Ala Val Ala Val Ala Glu Phe Ile Ala Glu Ser Pro Arg Leu Leu Arg	
374 379 384 389	
ctg gac ctt cgg gag aac gag atc aag aca ggc ggg ctc atg gca ctg	1433
Leu Asp Leu Arg Glu Asn Glu Ile Lys Thr Gly Gly Leu Met Ala Leu	
390 395 400 405	
tcg ttg gcc ctc aag gtg aac cac tca ctg ctg cgc ctg gac ctc gac	1481
Ser Leu Ala Leu Lys Val Asn His Ser Leu Leu Arg Leu Asp Leu Asp	
406 411 416 421	
cgt gaa ccc aag aaa gag gcg gtg aag agc ttc atc gag acg cag aag	1529
Arg Glu Pro Lys Lys Glu Ala Val Lys Ser Phe Ile Glu Thr Gln Lys	
422 427 432 437	
gcg ctg ctg gcc gag atc cag aac ggc tgc aag cgc aac ttg gtg ctg	1577
Ala Leu Leu Ala Glu Ile Gln Asn Gly Cys Lys Arg Asn Leu Val Leu	
438 443 448 453	
gcg cgg gag agg gag gag aag gag cag ccg cca cag ctg tcg gcc tcc	1625
Ala Arg Glu Arg Glu Glu Lys Glu Gln Pro Pro Gln Leu Ser Ala Ser	
454 459 464 469	
atg cct gag acc acc gcc acc gag ccc cag ccc gac gac gag ccc gcc	1673
Met Pro Glu Thr Thr Ala Thr Glu Pro Gln Pro Asp Asp Glu Pro Ala	
470 475 480 485	
gct ggg gtg cag aac ggg gcc ccc agc ccc gca ccc agc ccg gac tca	1721
Ala Gly Val Gln Asn Gly Ala Pro Ser Pro Ala Pro Ser Pro Asp Ser	
486 491 496 501	
gac tca gac tcg gac tcg gat ggg gag gaa gag gag gaa gag gaa ggg	1769
Asp Ser Asp Ser Asp Ser Asp Gly Glu Glu Glu Glu Glu Glu Glu Gly	
502 507 512 517	
gag agg gac gag acc ccc tcc ggg gcc att gac acc cgg gac aca ggg	1817
Glu Arg Asp Glu Thr Pro Ser Gly Ala Ile Asp Thr Arg Asp Thr Gly	
518 523 528 533	
tcc tct gag cct cag cca cca ccg gag ccg cct cgg tca ggg cca cca	1865
Ser Ser Glu Pro Gln Pro Pro Pro Glu Pro Pro Arg Ser Gly Pro Pro	
534 539 544 549	
ctg ccc aac ggc ctg aag ccc gag ttc gcc ctg gca ctg ccc cct gag	1913
Leu Pro Asn Gly Leu Lys Pro Glu Phe Ala Leu Ala Leu Pro Pro Glu	
550 555 560 565	

ccg ccc ccg ggg cct gag gtc aag ggg ggc agc tgc ggc ctg gag cac	1961
Pro Pro Pro Gly Pro Glu Val Lys Gly Gly Ser Cys Gly Leu Glu His	
566 571 576 581	
gaa ctg agc tgc tcc aag aac gag aag gag ctc gag gag ctg ctt ctg	2009
Glu Leu Ser Cys Ser Lys Asn Glu Lys Glu Leu Glu Glu Leu Leu Leu	
582 587 592 597	
gaa gcc agt cag gaa tcc ggg cag gag aca ctg tga cact ttagttccct	2059
Glu Ala Ser Gln Glu Ser Gly Gln Glu Thr Leu *	
598 603 608	
ttttccggtc ggtctgcgat gagctgaggc cagagccatg agaatctgct caccttcccc	2119
ccagccttcc tgaggcccag gatgccaggg gtggggggcca ttctggggcc cccctcccc	2179
cacagcaaca ctacaagggg tgcaggagct acagggagtg gccctccgcg cgtgactcaa	2239
gcacttctat ttatgagccc agcactggaa gactctgggg gtgaatggga ggagggggag	2299
caggaggagg aggaggtctc caaggacatc aggcgcctgt tctggagggg ccaggcttgc	2359
cctgcggagg gcaggcgtcc tgggtggtgg tgggatggtc ccctgtggcc ccgggcacag	2419
ggccggggcag gcagcctggt gccggagagg cgggtgcgtgc tgggtggtggt tgagatgcgc	2479
agaacagccc cagacagcgc aggccgggca ggggtggggg atgggagcag aggatcagag	2539
ctttcttttt ctcaagtgca ataaatctat caggagctg gggcgggagc agccggcact	2599
ccgggaccct gctgtccagg ccaactggagg ctgcgcctg agaggcacta cagcccttg	2659
ggggcgagtg gcatgggtgt gggtgagggg gggcagaggg ctggggctac tcctgtcgg	2719
gcaactctgt tcacaccttt tctaataaac tggggctggg ttcactttga aaaaaaaaaa	2779
a	2780

<210> 359
 <211> 533
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (239) .. (523)

<400> 359	
atttgaaacc gtcgtatag ccgatcccag ctggctagcg tttaaactta agcttggtac	60
cgagctcgga tccactagtc cagtgtggtg gaattctcaa gcccgattt cttaatctgt	120
tacctatctc ggcataattc ttcataaaaa cacaggtgct ctccctgccg atcctgtcca	180

actgatctct caaaccacca cccctttctac aaaacaacaa ctccctttcct tccctgggc 238
 atg gtt gga tac ttt tac ctt tgg ata cct ggt ttt gcc atc cta aca 286
 Met Val Gly Tyr Phe Tyr Leu Trp Ile Pro Gly Phe Ala Ile Leu Thr
 1 5 10 15

aaa cca tta tgt aaa ctc aca aaa gaa aac cta gct gat gcc ata gat 334
 Lys Pro Leu Cys Lys Leu Thr Lys Glu Asn Leu Ala Asp Ala Ile Asp 32
 17 22 27

cct aaa tcc ttt tcc cac tcc tct ttc cgt tcc ttg aag aca gca tta 382
 Pro Lys Ser Phe Ser His Ser Ser Phe Arg Ser Leu Lys Thr Ala Leu 48
 33 38 43

gag aat gct tcc aca cta gct ctc cct gac tca tcc caa ccc ttt ttc 430
 Glu Asn Ala Ser Thr Leu Ala Leu Pro Asp Ser Ser Gln Pro Phe Phe 64
 49 54 59

att aca cac agc cga agt gca ggg ctg tgt ggt cga aat tct tac aca 478
 Ile Thr His Ser Arg Ser Ala Gly Leu Cys Gly Arg Asn Ser Tyr Thr 80
 65 70 75

agg act ggg acc gct ccc tgt ggc ctt ttt atc caa aca act tga gct 526
 Arg Thr Gly Thr Ala Pro Cys Gly Leu Phe Ile Gln Thr Thr *
 81 86 91

tactgtt 533

<210> 360
 <211> 1770
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (105)..(1409)

<400> 360
 gaatatcgac acgccaagct tggcacgagg ggcggcgccg agctgaggtg gtgagggact 60

agctcccgga tgtggagaag ctggggagaa ggcgtgggag gaag atg gac tcg gtg 116
 Met Asp Ser Val
 1

gag aag ggg gcc gcc acc tcc gtc tcc aac ccg cgg ggg cga ccg tcc 164
 Glu Lys Gly Ala Ala Thr Ser Val Ser Asn Pro Arg Gly Arg Pro Ser 20
 5 10 15

cgg ggc cgg ccg ccg aag ctg cag cgc aac tot cgc ggc ggc cag ggc 212
 Arg Gly Arg Pro Pro Lys Leu Gln Arg Asn Ser Arg Gly Gly Gln Gly 36
 21 26 31

cga ggt gtg gag aag ccc ccg cac ctg gca gcc cta att ctg gcc cgg 260
 Arg Gly Val Glu Lys Pro Pro His Leu Ala Ala Leu Ile Leu Ala Arg 52
 37 42 47

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300

gga ggc agc aaa ggc atc ccc ctg aag aac att aag cac ctg gcg ggg	308
Gly Gly Ser Lys Gly Ile Pro Leu Lys Asn Ile Lys His Leu Ala Gly	
53 58 63 68	
gtc ccg ctc att ggc tgg gtc ctg cgt gcg gcc ctg gat tca ggg gcc	356
Val Pro Leu Ile Gly Trp Val Leu Arg Ala Ala Leu Asp Ser Gly Ala	
69 74 79 84	
ttc cag agt gta tgg gtt tcg aca gac cat gat gaa att gag aat gtg	404
Phe Gln Ser Val Trp Val Ser Thr Asp His Asp Glu Ile Glu Asn Val	
85 90 95 100	
gcc aaa caa ttt ggt gca caa gtt cat cga aga agt tct gaa gtt tca	452
Ala Lys Gln Phe Gly Ala Gln Val His Arg Arg Ser Ser Glu Val Ser	
101 106 111 116	
aaa gac agc tct acc tca cta gat gcc atc ata gaa ttt ctt aat tat	500
Lys Asp Ser Ser Thr Ser Leu Asp Ala Ile Ile Glu Phe Leu Asn Tyr	
117 122 127 132	
cat aat gag gtt gac att gta gga aat att caa gct act tct cca tgt	548
His Asn Glu Val Asp Ile Val Gly Asn Ile Gln Ala Thr Ser Pro Cys	
133 138 143 148	
tta cat cct act gat ctt caa aaa gtt gca gaa atg att cga gaa gaa	596
Leu His Pro Thr Asp Leu Gln Lys Val Ala Glu Met Ile Arg Glu Glu	
149 154 159 164	
gga tat gat tct gtt ttc tct gtt gtg aga cgc cat cag ttt cga tgg	644
Gly Tyr Asp Ser Val Phe Ser Val Val Arg Arg His Gln Phe Arg Trp	
165 170 175 180	
agt gaa att cag aaa gga gtt cgt gaa gtg acc gaa cct ctg aat tta	692
Ser Glu Ile Gln Lys Gly Val Arg Glu Val Thr Glu Pro Leu Asn Leu	
181 186 191 196	
aat cca gct aaa cgg cct cgt cga caa gac tgg gat gga gaa tta tat	740
Asn Pro Ala Lys Arg Pro Arg Arg Gln Asp Trp Asp Gly Glu Leu Tyr	
197 202 207 212	
gaa aat ggc tca ttt tat ttt gct aaa aga cat ttg ata gag atg ggt	788
Glu Asn Gly Ser Phe Tyr Phe Ala Lys Arg His Leu Ile Glu Met Gly	
213 218 223 228	
tac ttg cag ggt gga aaa atg gca tac tac gaa atg cga gct gaa cat	836
Tyr Leu Gln Gly Gly Lys Met Ala Tyr Tyr Glu Met Arg Ala Glu His	
229 234 239 244	
agt gtg gat ata gat gtg gat att gat tgg cct att gca gag caa aga	884
Ser Val Asp Ile Asp Val Asp Ile Asp Trp Pro Ile Ala Glu Gln Arg	
245 250 255 260	
gta tta aga tat ggc tat ttt ggc aaa gag aag ctt aag gaa ata aaa	932
Val Leu Arg Tyr Gly Tyr Phe Gly Lys Glu Lys Leu Lys Glu Ile Lys	
261 266 271 276	

ctt ttg gtt tgc aat att gat gga tgt ctc acc aat ggc cac att tat	980
Leu Leu Val Cys Asn Ile Asp Gly Cys Leu Thr Asn Gly His Ile Tyr	
277 282 287 292	
gta tca gga gac caa aaa gaa ata ata tct tat gat gta aaa gat gct	1028
Val Ser Gly Asp Gln Lys Glu Ile Ile Ser Tyr Asp Val Lys Asp Ala	
293 298 303 308	
att ggg ata agt tta tta aag aaa agt ggt att gag gtg agg cta atc	1076
Ile Gly Ile Ser Leu Leu Lys Lys Ser Gly Ile Glu Val Arg Leu Ile	
309 314 319 324	
tca gaa agg gcc tgt tca aag cag acg ctg tct tct tta aaa ctg gat	1124
Ser Glu Arg Ala Cys Ser Lys Gln Thr Leu Ser Ser Leu Lys Leu Asp	
325 330 335 340	
tgc aaa atg gaa gtc agt gta tca gac aag cta gca gtt gta gat gaa	1172
Cys Lys Met Glu Val Ser Val Ser Asp Lys Leu Ala Val Val Asp Glu	
341 346 351 356	
tgg aga aaa gaa atg ggc ctg tgc tgg aaa gaa gtg gca tat ctt gga	1220
Trp Arg Lys Glu Met Gly Leu Cys Trp Lys Glu Val Ala Tyr Leu Gly	
357 362 367 372	
aat gaa gtg tct gat gaa gag tgc ttg aag aga gtg ggc cta agt ggc	1268
Asn Glu Val Ser Asp Glu Glu Cys Leu Lys Arg Val Gly Leu Ser Gly	
373 378 383 388	
gct cct gct gat gcc tgt tct act gcc cag aag gct gtt gga tac att	1316
Ala Pro Ala Asp Ala Cys Ser Thr Ala Gln Lys Ala Val Gly Tyr Ile	
389 394 399 404	
tgc aaa tgt aat ggt ggc cgt ggt gcc atc cga gaa ttt gca gag cac	1364
Cys Lys Cys Asn Gly Gly Arg Gly Ala Ile Arg Glu Phe Ala Glu His	
405 410 415 420	
att tgc cta cta atg gaa aag gtt aat aat tca tgc caa aaa tag aaa	1412
Ile Cys Leu Leu Met Glu Lys Val Asn Asn Ser Cys Gln Lys *	
421 426 431	
ttagcgtaat attgagaaaa aatgataca gccttcttca gccagtttgc ttttattttt	1472
gattaagtaa attccatggt gtaatgttac agagagtgtg atttggtttg tgatatatat	1532
atattgtgct ctacttttct ctttacgcaa gataattatt tagagactga ttacagtctt	1592
tctcagatgtt ttagtaaatg caagtaagaa catcatcaaa gttcactttg tattgtaccc	1652
tgtaaaactg tgtgtttgtg tgctttcaaa gatgttgga ttttatttat ctggggacag	1712
tgtgtatggt aagacatgcc cttctattaa taaaactaca tttctcaaaa aaaaaaaaa	1770

<210> 361
<211> 1417

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (18)..(1208)

<400> 361

tgatataaca tcattcg	atg aga aga acc cca caa acc caa aaa aga gat	50
	Met Arg Arg Thr Pro Gln Thr Gln Lys Arg Asp	
	1 5	
ctc tcg agg atc cga att cgc ggc cgc gtc gac gcc ggg aac tgg cgt		98
Leu Ser Arg Ile Arg Ile Arg Gly Arg Val Asp Ala Gly Asn Trp Arg		
12 17 22 27		
gtg gga ctc cag aca gga gag gct gcg cct tcc ccg cac cgg gac ctt		146
Val Gly Leu Gln Thr Gly Glu Ala Ala Pro Ser Pro His Arg Asp Leu		
28 33 38 43		
cgc gac aca cca gat cct cgc ccc tgg ctc gcg cga acg cac agg atg		194
Arg Asp Thr Pro Asp Pro Arg Pro Trp Leu Ala Arg Thr His Arg Met		
44 49 54 59		
acc acc acc ctc gtg tct gcc acc atc ttc gac ttg agc gaa gtt tta		242
Thr Thr Thr Leu Val Ser Ala Thr Ile Phe Asp Leu Ser Glu Val Leu		
60 65 70 75		
tgc aag ggt aac aag atg ctc aac tat agt gct ccc agt gca ggg ggt		290
Cys Lys Gly Asn Lys Met Leu Asn Tyr Ser Ala Pro Ser Ala Gly Gly		
76 81 86 91		
tgc ctg ctg gac aga aag gca gtg ggc acc cct gct ggt ggg ggc ttc		338
Cys Leu Leu Asp Arg Lys Ala Val Gly Thr Pro Ala Gly Gly Gly Phe		
92 97 102 107		
cct cgg agg cac tca gtc acc ctg ccc agc tcc aag ttc cac cag aac		386
Pro Arg Arg His Ser Val Thr Leu Pro Ser Ser Lys Phe His Gln Asn		
108 113 118 123		
cag ctc ctc agc agc ctc aag ggt gag cca gcc ccc gct ctg agc tcg		434
Gln Leu Leu Ser Ser Leu Lys Gly Glu Pro Ala Pro Ala Leu Ser Ser		
124 129 134 139		
cga gac agc cgc ttc cga gac cgc tcc ttc tcg gaa ggg ggc gag cgg		482
Arg Asp Ser Arg Phe Arg Asp Arg Ser Phe Ser Glu Gly Gly Glu Arg		
140 145 150 155		
ctg ctg ccc acc cag aag cag ccc ggg ggc ggc cag gtc aac tcc agc		530
Leu Leu Pro Thr Gln Lys Gln Pro Gly Gly Gly Gln Val Asn Ser Ser		
156 161 166 171		
cgc tac aag acg gag ctg tgc cgc ccc ttt gag gaa aac ggt gcc tgt		578
Arg Tyr Lys Thr Glu Leu Cys Arg Pro Phe Glu Glu Asn Gly Ala Cys		
172 177 182 187		
aag tac ggg gac aag tgc cag ttc gca cac ggc atc cac gag ctc cgc		626

Lys	Tyr	Gly	Asp	Lys	Cys	Gln	Phe	Ala	His	Gly	Ile	His	Glu	Leu	Arg		
188					193					198					203		
agc	ctg	acc	cgc	cac	ccc	aag	tac	aag	acg	gag	ctg	tgc	cgc	acc	ttc	674	
Ser	Leu	Thr	Arg	His	Pro	Lys	Tyr	Lys	Thr	Glu	Leu	Cys	Arg	Thr	Phe		
204					209					214					219		
cac	acc	atc	ggc	ttt	tgc	ccc	tac	ggg	ccc	cgc	tgc	cac	ttc	atc	cac	722	
His	Thr	Ile	Gly	Phe	Cys	Pro	Tyr	Gly	Pro	Arg	Cys	His	Phe	Ile	His		
220					225					230					235		
aac	gct	gaa	gag	cgc	cgt	gcc	ctg	gcc	ggg	gcc	cgg	gac	ctc	tcc	gct	770	
Asn	Ala	Glu	Glu	Arg	Arg	Ala	Leu	Ala	Gly	Ala	Arg	Asp	Leu	Ser	Ala		
236					241					246					251		
gac	cgt	ccc	cgc	ctc	cag	cat	agc	ttt	agc	ttt	gct	ggg	ttt	ccc	agt	818	
Asp	Arg	Pro	Arg	Leu	Gln	His	Ser	Phe	Ser	Phe	Ala	Gly	Phe	Pro	Ser		
252					257					262					267		
gcc	gct	gcc	acc	gcc	gct	gcc	acc	ggg	ctg	ctg	gac	agc	ccc	acg	tcc	866	
Ala	Ala	Ala	Thr	Ala	Ala	Ala	Thr	Gly	Leu	Leu	Asp	Ser	Pro	Thr	Ser		
268					273					278					283		
atc	acc	cca	ccc	cct	att	ctg	agc	gcc	gat	gac	ctc	ctg	ggc	tca	cct	914	
Ile	Thr	Pro	Pro	Pro	Ile	Leu	Ser	Ala	Asp	Asp	Leu	Leu	Gly	Ser	Pro		
284					289					294					299		
acc	ctg	ccc	gat	ggc	acc	aat	aac	cct	ttt	gcc	ttc	tcc	agc	cag	gag	962	
Thr	Leu	Pro	Asp	Gly	Thr	Asn	Asn	Pro	Phe	Ala	Phe	Ser	Ser	Gln	Glu		
300					305					310					315		
ctg	gca	agc	ctc	ttt	gcc	cct	agc	atg	ggg	ctg	ccc	ggg	ggt	ggc	tcc	1010	
Leu	Ala	Ser	Leu	Phe	Ala	Pro	Ser	Met	Gly	Leu	Pro	Gly	Gly	Gly	Ser		
316					321					326					331		
ccg	acc	acc	ttc	ctc	ttc	cgg	ccc	atg	tcc	gag	tcc	cct	cac	atg	ttt	1058	
Pro	Thr	Thr	Phe	Leu	Phe	Arg	Pro	Met	Ser	Glu	Ser	Pro	His	Met	Phe		
332					337					342					347		
gac	tct	ccc	ccc	agc	cct	cag	gat	tct	ctc	tgc	gac	cag	gag	ggc	tac	1106	
Asp	Ser	Pro	Pro	Ser	Pro	Gln	Asp	Ser	Leu	Ser	Asp	Gln	Glu	Gly	Tyr		
348					353					358					363		
ctg	agc	agc	tcc	agc	agc	agc	cac	agt	ggc	tca	gac	tcc	ccg	acc	ttg	1154	
Leu	Ser	Ser	Ser	Ser	Ser	Ser	His	Ser	Gly	Ser	Asp	Ser	Pro	Thr	Leu		
364					369					374					379		
gac	aac	tca	aga	cgc	ctg	ccc	atc	ttc	agc	aga	ctt	tcc	atc	tca	gat	1202	
Asp	Asn	Ser	Arg	Arg	Leu	Pro	Ile	Phe	Ser	Arg	Leu	Ser	Ile	Ser	Asp		
380					385					390					395		
gac	taa	gccagggtag	ggagggacct	cctgggtcgac	gcgggccgcga	attcgggatcc										1258	
Asp	*																
396																	
tcgagagatc	tcttttttttg	ggtttggtgg	ggtatcttca	tcacogaata	gatagccaac											1318	

tcagaggaaa aaggtaagcc atgagcatag cgttcgagga gaggcagtga gtgatgtcgg 1378
 agcgagacat cgagcggagg acgaagaggt aggccgatg 1417

<210> 362
 <211> 1502
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (50)..(1072)

<400> 362
 gcacgagtga cactgcagct gcagtcgaacc tcttcccaat ttcaatgcg atg gac 55
 Met Asp
 1

ccg att cag aaa gct gta ata aac cat aca ttc ggg gtt cct ctt ccc 103
 Pro Ile Gln Lys Ala Val Ile Asn His Thr Phe Gly Val Pro Leu Pro
 3 8 13 18

cac cga aga aag caa atc ata tca tgc aac att tgc cag ttg aga ttt 151
 His Arg Arg Lys Gln Ile Ile Ser Cys Asn Ile Cys Gln Leu Arg Phe
 19 24 29 34

aat tct gat agc cag gct gcg gcc cac tac aaa ggc acg aaa cat gcc 199
 Asn Ser Asp Ser Gln Ala Ala Ala His Tyr Lys Gly Thr Lys His Ala
 35 40 45 50

aag aag ctc aaa gca ctg gaa gcc atg aaa aat aag cag aaa tct gta 247
 Lys Lys Leu Lys Ala Leu Glu Ala Met Lys Asn Lys Gln Lys Ser Val
 51 56 61 66

act gcc aag gac agc gca aag act acc ttc acc tcc atc act acc aat 295
 Thr Ala Lys Asp Ser Ala Lys Thr Thr Phe Thr Ser Ile Thr Thr Asn
 67 72 77 82

acc atc aat acc agc tct gac aaa aca gac ggt act gca ggg aca cca 343
 Thr Ile Asn Thr Ser Ser Asp Lys Thr Asp Gly Thr Ala Gly Thr Pro
 83 88 93 98

gca ata tca acg acg aca act gtg gaa atc cgc aaa agc agt gtt atg 391
 Ala Ile Ser Thr Thr Thr Thr Val Glu Ile Arg Lys Ser Ser Val Met
 99 104 109 114

aca act gag atc acc tct aaa gtg gaa aaa agc cca acg aca gcc act 439
 Thr Thr Glu Ile Thr Ser Lys Val Glu Lys Ser Pro Thr Thr Ala Thr
 115 120 125 130

ggc aat agc tca tgt cct tct act gag acc gag gaa gaa aag gca aaa 487
 Gly Asn Ser Ser Cys Pro Ser Thr Glu Thr Glu Glu Glu Lys Ala Lys
 131 136 141 146

cgg ctt ctt tac tgt tgg cta tgc aag gtt gct gtc aac tct gcc tcg	535
Arg Leu Leu Tyr Cys Ser Leu Cys Lys Val Ala Val Asn Ser Ala Ser	
147 152 157 162	
cag ctg gag gcg cac aac agt ggt act aag cac aaa acc atg tta gaa	583
Gln Leu Glu Ala His Asn Ser Gly Thr Lys His Lys Thr Met Leu Glu	
163 168 173 178	
gcc cgg aat gga agt ggc act atc aaa gcc ttt cct agg gca gga gtg	631
Ala Arg Asn Gly Ser Gly Thr Ile Lys Ala Phe Pro Arg Ala Gly Val	
179 184 189 194	
aaa ggc aaa gga cct gtt aat aaa gga aac aca ggc ctc caa aat aaa	679
Lys Gly Lys Gly Pro Val Asn Lys Gly Asn Thr Gly Leu Gln Asn Lys	
195 200 205 210	
aca ttt cac tgt gaa atc tgt gat gtg cac gtc aac tcg gaa acg caa	727
Thr Phe His Cys Glu Ile Cys Asp Val His Val Asn Ser Glu Thr Gln	
211 216 221 226	
ctt aaa cag cac att agc agt aga agg cac aaa gac aga gct gct ggg	775
Leu Lys Gln His Ile Ser Ser Arg Arg His Lys Asp Arg Ala Ala Gly	
227 232 237 242	
aag ccc ccg aaa cct aaa tac agt cct tac aac aaa cta cag aag aca	823
Lys Pro Pro Lys Pro Lys Tyr Ser Pro Tyr Asn Lys Leu Gln Lys Thr	
243 248 253 258	
gca cat cca ctg ggg gta aaa tta gta ttt tca aaa gaa cct tca aag	871
Ala His Pro Leu Gly Val Lys Leu Val Phe Ser Lys Glu Pro Ser Lys	
259 264 269 274	
cca ttg gct cca cga att cta cca aat cct cta gca gct gca gca gcc	919
Pro Leu Ala Pro Arg Ile Leu Pro Asn Pro Leu Ala Ala Ala Ala Ala	
275 280 285 290	
gca gca gca gtg gca gtg agt tcc ccc ttc agt ctt cga act gct cca	967
Ala Ala Ala Val Ala Val Ser Ser Pro Phe Ser Leu Arg Thr Ala Pro	
291 296 301 306	
gca gca aca ctg ttc cag act tct gcg ctt cct ccg gca ctc ctg cgg	1015
Ala Ala Thr Leu Phe Gln Thr Ser Ala Leu Pro Pro Ala Leu Leu Arg	
307 312 317 322	
cca gct ccc gga ccc att cgg acc gcc cac act cct gtg ctg ttt gct	1063
Pro Ala Pro Gly Pro Ile Arg Thr Ala His Thr Pro Val Leu Phe Ala	
323 328 333 338	
cct tac taa attccaa ataggagtaa ttgtactgca ataatttttc aaaaaacaaa	1119
Pro Tyr *	
339	
aaacaaaaca aacaaaagag aactatgcag tgtttattta tagtttaaag tataatctgaa	1179
gagccaggac ttttgatagt gaattgaaaa gggtataaaaa aagtggggga gggttggggg	1239
tgggagggag ggagtggtat tttctccaca ttaaagcatt cctottgaac gttgattgtt	1299

ttagaagtga tctccagcat tgatttgtag tggtatctag accttctgaa gcctctgtga 1359
 ctgtgctttt gggcacctgt ttccctctgc attgtctgtc ctgctttatg aaacaactat 1419
 acattgtcta agggcattaa ctgggtccaa tgtatataaa ataatttact ctgtagatta 1479
 aaatcgtaca aaaaaaaaaa aaa 1502

<210> 363
 <211> 4061
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (72)..(3062)

<400> 363
 aaattgtaaa ccagttgaat gctctgagca gcttagatga agatcaagat gactgcataa 60
 agcaagcaaa t atg cgt tca gct aaa tca gcc agt tcc tct gaa gag ctt 110
 Met Arg Ser Ala Lys Ser Ala Ser Ser Ser Glu Glu Leu
 1 5 10
 atc aac aaa ctt aac ttt ttg gat gaa gca gaa aag gac ttg gcc acc 158
 Ile Asn Lys Leu Asn Phe Leu Asp Glu Ala Glu Lys Asp Leu Ala Thr
 14 19 24 29
 gtg aat tca aat cca ttt gat gat cct gat gct gca gaa tta aat cca 206
 Val Asn Ser Asn Pro Phe Asp Asp Pro Asp Ala Ala Glu Leu Asn Pro
 30 35 40 45
 ttt gga gat cct gac tca gaa gaa cct atc act gaa aca gct tca cct 254
 Phe Gly Asp Pro Asp Ser Glu Glu Pro Ile Thr Glu Thr Ala Ser Pro
 46 51 56 61
 aga aaa aca gaa gac tct ttt tat aat aac agc tat aat ccc ttt aaa 302
 Arg Lys Thr Glu Asp Ser Phe Tyr Asn Asn Ser Tyr Asn Pro Phe Lys
 62 67 72 77
 gag gtg cag act cca cag tat ttg aac cca ttc gat gag cca gaa gca 350
 Glu Val Gln Thr Pro Gln Tyr Leu Asn Pro Phe Asp Glu Pro Glu Ala
 78 83 88 93
 ttt gtg acc ata aag gat tct cct ccc cag tct aca aaa aga aaa aat 398
 Phe Val Thr Ile Lys Asp Ser Pro Pro Gln Ser Thr Lys Arg Lys Asn
 94 99 104 109
 ata aga cct gtg gat atg agc aag tac ctc tat gct gat agt tct aaa 446
 Ile Arg Pro Val Asp Met Ser Lys Tyr Leu Tyr Ala Asp Ser Ser Lys
 110 115 120 125
 act gaa gaa gaa gaa gaa ttg gat gaa tca aat cct ttt tat gaa cct aaa 494

Thr	Glu	Glu	Glu	Glu	Leu	Asp	Glu	Ser	Asn	Pro	Phe	Tyr	Glu	Pro	Lys	
126					131					136					141	
tca	act	cct	cct	cca	aat	aat	ttg	gta	aat	cct	gtt	caa	gaa	cta	gaa	542
Ser	Thr	Pro	Pro	Pro	Asn	Asn	Leu	Val	Asn	Pro	Val	Gln	Glu	Leu	Glu	
142					147					152					157	
act	gaa	agg	cga	gtg	aaa	aga	aag	gcc	ccg	gct	cca	cca	gtc	ctc	tca	590
Thr	Glu	Arg	Arg	Val	Lys	Arg	Lys	Ala	Pro	Ala	Pro	Pro	Val	Leu	Ser	
158					163					168					173	
cca	aaa	aca	gga	gta	tta	aat	gaa	aac	aca	gtt	tct	gca	gga	aaa	gat	638
Pro	Lys	Thr	Gly	Val	Leu	Asn	Glu	Asn	Thr	Val	Ser	Ala	Gly	Lys	Asp	
174					179					184					189	
ctc	tct	act	tct	cct	aag	cca	agc	cct	ata	cca	agt	cct	gtt	ttg	ggg	686
Leu	Ser	Thr	Ser	Pro	Lys	Pro	Ser	Pro	Ile	Pro	Ser	Pro	Val	Leu	Gly	
190					195					200					205	
cga	aag	cca	aat	gct	agt	cag	tct	ttg	ctt	gta	tgg	tgt	aaa	gaa	gtt	734
Arg	Lys	Pro	Asn	Ala	Ser	Gln	Ser	Leu	Leu	Val	Trp	Cys	Lys	Glu	Val	
206					211					216					221	
aca	aag	aac	tac	cga	gga	gta	aaa	atc	acc	aat	ttt	act	aca	tcg	tgg	782
Thr	Lys	Asn	Tyr	Arg	Gly	Val	Lys	Ile	Thr	Asn	Phe	Thr	Thr	Ser	Trp	
222					227					232					237	
aga	aat	ggt	tta	tct	ttt	tgt	gca	ata	tta	cac	cac	ttt	aga	cca	gat	830
Arg	Asn	Gly	Leu	Ser	Phe	Cys	Ala	Ile	Leu	His	His	Phe	Arg	Pro	Asp	
238					243					248					253	
tta	att	gac	tac	aag	tct	ctg	aat	cct	caa	gat	att	aaa	gag	aac	aac	878
Leu	Ile	Asp	Tyr	Lys	Ser	Leu	Asn	Pro	Gln	Asp	Ile	Lys	Glu	Asn	Asn	
254					259					264					269	
aaa	aag	gca	tac	gat	gga	ttt	gcc	agc	ata	gga	att	tcc	cga	tta	ttg	926
Lys	Lys	Ala	Tyr	Asp	Gly	Phe	Ala	Ser	Ile	Gly	Ile	Ser	Arg	Leu	Leu	
270					275					280					285	
gaa	cct	tct	gat	atg	gta	tta	tta	gca	att	cct	gat	aaa	ctg	act	gtt	974
Glu	Pro	Ser	Asp	Met	Val	Leu	Leu	Ala	Ile	Pro	Asp	Lys	Leu	Thr	Val	
286					291					296					301	
atg	act	tat	ctc	tat	caa	ata	agg	gca	cat	ttc	agt	ggc	caa	gaa	cta	1022
Met	Thr	Tyr	Leu	Tyr	Gln	Ile	Arg	Ala	His	Phe	Ser	Gly	Gln	Glu	Leu	
302					307					312					317	
aat	gtc	gtt	cag	ata	gag	gaa	aac	agc	agt	aaa	agc	aca	tat	aaa	gtt	1070
Asn	Val	Val	Gln	Ile	Glu	Glu	Asn	Ser	Ser	Lys	Ser	Thr	Tyr	Lys	Val	
318					323					328					333	
gga	aac	tat	gaa	aca	gat	aca	aac	agt	tct	gtt	gat	caa	gaa	aaa	ttc	1118
Gly	Asn	Tyr	Glu	Thr	Asp	Thr	Asn	Ser	Ser	Val	Asp	Gln	Glu	Lys	Phe	
334					339					344					349	
tat	gca	gag	ctt	agt	gat	ctg	aag	cgg	gag	cct	gaa	cta	caa	cag	cct	1166
Tyr	Ala	Glu	Leu	Ser	Asp	Leu	Lys	Arg	Glu	Pro	Glu	Leu	Gln	Gln	Pro	

350	355	360	365	
atc agc gga gca gta gac ttc tta tca cag gat gac tct gta ttt gta				1214
Ile Ser Gly Ala Val Asp Phe Leu Ser Gln Asp Asp Ser Val Phe Val				
366	371	376	381	
aat gat agc ggg gtt gga gag tca gaa agt gag cat caa act cct gat				1262
Asn Asp Ser Gly Val Gly Glu Ser Glu Ser Glu His Gln Thr Pro Asp				
382	387	392	397	
gat cac ctt agt cca agc aca gcc tcc cct tac tgt cgc agg act aaa				1310
Asp His Leu Ser Pro Ser Thr Ala Ser Pro Tyr Cys Arg Arg Thr Lys				
398	403	408	413	
agt gac aca gaa ccc cag aag tct cag cag agc tct gga agg act tca				1358
Ser Asp Thr Glu Pro Gln Lys Ser Gln Gln Ser Ser Gly Arg Thr Ser				
414	419	424	429	
gga tct gat gac cct gga ata tgt tcc aat aca gat tca acc caa gca				1406
Gly Ser Asp Asp Pro Gly Ile Cys Ser Asn Thr Asp Ser Thr Gln Ala				
430	435	440	445	
cag gtt ttg tta ggc aaa aag aga cta ttg aaa gct gag act tta gaa				1454
Gln Val Leu Leu Gly Lys Lys Arg Leu Leu Lys Ala Glu Thr Leu Glu				
446	451	456	461	
ttg agt gac tta tat gtt agt gat aag aag aag gat atg tct cca ccc				1502
Leu Ser Asp Leu Tyr Val Ser Asp Lys Lys Lys Asp Met Ser Pro Pro				
462	467	472	477	
ttt att tgt gag gag aca gat gaa caa aag ctt caa act cta gac atc				1550
Phe Ile Cys Glu Glu Thr Asp Glu Gln Lys Leu Gln Thr Leu Asp Ile				
478	483	488	493	
ggt agt aac ttg gag aaa gaa aaa tta gag aat tcc aga tcc tta gaa				1598
Gly Ser Asn Leu Glu Lys Glu Lys Leu Glu Asn Ser Arg Ser Leu Glu				
494	499	504	509	
tgc aga tca gat cca gaa tct cct atc aaa caa aca agt tta tct cct				1646
Cys Arg Ser Asp Pro Glu Ser Pro Ile Lys Gln Thr Ser Leu Ser Pro				
510	515	520	525	
act tct aaa ctt gga tac tca tat agt aga gat cta gac ctt gct aag				1694
Thr Ser Lys Leu Gly Tyr Ser Tyr Ser Arg Asp Leu Asp Leu Ala Lys				
526	531	536	541	
aaa aaa cat gct tcc ctg agg cag acg gag tct gat cca gat gct gat				1742
Lys Lys His Ala Ser Leu Arg Gln Thr Glu Ser Asp Pro Asp Ala Asp				
542	547	552	557	
aga acc act tta aat cat gca gat cat tca tca aaa ata gtc cag cat				1790
Arg Thr Thr Leu Asn His Ala Asp His Ser Ser Lys Ile Val Gln His				
558	563	568	573	
cga ttg tta tct aga caa gaa gaa ctt aag gaa aga gca aga gtt ctg				1838
Arg Leu Leu Ser Arg Gln Glu Glu Leu Lys Glu Arg Ala Arg Val Leu				
574	579	584	589	

ctt gag caa gca aga aga gat gca gcc tta aag gcg ggg aat aag cac	1886
Leu Glu Gln Ala Arg Arg Asp Ala Ala Leu Lys Ala Gly Asn Lys His	
590 595 600 605	
aat acc aac aca gcc acc cca ttc tgc aac agg cag cta agt gat cag	1934
Asn Thr Asn Thr Ala Thr Pro Phe Cys Asn Arg Gln Leu Ser Asp Gln	
606 611 616 621	
caa gat gaa gag cga cgt cgg cag ctg aga gag aga gct cgt cag cta	1982
Gln Asp Glu Glu Arg Arg Arg Gln Leu Arg Glu Arg Ala Arg Gln Leu	
622 627 632 637	
ata gca gaa gct cga tct gga gtg aag atg tca gaa ctt ccc agc tat	2030
Ile Ala Glu Ala Arg Ser Gly Val Lys Met Ser Glu Leu Pro Ser Tyr	
638 643 648 653	
ggg gaa atg gct gca gaa aag ttg aaa gaa agg tca aag gca tct gga	2078
Gly Glu Met Ala Ala Glu Lys Leu Lys Glu Arg Ser Lys Ala Ser Gly	
654 659 664 669	
gat gaa aat gat aat att gag ata gat act aac gag gag atc cct gaa	2126
Asp Glu Asn Asp Asn Ile Glu Ile Asp Thr Asn Glu Glu Ile Pro Glu	
670 675 680 685	
ggc ttt gtt gta gga ggt gga gat gaa ctt act aac tta gaa aat gac	2174
Gly Phe Val Val Gly Gly Gly Asp Glu Leu Thr Asn Leu Glu Asn Asp	
686 691 696 701	
ctt gat act ccc gaa caa aac agt aag ttg gtg gac ttg aag ctg aag	2222
Leu Asp Thr Pro Glu Gln Asn Ser Lys Leu Val Asp Leu Lys Leu Lys	
702 707 712 717	
aag ctc cta gaa gtt cag cca cag gtg gca aat tca ccc tcc agt gct	2270
Lys Leu Leu Glu Val Gln Pro Gln Val Ala Asn Ser Pro Ser Ser Ala	
718 723 728 733	
gcc cag aaa gct gta act gag agc tca gag cag gac atg aaa agt ggc	2318
Ala Gln Lys Ala Val Thr Glu Ser Ser Glu Gln Asp Met Lys Ser Gly	
734 739 744 749	
aca gaa gat ctc cgg act gaa cga tta caa aaa aca aca gaa cgt ttt	2366
Thr Glu Asp Leu Arg Thr Glu Arg Leu Gln Lys Thr Thr Glu Arg Phe	
750 755 760 765	
aga aat cct gtt gtg ttc agc aaa gat tct aca gtc aga aaa act caa	2414
Arg Asn Pro Val Val Phe Ser Lys Asp Ser Thr Val Arg Lys Thr Gln	
766 771 776 781	
ctt cag tct ttc agc caa tat att gag aat aga cca gag atg aaa agg	2462
Leu Gln Ser Phe Ser Gln Tyr Ile Glu Asn Arg Pro Glu Met Lys Arg	
782 787 792 797	
cag aga tca ata cag gaa gat aca aag aaa gga aat gag gag aag gca	2510
Gln Arg Ser Ile Gln Glu Asp Thr Lys Lys Gly Asn Glu Glu Lys Ala	
798 803 808 813	

gcg ata act gaa act cag agg aag cca tca gaa gat gaa gtg ctt aat	2558
Ala Ile Thr Glu Thr Gln Arg Lys Pro Ser Glu Asp Glu Val Leu Asn	
814 819 824 829	
aaa ggg ttc aaa gac acc agt cag tat gta gta gga gaa ttg gca gca	2606
Lys Gly Phe Lys Asp Thr Ser Gln Tyr Val Val Gly Glu Leu Ala Ala	
830 835 840 845	
cta gag aat gag caa aag caa att gac acc cgt gcc gcg ctg gtg gag	2654
Leu Glu Asn Glu Gln Lys Gln Ile Asp Thr Arg Ala Ala Leu Val Glu	
846 851 856 861	
aag cgc ctt cgc tat ctc atg gac aca gga agg aac aca gaa gaa gaa	2702
Lys Arg Leu Arg Tyr Leu Met Asp Thr Gly Arg Asn Thr Glu Glu Glu	
862 867 872 877	
gaa gct atg atg cag gaa tgg ttt atg tta gtt aat aag aaa aat gcc	2750
Glu Ala Met Met Gln Glu Trp Phe Met Leu Val Asn Lys Lys Asn Ala	
878 883 888 893	
tta ata agg aga atg aat cag ctc tct ctt ctg gaa aaa gaa cat gat	2798
Leu Ile Arg Arg Met Asn Gln Leu Ser Leu Leu Glu Lys Glu His Asp	
894 899 904 909	
tta gaa cga cgg tat gag ctg ctg aac cgg gaa ttg agg gca atg cta	2846
Leu Glu Arg Arg Tyr Glu Leu Leu Asn Arg Glu Leu Arg Ala Met Leu	
910 915 920 925	
gcc att gaa gac tgg cag aag acc gag gcc cag aag cga cgc gaa cag	2894
Ala Ile Glu Asp Trp Gln Lys Thr Glu Ala Gln Lys Arg Arg Glu Gln	
926 931 936 941	
ctt ctg cta gat gag ctg gtg gcc ctg gtg aac aag cgc gat gcg ctc	2942
Leu Leu Leu Asp Glu Leu Val Ala Leu Val Asn Lys Arg Asp Ala Leu	
942 947 952 957	
gtc agg gac ctg gac gcg cag gag aag cag gcc gaa gaa gaa gat gag	2990
Val Arg Asp Leu Asp Ala Gln Glu Lys Gln Ala Glu Glu Glu Asp Glu	
958 963 968 973	
cat ttg gag cga act ctg gag caa aac aaa ggc aag atg gcc aag aaa	3038
His Leu Glu Arg Thr Leu Glu Gln Asn Lys Gly Lys Met Ala Lys Lys	
974 979 984 989	
gag gag aaa tgt gtt ctt cag tag ccatcagatc agaaagaatc tctcccaaca	3092
Glu Glu Lys Cys Val Leu Gln *	
990 995	
ttttagagtc ttgcttccca aaccagaaaa agtcagactc attgttgatt taaaactttt	3152
aacatttttgt ttggctggat tgtactactt tacctctact ttaccaccac cacccttttc	3212
ctccctcctt tccaaataat atacagaact ccaaaatagc ttcattttaag gatttttttg	3272
tgagttaaca atttcottga aatcctgtga aatagatttg cacagacacc ttgtgagtga	3332
ttggtattgg aggtgttcaa gaaactgttc gaaaaagaac aaaaacactt cctcgttat	3392

ccc tca gtc agc ggc ctc tcg cag ata acc aaa agc ctg tat atc agc	576
Pro Ser Val Ser Gly Leu Ser Gln Ile Thr Lys Ser Leu Tyr Ile Ser	
15 20 25 30	
aat ggt gtg gcc gcc aac aac aag ctc atg ctg tct agc aac cag atc	624
Asn Gly Val Ala Ala Asn Asn Lys Leu Met Leu Ser Ser Asn Gln Ile	
31 36 41 46	
acc atg gtc atc aat gtc tca gtg gag gta gtg aac acc ttg tat gag	672
Thr Met Val Ile Asn Val Ser Val Glu Val Val Asn Thr Leu Tyr Glu	
47 52 57 62	
gat atc cag tac atg cag gta cct gtg gct gac tcc cct aac tca cgt	720
Asp Ile Gln Tyr Met Gln Val Pro Val Ala Asp Ser Pro Asn Ser Arg	
63 68 73 78	
ctc tgt gac ttc ttt gac cct att gct gac cat atc cac agc gtg gag	768
Leu Cys Asp Phe Phe Asp Pro Ile Ala Asp His Ile His Ser Val Glu	
79 84 89 94	
atg aag cag ggc cgt act ttg ctg cac tgt gct gct ggt gtg agc cgc	816
Met Lys Gln Gly Arg Thr Leu Leu His Cys Ala Ala Gly Val Ser Arg	
95 100 105 110	
tca gct gcc ctg tgc ctc gcc tac ctc atg aag tac cac gcc atg tcc	864
Ser Ala Ala Leu Cys Leu Ala Tyr Leu Met Lys Tyr His Ala Met Ser	
111 116 121 126	
ctg ctg gac gcc cac acg tgg acc aag tca tgc cgg ccc atc atc cga	912
Leu Leu Asp Ala His Thr Trp Thr Lys Ser Cys Arg Pro Ile Ile Arg	
127 132 137 142	
ccc aac agc ggc ttt tgg gag cag ctc atc cac tat gag ttc caa ttg	960
Pro Asn Ser Gly Phe Trp Glu Gln Leu Ile His Tyr Glu Phe Gln Leu	
143 148 153 158	
ttt ggc aag aac act gtg cac atg gtc agt tcc cca gtg gga atg atc	1008
Phe Gly Lys Asn Thr Val His Met Val Ser Ser Pro Val Gly Met Ile	
159 164 169 174	
cct gac atc tat gag aag gaa gtc cgt ttg atg att cca ctg tga gcc	1056
Pro Asp Ile Tyr Glu Lys Glu Val Arg Leu Met Ile Pro Leu *	
175 180 185	
atccccacgag cccctgcatt ggagtcagag gtacagatct attgttgatc ttacaccaag	1116
atccaaactt gaacattcta cttttgttga tacagaaaaa aacagatgat gccttttatg	1176
agcacaaaaa agagttgctg tagcttttaa ctttataatc cattttttttt cagattaaac	1236
taattgtgag atggtgaaga taatttttct gccctgtgag tgacactggc caggggatag	1296
gttgaggcag atggtgccca gaagaaagag ggcagcacco attgcacatg gcaggcctgt	1356
atgcgtccgc tctagaggat ccaagcttac gtgcgcgt	1394

<210> 365
 <211> 7418
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(5103)

<400> 365

atg gtg ctg cgg aaa ctt tca aag aaa gat gtc acc aca aaa tta aaa	48
Met Val Leu Arg Lys Leu Ser Lys Lys Asp Val Thr Thr Lys Leu Lys	
1 5 10	
gct atg cag gaa ttt gga acc atg tgt aca gag aga gac aca gaa act	96
Ala Met Gln Glu Phe Gly Thr Met Cys Thr Glu Arg Asp Thr Glu Thr	
17 22 27 32	
gtg aaa gga gtt ctt cca tat tgg cca aga att ttt tgc aaa att tca	144
Val Lys Gly Val Leu Pro Tyr Trp Pro Arg Ile Phe Cys Lys Ile Ser	
33 38 43 48	
ctt gat cat gac cgt cgc gtc cga gaa gcc aca caa caa gct ttt gaa	192
Leu Asp His Asp Arg Arg Val Arg Glu Ala Thr Gln Gln Ala Phe Glu	
49 54 59 64	
aaa ctt acc ctt aaa gta aag aaa cag ttg gct ccc tac tta aaa agt	240
Lys Leu Thr Leu Lys Val Lys Lys Gln Leu Ala Pro Tyr Leu Lys Ser	
65 70 75 80	
tta atg gga tat tgg cta atg gct cag tgt gat act tac aca cca gct	288
Leu Met Gly Tyr Trp Leu Met Ala Gln Cys Asp Thr Tyr Thr Pro Ala	
81 86 91 96	
gcg ttt gca gca aaa gat gca ttt gaa gcg gct ttt cct cca agc aag	336
Ala Phe Ala Ala Lys Asp Ala Phe Glu Ala Ala Phe Pro Pro Ser Lys	
97 102 107 112	
caa cct gaa gcc ata gca ttt tgt aag gat gaa att aca agt gtg ctg	384
Gln Pro Glu Ala Ile Ala Phe Cys Lys Asp Glu Ile Thr Ser Val Leu	
113 118 123 128	
cag gat cat ctt ata aaa gaa aca cct gat aca ctc agt gac ccg caa	432
Gln Asp His Leu Ile Lys Glu Thr Pro Asp Thr Leu Ser Asp Pro Gln	
129 134 139 144	
act gtt cca gag gaa gaa aga gaa gct aaa ttc tac cgg gtt gta act	480
Thr Val Pro Glu Glu Arg Glu Ala Lys Phe Tyr Arg Val Val Thr	
145 150 155 160	
tgt tcc tta ttg gca tta aag aga tta ctt tgc ctt tta cct gat aat	528
Cys Ser Leu Leu Ala Leu Lys Arg Leu Leu Cys Leu Leu Pro Asp Asn	
161 166 171 176	

gag ctt gat tct ctg gag gag aaa ttt aag tct ctt tta tca cag aat	576
Glu Leu Asp Ser Leu Glu Glu Lys Phe Lys Ser Leu Leu Ser Gln Asn	
177 182 187 192	
aag ttt tgg aag tat gga aaa cac agt gta cct cag att cgc tca gct	624
Lys Phe Trp Lys Tyr Gly Lys His Ser Val Pro Gln Ile Arg Ser Ala	
193 198 203 208	
tat ttt gag tta gtc tct gca ttg tgc cag cgc att cca cag ttg atg	672
Tyr Phe Glu Leu Val Ser Ala Leu Cys Gln Arg Ile Pro Gln Leu Met	
209 214 219 224	
aaa gag gaa gca tcc aaa gtg agc cca tca gtt cta ctt agc att gat	720
Lys Glu Glu Ala Ser Lys Val Ser Pro Ser Val Leu Leu Ser Ile Asp	
225 230 235 240	
gac agt gac cca att gtc tgc cca gct ctc tgg gaa gct gta ctc tat	768
Asp Ser Asp Pro Ile Val Cys Pro Ala Leu Trp Glu Ala Val Leu Tyr	
241 246 251 256	
aca ctt aca act att gag gac tgt tgg ctt cat gta aat gca aaa aag	816
Thr Leu Thr Thr Ile Glu Asp Cys Trp Leu His Val Asn Ala Lys Lys	
257 262 267 272	
agt gtg ttt ccc aag ctg tca act gtg att cgt gaa ggt ggt cgg ggt	864
Ser Val Phe Pro Lys Leu Ser Thr Val Ile Arg Glu Gly Gly Arg Gly	
273 278 283 288	
cta gct act gtc ata tat cct tac ctt ctg cca ttc atc agc aag ctc	912
Leu Ala Thr Val Ile Tyr Pro Tyr Leu Leu Pro Phe Ile Ser Lys Leu	
289 294 299 304	
cct cat tcc atc aca aat cca aag ttg gat ttc ttc aaa aat ttc ctc	960
Pro His Ser Ile Thr Asn Pro Lys Leu Asp Phe Phe Lys Asn Phe Leu	
305 310 315 320	
acg tct cta gtt gct ggg ctg tca aca gag aga act aaa acc agc tct	1008
Thr Ser Leu Val Ala Gly Leu Ser Thr Glu Arg Thr Lys Thr Ser Ser	
321 326 331 336	
tca gag tcc tgc gca gta ata tct gct ttt tat gaa tgc tta cgt ttt	1056
Ser Glu Ser Ser Ala Val Ile Ser Ala Phe Tyr Glu Cys Leu Arg Phe	
337 342 347 352	
ata atg cag caa aac tta ggt gag gaa gag att gaa cag atg ctc gtc	1104
Ile Met Gln Gln Asn Leu Gly Glu Glu Glu Ile Glu Gln Met Leu Val	
353 358 363 368	
aat gat cag ttg atc cct ttt att gat gca gtt ctc aaa gac cca gga	1152
Asn Asp Gln Leu Ile Pro Phe Ile Asp Ala Val Leu Lys Asp Pro Gly	
369 374 379 384	
ttg caa cat ggg cag cta ttt aac cat tta gca gaa act cta agt tcc	1200
Leu Gln His Gly Gln Leu Phe Asn His Leu Ala Glu Thr Leu Ser Ser	
385 390 395 400	
tgg gaa gcc aaa gca gac acg gaa aaa gat gaa aaa aca gct cac aac	1248

Trp	Glu	Ala	Lys	Ala	Asp	Thr	Glu	Lys	Asp	Glu	Lys	Thr	Ala	His	Asn	
401					406					411					416	
ttg	gag	aac	gta	ctg	ata	cat	ttc	tgg	gaa	aga	ctg	tca	gag	atc	tgt	1296
Leu	Glu	Asn	Val	Leu	Ile	His	Phe	Trp	Glu	Arg	Leu	Ser	Glu	Ile	Cys	
417					422					427					432	
gtt	gcg	aaa	atc	agt	gag	cca	gaa	gct	gat	gtt	gag	tcc	gtt	ttg	ggt	1344
Val	Ala	Lys	Ile	Ser	Glu	Pro	Glu	Ala	Asp	Val	Glu	Ser	Val	Leu	Gly	
433					438					443					448	
gta	tct	aac	cta	tta	cag	gtg	ctt	cag	aag	ccg	aag	agc	tca	ttg	aag	1392
Val	Ser	Asn	Leu	Leu	Gln	Val	Leu	Gln	Lys	Pro	Lys	Ser	Ser	Leu	Lys	
449					454					459					464	
tca	agt	aaa	aaa	aaa	aat	ggc	aag	gtt	aga	ttt	gct	gat	gag	ata	ctt	1440
Ser	Ser	Lys	Lys	Lys	Asn	Gly	Lys	Val	Arg	Phe	Ala	Asp	Glu	Ile	Leu	
465					470					475					480	
gaa	agc	aat	aaa	gag	aat	gaa	aaa	tgt	gta	tct	tca	gaa	gga	gag	aag	1488
Glu	Ser	Asn	Lys	Glu	Asn	Glu	Lys	Cys	Val	Ser	Ser	Glu	Gly	Glu	Lys	
481					486					491					496	
att	gaa	ggc	tgg	gaa	tta	aca	act	gaa	cct	tct	ctc	act	cat	aat	tct	1536
Ile	Glu	Gly	Trp	Glu	Leu	Thr	Thr	Glu	Pro	Ser	Leu	Thr	His	Asn	Ser	
497					502					507					512	
tca	ggc	ctt	ttg	tct	cct	cta	agg	aaa	aaa	cct	ttg	gaa	gac	tta	gtc	1584
Ser	Gly	Leu	Leu	Ser	Pro	Leu	Arg	Lys	Lys	Pro	Leu	Glu	Asp	Leu	Val	
513					518					523					528	
tgt	aaa	ctc	gca	gat	ata	agt	att	aat	tat	gtc	aat	gaa	cga	aag	tca	1632
Cys	Lys	Leu	Ala	Asp	Ile	Ser	Ile	Asn	Tyr	Val	Asn	Glu	Arg	Lys	Ser	
529					534					539					544	
gag	caa	cat	cta	agg	ttt	ctt	tct	act	ctg	ctt	gac	tcc	ttt	tct	tca	1680
Glu	Gln	His	Leu	Arg	Phe	Leu	Ser	Thr	Leu	Leu	Asp	Ser	Phe	Ser	Ser	
545					550					555					560	
agc	cga	gta	ttt	aaa	atg	cta	ctt	ggc	gat	gaa	aaa	cag	agt	att	gtc	1728
Ser	Arg	Val	Phe	Lys	Met	Leu	Leu	Gly	Asp	Glu	Lys	Gln	Ser	Ile	Val	
561					566					571					576	
caa	gcc	aaa	cct	ctt	gaa	ata	gcc	aag	ctt	gta	caa	aaa	aat	cct	gcg	1776
Gln	Ala	Lys	Pro	Leu	Glu	Ile	Ala	Lys	Leu	Val	Gln	Lys	Asn	Pro	Ala	
577					582					587					592	
gtg	cag	ttt	tta	tac	cag	aaa	ctg	ata	ggc	tgg	cta	aat	gaa	gat	caa	1824
Val	Gln	Phe	Leu	Tyr	Gln	Lys	Leu	Ile	Gly	Trp	Leu	Asn	Glu	Asp	Gln	
593					598					603					608	
agg	aag	gat	ttt	ggc	ttc	ctg	gtg	gac	att	ttg	tac	agt	gct	ctc	cgg	1872
Arg	Lys	Asp	Phe	Gly	Phe	Leu	Val	Asp	Ile	Leu	Tyr	Ser	Ala	Leu	Arg	
609					614					619					624	
tgc	tgt	gac	aat	gat	atg	gaa	aga	aaa	aaa	gtc	ttg	gat	gat	cta	acc	1920
Cys	Cys	Asp	Asn	Asp	Met	Glu	Arg	Lys	Lys	Val	Leu	Asp	Asp	Leu	Thr	

625	630	635	640	
aag gtg gac ttg aaa tgg aat tct ctt ctt aag att att gaa aag gca				1968
Lys Val Asp Leu Lys Trp Asn Ser Leu Leu Lys Ile Ile Glu Lys Ala				
641	646	651	656	
tgt cct agt tca gat aaa cat gct tta gta act cct tgg ctc aaa ggc				2016
Cys Pro Ser Ser Asp Lys His Ala Leu Val Thr Pro Trp Leu Lys Gly				
657	662	667	672	
gat atc ctt ggt gag aaa ttg gtc aac ttg gca gat tgt ctt tgt aat				2064
Asp Ile Leu Gly Glu Lys Leu Val Asn Leu Ala Asp Cys Leu Cys Asn				
673	678	683	688	
gag gac ttg gaa tcc agg gta tct tca gaa tct cac ttc tca gaa aga				2112
Glu Asp Leu Glu Ser Arg Val Ser Ser Glu Ser His Phe Ser Glu Arg				
689	694	699	704	
tgg act ctt cta agc ttg gta tta tcc caa cat gtt aaa aat gat tac				2160
Trp Thr Leu Leu Ser Leu Val Leu Ser Gln His Val Lys Asn Asp Tyr				
705	710	715	720	
ttg att gga gac gta tat gtt gaa aga atc att gtt aga ctt cat gaa				2208
Leu Ile Gly Asp Val Tyr Val Glu Arg Ile Ile Val Arg Leu His Glu				
721	726	731	736	
act tta ttc aaa aaa aaa tta tca gaa gct gaa agc agt gac tca				2256
Thr Leu Phe Lys Lys Lys Lys Leu Ser Glu Ala Glu Ser Ser Asp Ser				
737	742	747	752	
tca gtg tct ttt atc tgt gat gtg gcc tat aac tat ttc agc tca gcg				2304
Ser Val Ser Phe Ile Cys Asp Val Ala Tyr Asn Tyr Phe Ser Ser Ala				
753	758	763	768	
aaa gga tgc ttg cta atg cca tca tct gaa gat tta tta tta act ctc				2352
Lys Gly Cys Leu Leu Met Pro Ser Ser Glu Asp Leu Leu Leu Thr Leu				
769	774	779	784	
ttt cag tta tgt gct cag agc aaa gaa aaa aca cat ttg cca gat ttt				2400
Phe Gln Leu Cys Ala Gln Ser Lys Glu Lys Thr His Leu Pro Asp Phe				
785	790	795	800	
ctt atc tgt aaa ctg aaa aat act tgg ctc tct ggt gta aat tta ttg				2448
Leu Ile Cys Lys Leu Lys Asn Thr Trp Leu Ser Gly Val Asn Leu Leu				
801	806	811	816	
gtt cat caa act gac agt tca tat aaa gag agt acc ttc cta cat ttg				2496
Val His Gln Thr Asp Ser Ser Tyr Lys Glu Ser Thr Phe Leu His Leu				
817	822	827	832	
tct gct ctg tgg ctg aag aac caa gtt cag gct tca tct ttg gat atc				2544
Ser Ala Leu Trp Leu Lys Asn Gln Val Gln Ala Ser Ser Leu Asp Ile				
833	838	843	848	
aac agt ctc caa gtc ctc ttg tct gct gtt gat gat ttg cta aat aca				2592
Asn Ser Leu Gln Val Leu Leu Ser Ala Val Asp Asp Leu Leu Asn Thr				
849	854	859	864	

ctt cta gag agt gaa gat tct tat ctt atg gga gtt tat att gga agt	2640
Leu Leu Glu Ser Glu Asp Ser Tyr Leu Met Gly Val Tyr Ile Gly Ser	
865 870 875 880	
gta atg ccg aac gac agt gaa tgg gaa aag atg agg cag tct ctt cct	2688
Val Met Pro Asn Asp Ser Glu Trp Glu Lys Met Arg Gln Ser Leu Pro	
881 886 891 896	
atg cag tgg tta cat aga cct ctt tta gag gga aga ttg agt ttg aat	2736
Met Gln Trp Leu His Arg Pro Leu Leu Glu Gly Arg Leu Ser Leu Asn	
897 902 907 912	
tat gaa tgt ttc aaa aca gat ttt aag gaa cag gac ¹ ata aag aca ctt	2784
Tyr Glu Cys Phe Lys Thr Asp Phe Lys Glu Gln Asp Ile Lys Thr Leu	
913 918 923 928	
ccc agc cat ttg tgt act tca gca tta ttg agc aaa atg gtc tta att	2832
Pro Ser His Leu Cys Thr Ser Ala Leu Leu Ser Lys Met Val Leu Ile	
929 934 939 944	
gca ctg aga aag gaa aca gtc tta gaa aat aat gag ctt gag aaa ata	2880
Ala Leu Arg Lys Glu Thr Val Leu Glu Asn Asn Glu Leu Glu Lys Ile	
945 950 955 960	
att gca gaa ctg ctt tat tca ctg cag tgg tgt gaa gaa tta gat aac	2928
Ile Ala Glu Leu Leu Tyr Ser Leu Gln Trp Cys Glu Glu Leu Asp Asn	
961 966 971 976	
cca cct att ttt cta att gga ttt tgt gaa ata ctt caa aaa atg aat	2976
Pro Pro Ile Phe Leu Ile Gly Phe Cys Glu Ile Leu Gln Lys Met Asn	
977 982 987 992	
att acg tat gat aac tta cgt gta ctt ggt aat acg tcg ggc ctt ttg	3024
Ile Thr Tyr Asp Asn Leu Arg Val Leu Gly Asn Thr Ser Gly Leu Leu	
993 998 1003 1008	
cag ctg tta ttt aac agg tcc aga gaa cat ggc aca ctg tgg tct ctt	3072
Gln Leu Leu Phe Asn Arg Ser Arg Glu His Gly Thr Leu Trp Ser Leu	
1009 1014 1019 1024	
att att gct aag ttg atc ctt tcc cga agc att tca tct gat gaa gta	3120
Ile Ile Ala Lys Leu Ile Leu Ser Arg Ser Ile Ser Ser Asp Glu Val	
1025 1030 1035 1040	
aaa cca cat tat aag aga aaa gaa agt ttt ttt cca cta act gaa ggc	3168
Lys Pro His Tyr Lys Arg Lys Glu Ser Phe Phe Pro Leu Thr Glu Gly	
1041 1046 1051 1056	
aat ttg cat acc att caa agt cta tgt cca ttt ttg tca aaa aaa aaa	3216
Asn Leu His Thr Ile Gln Ser Leu Cys Pro Phe Leu Ser Lys Lys Lys	
1057 1062 1067 1072	
aaa aaa gaa ttt agt gct caa tgt ata cct gct ctt ttg ggc tgg act	3264
Lys Lys Glu Phe Ser Ala Gln Cys Ile Pro Ala Leu Leu Gly Trp Thr	
1073 1078 1083 1088	

aag aaa gat ctt tgc agc act aat gga ggt ttt gga cat ctt gcc att	3312
Lys Lys Asp Leu Cys Ser Thr Asn Gly Gly Phe Gly His Leu Ala Ile	
1089 1094 1099 1104	
ttc aat tct tgt ctg caa acc aaa agt ata gat gat gga gag cta tta	3360
Phe Asn Ser Cys Leu Gln Thr Lys Ser Ile Asp Asp Gly Glu Leu Leu	
1105 1110 1115 1120	
cat gga ata tta aaa atc ata ata tcc tgg aag aaa gag cat gaa gat	3408
His Gly Ile Leu Lys Ile Ile Ile Ser Trp Lys Lys Glu His Glu Asp	
1121 1126 1131 1136	
att ttt ctt ttc agt tgt aat cta tca gaa gca agt cca gag gta ctg	3456
Ile Phe Leu Phe Ser Cys Asn Leu Ser Glu Ala Ser Pro Glu Val Leu	
1137 1142 1147 1152	
ggt gta aat ata gaa ata atc cgg ttt ctt tcc ctg ttt ctg aaa tac	3504
Gly Val Asn Ile Glu Ile Ile Arg Phe Leu Ser Leu Phe Leu Lys Tyr	
1153 1158 1163 1168	
tgc tca tcc cct ttg gca gag agt gag tgg gac ttc atc atg tgc tcc	3552
Cys Ser Ser Pro Leu Ala Glu Ser Glu Trp Asp Phe Ile Met Cys Ser	
1169 1174 1179 1184	
atg ttg gct tgg ttg gag aca aca agt gag aat cag gca ttg tat tct	3600
Met Leu Ala Trp Leu Glu Thr Thr Ser Glu Asn Gln Ala Leu Tyr Ser	
1185 1190 1195 1200	
att cca ctt gtg caa ctg ttt gcc tgt gtc agc tgt gat ttg gcc tgt	3648
Ile Pro Leu Val Gln Leu Phe Ala Cys Val Ser Cys Asp Leu Ala Cys	
1201 1206 1211 1216	
gac ctc agt gct ttc ttt gat tcc aca act ctg gat acc att ggc aat	3696
Asp Leu Ser Ala Phe Phe Asp Ser Thr Thr Leu Asp Thr Ile Gly Asn	
1217 1222 1227 1232	
ctt cct gta aat cta atc agt gaa tgg aaa gaa ttt ttt tcc caa ggc	3744
Leu Pro Val Asn Leu Ile Ser Glu Trp Lys Glu Phe Phe Ser Gln Gly	
1233 1238 1243 1248	
atc cac agt ttg ctt tta cct att ttg gtg act gtt aca gga gaa aac	3792
Ile His Ser Leu Leu Leu Pro Ile Leu Val Thr Val Thr Gly Glu Asn	
1249 1254 1259 1264	
aaa gat gtg tct gaa aca tcc ttt cag aat gca atg ctg aaa ccc atg	3840
Lys Asp Val Ser Glu Thr Ser Phe Gln Asn Ala Met Leu Lys Pro Met	
1265 1270 1275 1280	
tgt gaa aca tta acg tat atc tca aag gaa cag cta ttg agt cac aaa	3888
Cys Glu Thr Leu Thr Tyr Ile Ser Lys Glu Gln Leu Leu Ser His Lys	
1281 1286 1291 1296	
ctt cct gca aga tta gtt gct gac caa aaa aca aac tta cca gaa tat	3936
Leu Pro Ala Arg Leu Val Ala Asp Gln Lys Thr Asn Leu Pro Glu Tyr	
1297 1302 1307 1312	
ctc cag act ttg tta aat aca ttg gcc cca tta ctc ctc ttc aga gct	3984

Leu Gln Thr Leu Leu Asn Thr Leu Ala Pro Leu Leu Leu Phe Arg Ala	
1313 1318 1323 1328	
agg cct gtg caa att gct gtt tat cat atg cta tac aaa ttg atg cct	4032
Arg Pro Val Gln Ile Ala Val Tyr His Met Leu Tyr Lys Leu Met Pro	
1329 1334 1339 1344	
gaa tta cca cag tat gat cag gat aat cta aag tca tac gga gat gaa	4080
Glu Leu Pro Gln Tyr Asp Gln Asp Asn Leu Lys Ser Tyr Gly Asp Glu	
1345 1350 1355 1360	
gaa gaa gag cca gcc ttg tca cca cca gca gca ctg atg tct ctt ctt	4128
Glu Glu Glu Pro Ala Leu Ser Pro Pro Ala Ala Leu Met Ser Leu Leu	
1361 1366 1371 1376	
agc att caa gag gac tta cta gaa aat gtt ttg ggg tgt att cct gtt	4176
Ser Ile Gln Glu Asp Leu Leu Glu Asn Val Leu Gly Cys Ile Pro Val	
1377 1382 1387 1392	
gga cag ata gtt act att aaa cca ctg agt gaa gac ttc tgt tat gtt	4224
Gly Gln Ile Val Thr Ile Lys Pro Leu Ser Glu Asp Phe Cys Tyr Val	
1393 1398 1403 1408	
ctg gga tac ctt ctc act tgg aaa tta ata cta act ttc ttc aaa gct	4272
Leu Gly Tyr Leu Leu Thr Trp Lys Leu Ile Leu Thr Phe Phe Lys Ala	
1409 1414 1419 1424	
gca tca tca cag ctt cgg gct ttg tat tcc atg tat ctt cgg aaa aca	4320
Ala Ser Ser Gln Leu Arg Ala Leu Tyr Ser Met Tyr Leu Arg Lys Thr	
1425 1430 1435 1440	
aag agt ttg aat aaa ttg ctc tat cac ctg ttc agg ctt atg cca gaa	4368
Lys Ser Leu Asn Lys Leu Leu Tyr His Leu Phe Arg Leu Met Pro Glu	
1441 1446 1451 1456	
aat cca acc tat gca gag aca gca gtt gag gtc cca aat aag gac cct	4416
Asn Pro Thr Tyr Ala Glu Thr Ala Val Glu Val Pro Asn Lys Asp Pro	
1457 1462 1467 1472	
aaa aca ttc ttt act gag gag ctc cag ctg agt att aga gaa aca aca	4464
Lys Thr Phe Phe Thr Glu Glu Leu Gln Leu Ser Ile Arg Glu Thr Thr	
1473 1478 1483 1488	
atg ctt cca tac cac att cca cac ttg gct tgt tca gtc tat cat atg	4512
Met Leu Pro Tyr His Ile Pro His Leu Ala Cys Ser Val Tyr His Met	
1489 1494 1499 1504	
aca tta aaa gac ttg cct gcc atg gtt agg ttg tgg tgg aat agc agt	4560
Thr Leu Lys Asp Leu Pro Ala Met Val Arg Leu Trp Trp Asn Ser Ser	
1505 1510 1515 1520	
gag aag cgt gtt ttc aat att gtg gat aga ttt aca agc aag tat gtc	4608
Glu Lys Arg Val Phe Asn Ile Val Asp Arg Phe Thr Ser Lys Tyr Val	
1521 1526 1531 1536	
agc agt gtt ctt tct ttt caa gaa ata tct tct gta caa aca agt aca	4656
Ser Ser Val Leu Ser Phe Gln Glu Ile Ser Ser Val Gln Thr Ser Thr	

1537	1542	1547	1552	
caa cta ttt aat ggc atg acg gtt aaa gct cga gct act act cga gag				4704
Gln Leu Phe Asn Gly Met Thr Val Lys Ala Arg Ala Thr Thr Arg Glu				
1553	1558	1563	1568	
gta atg gct act tat act att gag gac ata gtt att gaa ctt ata ata				4752
Val Met Ala Thr Tyr Thr Ile Glu Asp Ile Val Ile Glu Leu Ile Ile				
1569	1574	1579	1584	
caa ctg cct tca aat tat cca ctg ggt tca ata ata gta gaa agt ggg				4800
Gln Leu Pro Ser Asn Tyr Pro Leu Gly Ser Ile Ile Val Glu Ser Gly				
1585	1590	1595	1600	
aaa aga gta gga gta gct gtt cag cag tgg cgg aac tgg atg ctg cag				4848
Lys Arg Val Gly Val Ala Val Gln Gln Trp Arg Asn Trp Met Leu Gln				
1601	1606	1611	1616	
tta agc act tac ctc acc cat cag aat gga agt att atg gaa ggc tta				4896
Leu Ser Thr Tyr Leu Thr His Gln Asn Gly Ser Ile Met Glu Gly Leu				
1617	1622	1627	1632	
gct tta tgg aaa aat aac gta gac aaa cgt ttt gag ggt gtt gaa gat				4944
Ala Leu Trp Lys Asn Asn Val Asp Lys Arg Phe Glu Gly Val Glu Asp				
1633	1638	1643	1648	
tgc atg atc tgt ttc tca gtc att cac ggt ttc aac tat tcc ctt ccc				4992
Cys Met Ile Cys Phe Ser Val Ile His Gly Phe Asn Tyr Ser Leu Pro				
1649	1654	1659	1664	
aaa aaa gcc tgt aga aca tgc aag aaa aaa ttc cat tca gcc tgc ttg				5040
Lys Lys Ala Cys Arg Thr Cys Lys Lys Lys Phe His Ser Ala Cys Leu				
1665	1670	1675	1680	
tac aaa tgg ttt aca tct agc aac aaa tcc act tgt cca ctg tgt cgt				5088
Tyr Lys Trp Phe Thr Ser Ser Asn Lys Ser Thr Cys Pro Leu Cys Arg				
1681	1686	1691	1696	
gag acg ttt ttc tga gatttttttc actggaaggg atccctgaag tacatcaaac				5143
Glu Thr Phe Phe *				
1697				
aaaggcattg gatttggatc cgtctgaaaag tgtggatgtg gggaagccag tgagcattac				5203
ttttaaatag gaccttctct ggaaaaattat tttggttaat gtaataatcc taaaatcagg				5263
tttacttaac tttagattgc tttgtaaattg tttggaaact ttctttttaca aaagaatatt				5323
acatatttga gagaaaatat ttctattaat ggtttaattt ctttgtatat ttaaaaaataa				5383
atatgaaaaa cccctaaatt acagaattgg aatttgtgaa aagattgcac aactatatta				5443
ttgataaacc cattccgttt gttgatctgt gttttagaat agtccaagtg aagcaaaacg				5503
aactgagaga gctgatttac atctatagat attttaagcc ttattttatta gttatgacaa				5563
taaattagta ttctgatatt tgtagattat tttaatgata aaaatgacac taagctatta				5623

1000 900 800 700 600 500 400 300 200 100 0

atacggcttg	tcttaagata	tctggaggca	tgctctgaaa	tcctatataa	aagagtttaa	5683
actgaacttt	aaggtgcctc	catttatcaa	gggttatgaa	actcagaaaa	ttaaattcct	5743
gatgctgacc	tttttgcttg	tgggagaatt	atttctatat	attagtgaaa	tttgaattgt	5803
aaacttgctca	gtgaatttat	cactctgagc	gagtctctag	agggtgagaa	tttgagagaa	5863
atagtaattt	gattatttca	ttcatgaagc	ggagtggtag	ttatccttct	attgagaggg	5923
aagaaataaa	tgagtattac	tgaaacttaa	agatcagtgg	aaaaaaaaaa	catttaaaaa	5983
tgttgtagga	gactttcaat	tttgaagca	aactgagcta	ttcttaccag	ccaaagttaa	6043
actaaataag	agacttgggg	gagcaaagt	ttttcagcct	tcagaaatga	aagttaagga	6103
ttttagcact	aggtaaaatt	cagtataata	ggctgaagt	gagtaagtga	aaacctgcct	6163
tttgccactc	ttaaaaattg	tgcccaaaat	ataaaagtgt	ggaacttttag	aacttggaat	6223
aattttattg	cagtcttcca	ttacatggaa	atagcatatc	taatatctag	gttacttgag	6283
agaccagcta	atcatctctg	ttgcacatgt	ttaattggca	aaaagcaatt	catgataaat	6343
aaaattactg	ctttccatct	actgggtaaa	atgactattg	aaatagtatg	aatgtggtca	6403
gaggattata	gttgagagt	aagtactatg	tgtgagttat	agatctctcg	aattatattt	6463
atagatgcag	tgtcctgccc	agttttgttt	gcctcctaca	ttttactgta	aaatatttat	6523
tgtctcttag	ccttgagcct	ctgagggtca	gtaagtgaag	tacagatagc	aaaattttac	6583
tacctogtta	acccttttct	taaaatattc	tctatctttc	tatgtctctt	totgacatag	6643
taatcccaaa	ggattgtggt	actccccgtg	aaagttatta	cttttccttt	aaaaatgggt	6703
ttataataag	actgttttaa	acctttccag	tattggtaca	tcttggtctc	tggcccaaac	6763
ccaagcaga	aaagaaaatg	gaataatgga	gcattgtttt	tccacattag	tattagggca	6823
tcagattcct	ggtgaaacac	tataattaag	tagttataat	taaataactg	ttcttcatac	6883
ttaggactct	taatacattt	ctttaagact	tgtaagtata	attgtaaagc	ttgttaactg	6943
tttatatact	aaagaaaaag	ctttacaaga	taagactgaa	attcagaata	ccacattaaa	7003
gttttatctg	tacagcgttg	acaactctaa	ctaaaaggat	tacagccctt	aaaatttttag	7063
cttaaggaca	ttttaaaatt	gcatgagatt	agcaaaatta	ttaattttaa	accccaaagt	7123
aaattgcaaa	ttttaaaatt	tatttttgac	tcttttatca	catgctocaa	tgtatgtaca	7183
taagtgtctg	tggcttaaat	aatatgttgt	tatttgatac	atttttgtgg	tgcaagtaat	7243
taatgttatt	atttgattgt	tataccatat	gtgccatta	aaattctttt	taattaaaaa	7303

tatttcaa atgcagaaaa ataataatat aaatgccctt gtacccttca cataactattt 7363
 tgccatattt gcttctgatt tttaaataaa taaaatgtta ctcttttgta cttct 7418

<210> 366
 <211> 1497
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (317)..(751)

<400> 366
 aactagtcca gtgcgggtgga attcgggtgga tggatgggtg ggtagatgaa tggatgcata 60
 gatgaatgta tcagtggatg gatagttggc tagatgggtg ggttgggtgga tgaatggcag 120
 agcttgcacc tgccagtcca totgacatca aagccagtgt ctctaattggg gacaccaccc 180
 tcctctgcag caggaggcag agctgtggga tgaatgaggt tcgccagggtc tcccttacct 240
 atcctgggtc cccagctcct tctcactctc ttccttgca gcctcgaagc ggaggatccc 300
 tgtgtcccag ccgggc atg gcc gac ccc cac cag ctt ttc gat gac aca 349
 Met Ala Asp Pro His Gln Leu Phe Asp Asp Thr
 1 5
 agt tca gcc cag agc cgg ggc tat ggg gcc cag cgg gca cct ggt ggc 397
 Ser Ser Ala Gln Ser Arg Gly Tyr Gly Ala Gln Arg Ala Pro Gly Gly
 12 17 22 27
 cta agt tat cct gca gcc tct ccc acg ccc cat gca gcc ttc ctg gct 445
 Leu Ser Tyr Pro Ala Ala Ser Pro Thr Pro His Ala Ala Phe Leu Ala
 28 33 38 43
 gac ccg gtg tcc aac atg gcc atg gcc tat ggg agc agc ctg gcc gcg 493
 Asp Pro Val Ser Asn Met Ala Met Ala Tyr Gly Ser Ser Leu Ala Ala
 44 49 54 59
 cag ggc aag gag ctg gtg gat aag aac gtg agt ggg cgg ggc tgg tgg 541
 Gln Gly Lys Glu Leu Val Asp Lys Asn Val Ser Gly Arg Gly Trp Trp
 60 65 70 75
 gag tgg ggg gat gca cgg ggc cac agg gct tca gac ttg agc tct gcc 589
 Glu Trp Gly Asp Ala Arg Gly His Arg Ala Ser Asp Leu Ser Ser Ala
 76 81 86 91
 tcc cca gat cga ccg ctt cat ccc cat cac caa gct caa gta tta ctt 637
 Ser Pro Asp Arg Pro Leu His Pro His His Gln Ala Gln Val Leu Leu
 92 97 102 107
 tgc tgt gga cac cat gta tgt ggg cag aaa gct ggg cct gct gtt ctt 685
 Cys Cys Gly His His Val Cys Gly Gln Lys Ala Gly Pro Ala Val Leu

108	113	118	123	
ccc cta cct aca cca gga ctg gga agt gca gta cca aca gga cac ccc				733
Pro Leu Pro Thr Pro Gly Leu Gly Ser Ala Val Pro Thr Gly His Pro				
124	129	134	139	
ggg ggc ccc ccg ctt tga cgtcaa tgccccggac ctctacattc cagcaatggc				787
Gly Gly Pro Pro Leu *				
140	145			
tttcatcacc tacgttttgg tggctgggtct tgcgctgggg acccaggata gggttctcccc				847
agacctcctg gggctgcaag cgagctcagc cctggccttg ctgaccttg aggtgctggc				907
catcctgctc agcctctatc tggctactgt caacaccgac ctcaccacca tcgacctggg				967
ggccttcttg ggctacaaat atgtcgggat gattggcggg gtcctcatgg gcctgctctt				1027
cggaagatt ggctactacc tgggtgctggg ctgggtgctgc gtagccatct ttgtgttcat				1087
gatccggacg ctgctggctga agatcttggc agacgcagca gctgaggggg tcccgggtgcg				1147
tggggccccg aaccagctgc gcatgtacct gaccatggcg gtggcggcg cgagcctat				1207
gctcatgtac tggctcacct tccacctggg gcggtgagcg cggccgctga acctcccgt				1267
gctgctgctg ctgctggggg ccactgtggc cgccgaactc atctcctgcc tgcaggcccc				1327
aagggtccacc ctgtctggcc acaggccacc gcctccatcc catgtcccgc ccagccccgc				1387
ccccaaacca aggtgctgag agatctccag ctgcacaggc caccgcccc aaggcgtggcc				1447
gctgttacag aaacaataaa ccctgatggg catggcaaaa aaaaaaaaaa				1497

<210> 367
 <211> 973
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (375)..(599)

<220>
 <221> misc_feature
 <222> (1)...(973)
 <223> n = a,t,c or g

gtgtgtgggg aggggtgtata tggagaagga gccccaaagaa aggatcagaa cggagaccac	60
tgccacctga tgtttcctgc aggggctgca ctgtgtctct ggctgagggtc aactgacac	120
ctgggtgggtca ctgggtcactc gcagtcttaa atctagtagg gccgaaagta ctagaaggag	180

gttgtccaga gaggtctgcc ctcaaaatgc tcctgaaaga tgcttgctta tgcttttctt 240
 taaaaattat ttctggggaa gggcggggag tggtcacagg atcttatatt ctctttattt 300
 ttacttaatt tgcattgtat ttttagaact ccccttttta agggtcacat tttgcctcag 360
 aaaaccctgt ctga atg tct cct gtt tgt cgg tca gga ctg act ctg cct 410
 Met Ser Pro Val Cys Arg Ser Gly Leu Thr Leu Pro
 1 5 10
 ttt ctt tcc ttt tcc atg tgc cac tcc tgt cct ccc ttt gcc ctg cct 458
 Phe Leu Ser Phe Ser Met Cys His Ser Cys Pro Pro Phe Ala Leu Pro
 13 18 23 28
 gat ttc tgc act gtc ctg tcc cac ctg tct gtc tcc tct tgg ttt tgc 506
 Asp Phe Cys Thr Val Leu Ser His Leu Ser Val Ser Ser Trp Phe Cys
 29 34 39 44
 ccg tgt cag cct ccc ctt ccg tgc cct ctg ccc ccc ttg cag aac aag 554
 Pro Cys Gln Pro Pro Leu Pro Cys Pro Leu Pro Pro Leu Gln Asn Lys
 45 50 55 60
 acc gcg aaa ggc agc ctg agc aca gag cag tgg gag cgg ggg tga ggg 602
 Thr Ala Lys Gly Ser Leu Ser Thr Glu Gln Ser Glu Arg Gly *
 61 66 71
 gggcagtggtg ctctgtggaa tggaaaggac agcaagcaca ggtgagtcgg ggccaccggg 662
 ctccctgcat cctgccccgg ctcccagcag gcgtcgttgc ctctgccctc ctgctcgtc 722
 tatgctctgc caccagcatt tcattcctgtg gatgacaacg ccagggtggat gcagtgttct 782
 tccattgggtt acttagctcc ccagattatc tgtggaaagg agtgggggct tctaaactgt 842
 ccactgccaa tgggggtgcag ggtgactgtt cctgaaggca gcccttcagg gcacagctgg 902
 ccaggggtgg ccttgtgagt ngacacaaca ggcttttagg tctctttctt gggcaagggc 962
 atctcttgcc a 973

<210> 368
 <211> 839
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (61) .. (429)

<400> 368
 gctacctatc cggaagggtc atatctgaaa gggtttgcct gtcgcgtcat gtaacttgaa 60
 atg tgg aat ttt acc ctt ata tca aag gta aag att tcc cgg gag gtg 108

Met	Trp	Asn	Phe	Thr	Leu	Ile	Ser	Lys	Val	Lys	Ile	Ser	Arg	Glu	Val	
1				5					10					15		
act	atg	att	gcc	agc	aaa	ttc	ggt	atc	ggc	cag	cag	gtc	cgc	cat	tcc	156
Thr	Met	Ile	Ala	Ser	Lys	Phe	Gly	Ile	Gly	Gln	Gln	Val	Arg	His	Ser	
17					22				27					32		
ctg	tta	ggt	tat	ctc	gga	gtg	gtc	gtg	gat	atc	gac	ccg	gtt	tat	tcg	204
Leu	Leu	Gly	Tyr	Leu	Gly	Val	Val	Val	Asp	Ile	Asp	Pro	Val	Tyr	Ser	
33					38				43					48		
ctc	tct	gaa	ccg	tcg	cct	gat	gag	ctg	gcg	gtg	aat	gac	gag	ctt	cgc	252
Leu	Ser	Glu	Pro	Ser	Pro	Asp	Glu	Leu	Ala	Val	Asn	Asp	Glu	Leu	Arg	
49					54				59					64		
gcc	gct	ccg	tgg	tat	cac	gta	gtg	atg	gag	gac	gat	aac	ggc	cta	ccg	300
Ala	Ala	Pro	Trp	Tyr	His	Val	Val	Met	Glu	Asp	Asp	Asn	Gly	Leu	Pro	
65					70				75					80		
gtt	cat	acc	tac	ctg	gct	gaa	gcc	cag	cta	agt	agc	gaa	ttg	cag	gat	348
Val	His	Thr	Tyr	Leu	Ala	Glu	Ala	Gln	Leu	Ser	Ser	Glu	Leu	Gln	Asp	
81					86				91					96		
gaa	cat	cct	gaa	cag	cca	tcc	atg	gat	gag	ctg	gcg	cag	acc	atc	cgc	396
Glu	His	Pro	Glu	Gln	Pro	Ser	Met	Asp	Glu	Leu	Ala	Gln	Thr	Ile	Arg	
97					102				107					112		
aaa	caa	ctc	cag	gcc	ccg	cgt	ctg	cgt	aac	taa	tcctgaa	caa	atccccg			447
Lys	Gln	Leu	Gln	Ala	Pro	Arg	Leu	Arg	Asn	*						
113					118				123							
gaagggttttt	gccttcgagg	gatttttttat	ttggccaggc	ccaggcgagg	gatctcaata											507
gccggggcagc	gatccatcac	cacatttaac	ccggcatccc	gtgccagtac	tgcgcgttgc											567
tcattaatca	ccccagttg	catccagaga	gttttcgcgc	caatggcaat	agcttctgt											627
gccacgcccc	acgccgcttc	tgaattacgg	aaaacatcga	ccatatcgac	tttttcggga											687
acgtctgcc	gcgtgccata	ccccttctgg	cccagcagcg	ttttgccggc	aacttttggc											747
gaaaccggaa	tgacgtgata	cccctggctg	agtagatatt	tcatacgcg	atagctggga											807
cgatcggggt	tgctgcttgc	cccaccagc	gc													839

<210> 369
 <211> 3388
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (296) .. (2413)

<400> 369

ccatgacgat gttgattaca ggtcgtgct acttacgcca gcttgaacct taccctaact 60

aaaggaaca caggctggag ctcaaggatc cttaattaa ttaatcccc ccccccccg 120

gggcgcgacc atctgcgctg cggcgccggc gactcagcgc tgectcagtc tgcgggtgggc 180

agcggaggag tcgtgtcgtg cctgagagcg cagctgtgct cctgggcacc gcgcagtccg 240

ccccgcggc tcctggccag accacccta ggacccctg cccaagtcg cagcc atg 298
Met
1

aac tac ctg cgg cgc cgc ctg tgc gac agc aac ttt atg gcc aat ctg 346
Asn Tyr Leu Arg Arg Arg Leu Ser Asp Ser Asn Phe Met Ala Asn Leu
2 7 12 17

cca aat ggg tac atg aca gac ctg cag cgt ccg cag ccg ccc cca ccg 394
Pro Asn Gly Tyr Met Thr Asp Leu Gln Arg Pro Gln Pro Pro Pro Pro
18 23 28 33

ccg ccc ggt gcc cac agc ccc gga gcc acg ccc ggt ccc ggg acc gcc 442
Pro Pro Gly Ala His Ser Pro Gly Ala Thr Pro Gly Pro Gly Thr Ala
34 39 44 49

act gcc gag agg tcc tcc ggg gtc gcc cca gcg gcc tct ccg gcc gcc 490
Thr Ala Glu Arg Ser Ser Gly Val Ala Pro Ala Ala Ser Pro Ala Ala
50 55 60 65

cct agc ccc ggg tcc tgc ggg ggc ggt ggc ttc ttc tgc tgc ctg tcc 538
Pro Ser Pro Gly Ser Ser Gly Gly Gly Gly Phe Phe Ser Ser Leu Ser
66 71 76 81

aac gcg gtc aag cag acc acg gcg gcg gca gct gcc acc ttc agc gag 586
Asn Ala Val Lys Gln Thr Thr Ala Ala Ala Ala Ala Thr Phe Ser Glu
82 87 92 97

cag gtg ggc ggc ggc tct ggg ggc gca ggc cgc ggg gga gcc gcc tcc 634
Gln Val Gly Gly Gly Ser Gly Gly Ala Gly Arg Gly Gly Ala Ala Ser
98 103 108 113

agg gtg ctg ctg gtc atc gac gag ccg cac acc gac tgg gca aaa tac 682
Arg Val Leu Leu Val Ile Asp Glu Pro His Thr Asp Trp Ala Lys Tyr
114 119 124 129

ttc aaa ggg aaa aag atc cat gga gaa att gac att aaa gta gaa cag 730
Phe Lys Gly Lys Lys Ile His Gly Glu Ile Asp Ile Lys Val Glu Gln
130 135 140 145

gcc gaa ttc tct gat ctg aac ctt gtg gcc cat gcc aat ggt gga ttc 778
Ala Glu Phe Ser Asp Leu Asn Leu Val Ala His Ala Asn Gly Gly Phe
146 151 156 161

tct gtg gat atg gaa gtt ctt cgg aat ggg gtg aag gtc gtg cgg tct 826
Ser Val Asp Met Glu Val Leu Arg Asn Gly Val Lys Val Val Arg Ser
162 167 172 177

ctg aag ccg gat ttt gtg ctg atc cgc cag cac gcc ttc agc atg gca	874
Leu Lys Pro Asp Phe Val Leu Ile Arg Gln His Ala Phe Ser Met Ala	
178 183 188 193	
cgc aac gga gac tac cgc agt ttg gtc att ggg ctg cag tat gct gga	922
Arg Asn Gly Asp Tyr Arg Ser Leu Val Ile Gly Leu Gln Tyr Ala Gly	
194 199 204 209	
atc ccc agt gtt aac tcc ttg cat tct gtc tac aac ttc tgt gac aag	970
Ile Pro Ser Val Asn Ser Leu His Ser Val Tyr Asn Phe Cys Asp Lys	
210 215 220 225	
ccc tgg gtg ttt gcc cag atg gtt cga ctg cat aag aaa ctg ggg aca	1018
Pro Trp Val Phe Ala Gln Met Val Arg Leu His Lys Lys Leu Gly Thr	
226 231 236 241	
gaa gaa ttc cct cta att gat cag acc ttc tac ccc aat cac aaa gaa	1066
Glu Glu Phe Pro Leu Ile Asp Gln Thr Phe Tyr Pro Asn His Lys Glu	
242 247 252 257	
atg ctc agc agt aca acg tac ccc gtg gtt gtg aag atg ggg cac gca	1114
Met Leu Ser Ser Thr Thr Tyr Pro Val Val Val Lys Met Gly His Ala	
258 263 268 273	
cac tct ggg atg ggc aag gtc aag gtt gac aac cag cat gac ttc cag	1162
His Ser Gly Met Gly Lys Val Lys Val Asp Asn Gln His Asp Phe Gln	
274 279 284 289	
gac atc gca agt gtc gtg gca ctg acc aag acg tat gcc act gcc gag	1210
Asp Ile Ala Ser Val Val Ala Leu Thr Lys Thr Tyr Ala Thr Ala Glu	
290 295 300 305	
ccc ttc atc gat gcc aaa tat gac gtg cgt gtc cag aag att ggg cag	1258
Pro Phe Ile Asp Ala Lys Tyr Asp Val Arg Val Gln Lys Ile Gly Gln	
306 311 316 321	
aac tac aag gcc tac atg agg acg tca gtg tca ggg aac tgg aag acc	1306
Asn Tyr Lys Ala Tyr Met Arg Thr Ser Val Ser Gly Asn Trp Lys Thr	
322 327 332 337	
aat act ggc tct gcg atg ctg gag caa att gcc atg tct gac aga tac	1354
Asn Thr Gly Ser Ala Met Leu Glu Gln Ile Ala Met Ser Asp Arg Tyr	
338 343 348 353	
aag ctg tgg gtg gac acg tgc tca gag att ttt ggg gga ctg gac atc	1402
Lys Leu Trp Val Asp Thr Cys Ser Glu Ile Phe Gly Gly Leu Asp Ile	
354 359 364 369	
tgc gca gtg gaa gcg cta cat ggc aag gac gga agg gat cac atc att	1450
Cys Ala Val Glu Ala Leu His Gly Lys Asp Gly Arg Asp His Ile Ile	
370 375 380 385	
gag gtg gtg ggt tcc tcc atg ccg ctc att ggt gac cac cag gat gaa	1498
Glu Val Val Gly Ser Ser Met Pro Leu Ile Gly Asp His Gln Asp Glu	
386 391 396 401	
gac aaa cag ctc atc gta gag ctc gtg gtc aac aag atg gct cag gcc	1546

Asp	Lys	Gln	Leu	Ile	Val	Glu	Leu	Val	Val	Asn	Lys	Met	Ala	Gln	Ala		
402					407					412					417		
ctg	ccc	cgg	cag	cga	cag	cgc	gat	gcc	tcc	cct	ggc	agg	ggc	tcc	cat	1594	
Leu	Pro	Arg	Gln	Arg	Gln	Arg	Asp	Ala	Ser	Pro	Gly	Arg	Gly	Ser	His		
418					423					428					433		
ggc	cag	act	ccg	tcc	cca	ggg	gcc	ctg	ccc	ttg	ggc	cgc	cag	acc	tcc	1642	
Gly	Gln	Thr	Pro	Ser	Pro	Gly	Ala	Leu	Pro	Leu	Gly	Arg	Gln	Thr	Ser		
434					439					444					449		
cag	cag	ccc	gca	ggg	ccc	ccg	gct	cag	cag	cga	ccc	cca	cca	cag	ggc	1690	
Gln	Gln	Pro	Ala	Gly	Pro	Pro	Ala	Gln	Gln	Arg	Pro	Pro	Pro	Gln	Gly		
450					455					460					465		
ggc	cct	cca	cag	ccg	ggt	cca	ggc	ccc	cag	cgc	cag	gga	ccc	cca	ttg	1738	
Gly	Pro	Pro	Gln	Pro	Gly	Pro	Gly	Pro	Gln	Arg	Gln	Gly	Pro	Pro	Leu		
466					471					476					481		
cag	cag	cgc	ccg	ccc	ccg	cag	ggc	cag	cag	cac	ctt	tca	ggc	ctt	gga	1786	
Gln	Gln	Arg	Pro	Pro	Pro	Gln	Gly	Gln	Gln	His	Leu	Ser	Gly	Leu	Gly		
482					487					492					497		
ccc	cca	gct	ggc	agc	ccc	ctg	ccc	cag	cgc	ctt	cca	agt	ccc	acc	tca	1834	
Pro	Pro	Ala	Gly	Ser	Pro	Leu	Pro	Gln	Arg	Leu	Pro	Ser	Pro	Thr	Ser		
498					503					508					513		
gcg	ccc	cag	cag	ccc	gcg	tcc	cag	gcc	gcg	ccg	ccg	acc	cag	ggt	caa	1882	
Ala	Pro	Gln	Gln	Pro	Ala	Ser	Gln	Ala	Ala	Pro	Pro	Thr	Gln	Gly	Gln		
514					519					524					529		
ggc	cgc	caa	tcc	cgg	cca	gtg	gcg	gga	ggc	ccc	ggg	gcg	cct	cca	gca	1930	
Gly	Arg	Gln	Ser	Arg	Pro	Val	Ala	Gly	Gly	Pro	Gly	Ala	Pro	Pro	Ala		
530					535					540					545		
gcc	cgc	ccg	ccc	gcc	tct	ccg	tct	ccc	cag	cgc	cag	gcg	ggc	ccc	cca	1978	
Ala	Arg	Pro	Pro	Ala	Ser	Pro	Ser	Pro	Gln	Arg	Gln	Ala	Gly	Pro	Pro		
546					551					556					561		
cag	gct	acc	cgt	cag	aca	tcc	gtc	tct	ggc	ccg	gct	ccg	cca	aag	gcc	2026	
Gln	Ala	Thr	Arg	Gln	Thr	Ser	Val	Ser	Gly	Pro	Ala	Pro	Pro	Lys	Ala		
562					567					572					577		
tct	ggg	gcc	cca	ccg	ggc	ggg	cag	cag	cgc	cag	ggc	ccg	ccc	cag	aaa	2074	
Ser	Gly	Ala	Pro	Pro	Gly	Gly	Gln	Gln	Arg	Gln	Gly	Pro	Pro	Gln	Lys		
578					583					588					593		
ccc	cca	ggc	cca	gcc	ggc	ccc	aca	cgc	cag	gcc	agc	cag	gcg	ggt	ccc	2122	
Pro	Pro	Gly	Pro	Ala	Gly	Pro	Thr	Arg	Gln	Ala	Ser	Gln	Ala	Gly	Pro		
594					599					604					609		
gtg	ccc	cgc	act	ggg	cca	ccc	acc	acg	cag	cag	cct	cgg	ccc	agc	ggc	2170	
Val	Pro	Arg	Thr	Gly	Pro	Pro	Thr	Thr	Gln	Gln	Pro	Arg	Pro	Ser	Gly		
610					615					620					625		
ccg	ggc	ccc	gct	gga	cgt	ccc	aaa	cca	cag	ctg	gcc	cag	aaa	ccc	agc	2218	
Pro	Gly	Pro	Ala	Gly	Arg	Pro	Lys	Pro	Gln	Leu	Ala	Gln	Lys	Pro	Ser		

626	631	636	641	
cag gac gtg ccg cca	ccc gcc acc gcc gct	gca ggg gga cct ccg cac		2266
Gln Asp Val Pro Pro	Pro Ala Thr Ala Ala	Ala Gly Gly Pro Pro His		
642	647	652	657	
ccc cag ctc aac aaa	tcc cag tot ctg acc	aat gcc ttc aac ctt cca		2314
Pro Gln Leu Asn Lys	Ser Gln Ser Leu Thr	Asn Ala Phe Asn Leu Pro		
658	663	668	673	
gag cca gcc ccg ccc	agg ccc agc ctt agc	cag gac gag gtg aaa gct		2362
Glu Pro Ala Pro Pro	Arg Pro Ser Leu Ser	Gln Asp Glu Val Lys Ala		
674	679	684	689	
gag acc atc cgc agc	ctg agg aag tct ttc	gcc agc ctc ttc tcc gac		2410
Glu Thr Ile Arg Ser	Leu Arg Lys Ser Phe	Ala Ser Leu Phe Ser Asp		
690	695	700	705	
tga tacc ccactctgag	aacccccaaaa	tccttgggca acccttctct	gggccctgaa	2467
*				
706				
tccattttctc acttttggag	tctccaaatc ccttgagaac	ccatctcccg gttctccaag		2527
attccacctc tcattcctca	agatccccga gtaccttgag	aaacctgact cctcctggcc		2587
ctaaatccgg ttctcacatg	tggaatcccc aagtcctttt	agaacccac tegtggtcac		2647
ttcaggatct acttctgttt	tagaacctcc acattcctga	agacctccgc ccttggtttc		2707
cccagagggc gttttccttc	ctggaagtgc ccaaatacca	ggcaacccat tgcagaatcc		2767
cttctctggag ccttgaagtt	cctggaaaac cctatttttg	gtcccaaate tctccagcac		2827
acctattttcc catcataatt	ttccaaatcc tcaagaaacc	cctactgttg agccccttcc		2887
catggatctt ccatccctct	gaagatccac atcttcaa	at gccacccaac acctagcccc		2947
acaaggattt cctttcacca	gctcccctca acctcattca	ataccttggg agcccctccc		3007
acttccagga cccctcggtt	ccccagggc cccctcccc	agtttctctgc ctctgacagc		3067
tgtctttaaa tatgaaaact	ccacccatct tcccagaatc	ctttgcacac ggaaggccag		3127
tggtctccgc ttccccacct	ttgctgtggt gtctgtgtct	gtgactgacg tggcctcctt		3187
ttgtgccgtg cttggcatat	gtggctctcg ttcacgtg	gc cctgtggt gatgcgtgca		3247
gtgacgtgt ttatgtggtc	cgcacctccc cctgaccttc	actccttgcc tggactcacc		3307
ccaccttca gcggtctga	acccaagag aagagtcggg	aaacaaaata aacaagcaaa		3367
ggcccagcaa aaaaaaaaaa	a			3388

<210> 370
 <211> 1136
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (353)..(727)

<400> 370
 ggaattcaat gctgcacaag ctctgagccc tcctggggct ggaagttcc tctgatggga 60
 ggtgtgtggt ggccatccca tcctgtgta agacctgggg aaaccactct tcaaggttca 120
 ggaggaggga gggcgggccc cgacccttaa ccagagcgag gttgttgctt tgtgtccaca 180
 gggaccagga gcgaaccatg atgccaggta ggaggggctg actggggcct gcgagcgct 240
 gcctttcctg ctgggcagag gccctccaca tggggccaag cgggcccggg acaggagggc 300
 agtcagatgg gcagggcctg agagcctccc tcctctcct aggtccctaa tc atg 355
 Met
 1
 gac tcc cca aga gct ggc acc cac cag ggc ccc ctc gat gca gag aca 403
 Asp Ser Pro Arg Ala Gly Thr His Gln Gly Pro Leu Asp Ala Glu Thr
 2 7 12 17
 gag gtc ggt gct gac cgc tgc acg tcg act gcc tac cag gag cag agg 451
 Glu Val Gly Ala Asp Arg Cys Thr Ser Thr Ala Tyr Gln Glu Gln Arg
 18 23 28 33
 ccc cag gtg gag caa gtt ggc aaa cag gct cct ctc tcc cca ggg ctg 499
 Pro Gln Val Glu Gln Val Gly Lys Gln Ala Pro Leu Ser Pro Gly Leu
 34 39 44 49
 ccg gca atg ggg ggg cct ggc ccc ggc ccc tgt gag gac ccc gcg ggt 547
 Pro Ala Met Gly Gly Pro Gly Pro Gly Pro Cys Glu Asp Pro Ala Gly
 50 55 60 65
 gct ggg gga gca ggt gca ggg ggc tcc gag ccc ctg gtg act gtc acc 595
 Ala Gly Gly Ala Gly Ala Gly Gly Ser Glu Pro Leu Val Thr Val Thr
 66 71 76 81
 gtg cag tgc gcc ttc aca gtg gcc ctg agg gca cga aga gga gcc gac 643
 Val Gln Cys Ala Phe Thr Val Ala Leu Arg Ala Arg Arg Gly Ala Asp
 82 87 92 97
 ctg tcc agc ctg cgg gca ctg ctg ggc caa gcc cct ccc tca cca ggc 691
 Leu Ser Ser Leu Arg Ala Leu Leu Gly Gln Ala Pro Pro Ser Pro Gly
 98 103 108 113
 cca gct tgg gca act cag tta cct agc ccc agg tga ggac gggcactggg 741
 Pro Ala Trp Ala Thr Gln Leu Pro Ser Pro Arg *
 114 119 124
 tccccatccc cgaggaggag tcgctgcaga gggcctggca ggacgcagct gcctgcccc 801

```

gggggctgca gctgcagtgc aggggagccg ggggtcggcc ggtcctctac caggtggtgg      861
cccagcacag ctactccgcc caggggccag aggacctggg cttccgacag ggggacacgg      921
tggacgtcct gtgtgaagtg gaccaggcat ggctggaggg ccactgtgac ggccgcatcg      981
gcatcttccc caagtgttc gtggtccccg ccggccctcg gatgtcagga gccccggcc      1041
gcctgccccg atcccagcag ggagatcagc cctaattgatg ctgtgtccat gatgctttta      1101
ataaaaacaa cccccactgc aaaaaaaaaa aaaaaa                                1136

```

```

<210> 371
<211> 2575
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (225)..(1568)

<220>
<221> misc_feature
<222> (1)...(2575)
<223> n = a,t,c or g

```

```

<400> 371
taagcttgcg gccgccgccc gccaccgcg cgctcgcttg accgcggcgc ccgcccccg      60
ccgccccgcg ccgtccccct gccgcgatgc cctcccttcg gggccccggc ggccccgcgc      120
cctgctaggc tgcggcggca tggccccgcg gcccggcgcg acctctgcgg attgcatcg      180
tgtgtggcgg cggggcatgc ccagagcacc gggcacggcc ttca atg ggc gag gac      236
                               Met Gly Glu Asp
                               1

```

```

acg gac acg cgg aaa att aac cac agc ttc ctg ogg gac cac agc tat      284
Thr Asp Thr Arg Lys Ile Asn His Ser Phe Leu Arg Asp His Ser Tyr
  5                      10                      15                      20

gtg act gaa gct gac atc atc tct acc gtt gag ttc aac cac acg gga      332
Val Thr Glu Ala Asp Ile Ile Ser Thr Val Glu Phe Asn His Thr Gly
  21                      26                      31                      36

gag ctg ctg gcc aca ggt gac aag ggc ggc cgg gtc gtc atc ttc cag      380
Glu Leu Leu Ala Thr Gly Asp Lys Gly Gly Arg Val Val Ile Phe Gln
  37                      42                      47                      52

cgg gaa cca gag agt aaa aat gcg ccc cac agc cag ggc gaa tac gac      428
Arg Glu Pro Glu Ser Lys Asn Ala Pro His Ser Gln Gly Glu Tyr Asp
  53                      58                      63                      68

```


gtg tac agc act ttc cag agc cac gag ccg gag ttt gac tat ctc aag	476
Val Tyr Ser Thr Phe Gln Ser His Glu Pro Glu Phe Asp Tyr Leu Lys	
69 74 79 84	
agc ctg gag ata gag gag aag atc aac aag atc aag tgg ctc cca cag	524
Ser Leu Glu Ile Glu Glu Lys Ile Asn Lys Ile Lys Trp Leu Pro Gln	
85 90 95 100	
cag aac gcc gcc cac tca ctc ctg tcc acc aac gat aaa act atc aaa	572
Gln Asn Ala Ala His Ser Leu Leu Ser Thr Asn Asp Lys Thr Ile Lys	
101 106 111 116	
tta tgg aag att acc gaa cga gat aaa agg ccc gaa gga tac aac ctg	620
Leu Trp Lys Ile Thr Glu Arg Asp Lys Arg Pro Glu Gly Tyr Asn Leu	
117 122 127 132	
aag gat gaa gag ggg aaa ctt aag gac ctg tcc acg gtg acg tca ctg	668
Lys Asp Glu Glu Gly Lys Leu Lys Asp Leu Ser Thr Val Thr Ser Leu	
133 138 143 148	
cag gtg cca gtg ctg aag ccc atg gat ctg atg gtg gag gtg agc cct	716
Gln Val Pro Val Leu Lys Pro Met Asp Leu Met Val Glu Val Ser Pro	
149 154 159 164	
cgg agg atc ttt gcc aat ggc cac acc tac cac atc aac tcc atc tcc	764
Arg Arg Ile Phe Ala Asn Gly His Thr Tyr His Ile Asn Ser Ile Ser	
165 170 175 180	
gtc aac agt gac tgc gag acc tac atg tgc gcg gat gac ctg cgc atc	812
Val Asn Ser Asp Cys Glu Thr Tyr Met Ser Ala Asp Asp Leu Arg Ile	
181 186 191 196	
aac ctc tgg cac ctg gcc atc acc gac agg agc ttc aac atc gtg gac	860
Asn Leu Trp His Leu Ala Ile Thr Asp Arg Ser Phe Asn Ile Val Asp	
197 202 207 212	
atc aag ccg gcc aac atg gag gac ctt acg gag gtg atc aca gca tct	908
Ile Lys Pro Ala Asn Met Glu Asp Leu Thr Glu Val Ile Thr Ala Ser	
213 218 223 228	
gag ttc cat ccg cac cac tgc aac ctc ttc gtc tac agc agc agc aag	956
Glu Phe His Pro His His Cys Asn Leu Phe Val Tyr Ser Ser Ser Lys	
229 234 239 244	
ggc tcc ctg cgg ctc tgc gac atg cgg gca gct gcc ctg tgt gac aag	1004
Gly Ser Leu Arg Leu Cys Asp Met Arg Ala Ala Ala Leu Cys Asp Lys	
245 250 255 260	
cat tcc aag ctc ttt gaa gag cct gag gac ccc agt aac cgc tca ttc	1052
His Ser Lys Leu Phe Glu Glu Pro Glu Asp Pro Ser Asn Arg Ser Phe	
261 266 271 276	
ttc tgc gaa atc atc tcc tcc gtg tcc gac gtg aag ttc agc cac agc	1100
Phe Ser Glu Ile Ile Ser Ser Val Ser Asp Val Lys Phe Ser His Ser	
277 282 287 292	
ggc cgc tac atg ctc acc cgg gac tac ctt aca gtc aag gtc tgg gac	1148

Gly	Arg	Tyr	Met	Leu	Thr	Arg	Asp	Tyr	Leu	Thr	Val	Lys	Val	Trp	Asp	
293					298					303					308	
ctg	aac	atg	gag	gca	aga	ccc	ata	gag	acc	tac	cag	gtc	cat	gac	tac	1196
Leu	Asn	Met	Glu	Ala	Arg	Pro	Ile	Glu	Thr	Tyr	Gln	Val	His	Asp	Tyr	
309					314					319					324	
ctt	cgg	agc	aag	ctc	tgt	tcc	ctg	tac	gag	aac	gac	tgc	att	ttc	gac	1244
Leu	Arg	Ser	Lys	Leu	Cys	Ser	Leu	Tyr	Glu	Asn	Asp	Cys	Ile	Phe	Asp	
325					330					335					340	
aag	ttt	gaa	tgt	gcc	tgg	aac	ggg	agc	gac	agc	gtc	atc	atg	acc	ggg	1292
Lys	Phe	Glu	Cys	Ala	Trp	Asn	Gly	Ser	Asp	Ser	Val	Ile	Met	Thr	Gly	
341					346					351					356	
gcc	tac	aac	aac	ttc	ttc	cgc	atg	ttc	gat	cgg	aac	acc	aag	cgg	gac	1340
Ala	Tyr	Asn	Asn	Phe	Phe	Arg	Met	Phe	Asp	Arg	Asn	Thr	Lys	Arg	Asp	
357					362					367					372	
gtg	acc	ctg	gag	gcc	tcg	agg	gaa	agc	agc	aag	ccc	cgg	gct	gtg	ctc	1388
Val	Thr	Leu	Glu	Ala	Ser	Arg	Glu	Ser	Ser	Lys	Pro	Arg	Ala	Val	Leu	
373					378					383					388	
aag	cca	cgg	cgc	gtg	tgc	gtg	ggg	ggc	aag	cgc	cgg	cgt	gat	gac	atc	1436
Lys	Pro	Arg	Arg	Val	Cys	Val	Gly	Gly	Lys	Arg	Arg	Arg	Asp	Asp	Ile	
389					394					399					404	
agt	gtg	gac	agc	ttg	gac	ttc	acc	aag	aag	atc	ctg	cac	acg	gcc	tgg	1484
Ser	Val	Asp	Ser	Leu	Asp	Phe	Thr	Lys	Lys	Ile	Leu	His	Thr	Ala	Trp	
405					410					415					420	
cac	ccg	gct	gag	aac	atc	att	gcc	atc	gcc	gcc	acc	aac	aac	ctg	tac	1532
His	Pro	Ala	Glu	Asn	Ile	Ile	Ala	Ile	Ala	Ala	Thr	Asn	Asn	Leu	Tyr	
421					426					431					436	
atc	ttc	cag	gac	aag	gta	aac	tct	gac	atg	cac	tag	gtat	gtgcagttcc			1582
Ile	Phe	Gln	Asp	Lys	Val	Asn	Ser	Asp	Met	His	*					
437					442					447						
cgccccctgc	cacccagcct	catgcaagtc	atccccgaca	tgaccttcac	gaccgcaatg											1642
caaggagggg	aagaaagtca	cagcactgat	gaggacagct	gcagaggtgg	cagtgtgtgg											1702
acacaggaag	tttgggcccc	ctccctgccc	cagctttcct	aggccagaat	tgtgtttggc											1762
agtaattgtc	tgtttaaaaa	aataaaaagg	aaaggaagcg	ttcaccgcca	caaatacataa											1822
aatggacatg	actgtggagt	cttacagttc	agggttcttt	cattcacgtc	ccttcctgtc											1882
tcggtctgcg	gtctttacca	catcaatagg	actttttatg	cgcccggtt	aatttttcac											1942
tccagtgcgt	cctgtttgcag	ggaccggagc	tgatgggagc	tgcttctccc	ccatgcctca											2002
ctgggtcccag	atcagggctc	cagggacaga	tgatgagtct	caaacgagcc	agccaggggt											2062
tcttttggtt	ataaatgggg	caattcgccc	tgtctcagag	ctgatgacct	caccgttggt											2122

```

ttttggatgg tgaattcatg ctgagaatgt gcagatgcaa gctcctctcc taggtcttct 2182
gaatgtcttg aaacatccca ggtcccaggt ctggtgcggt ttcccagag gagcggagtg 2242
gggtttgtct tctgtgtgcc tgtgtctca tctgattcac ctgccatttg ctgagcctct 2302
gctgtgtacc aggctgggtg ctcagcccta gaggcagttg acttaccctc tgcagccctc 2362
cctgccgcct cacccttcag cattcactgg gcaccttccc ggagcggaca ctgactccca 2422
tgcacgattt tttggaatct tcctcctgac tgtgaggtgg gtgttcattc atttctcca 2482
taaacaccaa cttctcgaag cgtgcctcgt gccaaagctgg cgtaatgtgg ttacgatgtc 2542
ttcattnttc aggcnnccggg ccgcttacat cct 2575

```

```

<210> 372
<211> 7393
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (118)..(3012)

```

```

<400> 372
taagcttgct tgttcttttg gccgaagcgg cctacggctg cgagaagacg acagaagggg 60

gacgtcaagg ccagcccttc ctcagctaata aagcggaaaa acaaaccctt ttcagac 117
atg gag ctg aat tct agc tca gag gac tcc aaa ggg agc aag cgt gtc 165
Met Glu Leu Asn Ser Ser Ser Glu Asp Ser Lys Gly Ser Lys Arg Val
1 5 10 15

cgt act aat tcc atg ggc tca gcc act ggc ccc ctt cct ggg aca aag 213
Arg Thr Asn Ser Met Gly Ser Ala Thr Gly Pro Leu Pro Gly Thr Lys
17 22 27 32

gta gaa ccc act gtt ctg gac aga aac tgc ccc tcc ccc gtc cta att 261
Val Glu Pro Thr Val Leu Asp Arg Asn Cys Pro Ser Pro Val Leu Ile
33 38 43 48

gac tgt ccc cac cca aac tgc aac aag aag tac aag cac atc aat gga 309
Asp Cys Pro His Pro Asn Cys Asn Lys Lys Tyr Lys His Ile Asn Gly
49 54 59 64

ctt aag tac cac caa gct cat gcc cat aca gat gat gac agc aag ccg 357
Leu Lys Tyr His Gln Ala His Ala His Thr Asp Asp Asp Ser Lys Pro
65 70 75 80

gaa gcg gat ggg gac agt gag tac gga gag gaa cct att ctc cat gca 405
Glu Ala Asp Gly Asp Ser Glu Tyr Gly Glu Glu Pro Ile Leu His Ala
81 86 91 96

gat ctt ggg agc tgc aac ggt gca tct gtc tca caa aaa ggt tcc ttg 453

```

Asp	Leu	Gly	Ser	Cys	Asn	Gly	Ala	Ser	Val	Ser	Gln	Lys	Gly	Ser	Leu	
97					102					107					112	
tcc	cct	gcc	cgc	tca	gct	acc	ccc	aaa	gtt	cga	ctt	gta	gag	ccc	cat	501
Ser	Pro	Ala	Arg	Ser	Ala	Thr	Pro	Lys	Val	Arg	Leu	Val	Glu	Pro	His	
113					118					123					128	
agc	cct	tct	cct	tca	agc	aaa	ttc	agc	aca	aaa	ggc	ctc	tgt	aag	aaa	549
Ser	Pro	Ser	Pro	Ser	Ser	Lys	Phe	Ser	Thr	Lys	Gly	Leu	Cys	Lys	Lys	
129					134					139					144	
aag	ttg	agt	ggg	gaa	ggg	gac	aca	gac	ctt	ggg	gcc	tta	tcc	aat	gat	597
Lys	Leu	Ser	Gly	Glu	Gly	Asp	Thr	Asp	Leu	Gly	Ala	Leu	Ser	Asn	Asp	
145					150					155					160	
ggc	tct	gat	gat	gga	ccc	tca	gtg	atg	gat	gaa	aca	agc	aat	gat	gcc	645
Gly	Ser	Asp	Asp	Gly	Pro	Ser	Val	Met	Asp	Glu	Thr	Ser	Asn	Asp	Ala	
161					166					171					176	
ttt	gat	tct	tta	gaa	agg	aag	tgt	atg	gaa	aaa	gaa	aaa	tgt	aaa	aaa	693
Phe	Asp	Ser	Leu	Glu	Arg	Lys	Cys	Met	Glu	Lys	Glu	Lys	Cys	Lys	Lys	
177					182					187					192	
ccc	tct	agt	tta	aaa	cct	gaa	aag	att	cct	tcc	aag	agc	cta	aag	tca	741
Pro	Ser	Ser	Leu	Lys	Pro	Glu	Lys	Ile	Pro	Ser	Lys	Ser	Leu	Lys	Ser	
193					198					203					208	
gcc	cgt	ccc	att	gcc	cct	gcc	atc	ccc	cca	cag	caa	atc	tac	acc	ttc	789
Ala	Arg	Pro	Ile	Ala	Pro	Ala	Ile	Pro	Pro	Gln	Gln	Ile	Tyr	Thr	Phe	
209					214					219					224	
cag	aca	gcc	acc	ttc	aca	gca	gcg	agc	cca	ggc	tct	tcc	tca	ggc	ttg	837
Gln	Thr	Ala	Thr	Phe	Thr	Ala	Ala	Ser	Pro	Gly	Ser	Ser	Ser	Gly	Leu	
225					230					235					240	
acc	gcc	aca	gtg	gca	caa	gcc	atg	ccc	aac	agt	ccc	caa	ctc	aag	ccc	885
Thr	Ala	Thr	Val	Ala	Gln	Ala	Met	Pro	Asn	Ser	Pro	Gln	Leu	Lys	Pro	
241					246					251					256	
att	cag	ccc	aag	ccc	act	gtt	atg	gga	gaa	cct	ttc	aca	gtc	aac	cct	933
Ile	Gln	Pro	Lys	Pro	Thr	Val	Met	Gly	Glu	Pro	Phe	Thr	Val	Asn	Pro	
257					262					267					272	
gcc	ttg	act	cca	gcc	aag	gac	aag	aaa	aag	aaa	gac	aaa	aaa	aag	aag	981
Ala	Leu	Thr	Pro	Ala	Lys	Asp	Lys	Lys	Lys	Lys	Asp	Lys	Lys	Lys	Lys	
273					278					283					288	
gaa	tct	tca	aag	gaa	ctt	gaa	agt	cct	ctg	acc	cct	ggg	aag	gtg	tgt	1029
Glu	Ser	Ser	Lys	Glu	Leu	Glu	Ser	Pro	Leu	Thr	Pro	Gly	Lys	Val	Cys	
289					294					299					304	
cga	gca	gag	gaa	ggc	aaa	agc	cca	ttc	agg	gaa	tct	tca	gga	aat	ggg	1077
Arg	Ala	Glu	Glu	Gly	Lys	Ser	Pro	Phe	Arg	Glu	Ser	Ser	Gly	Asn	Gly	
305					310					315					320	
atg	aaa	atg	gag	ggg	ctc	cta	aat	ggc	tca	tca	gac	ccc	cac	caa	agc	1125
Met	Lys	Met	Glu	Gly	Leu	Leu	Asn	Gly	Ser	Ser	Asp	Pro	His	Gln	Ser	

321	326	331	336	
cga ctg gct agc atc aag gct gaa gcc gac aag atc tac agt ttc acg				1173
Arg Leu Ala Ser Ile Lys Ala Glu Ala Asp Lys Ile Tyr Ser Phe Thr				
337	342	347	352	
gac aat gcc ccc agc cct tcc att gga ggc agt agc cgc ctt gaa aac				1221
Asp Asn Ala Pro Ser Pro Ser Ile Gly Gly Ser Ser Arg Leu Glu Asn				
353	358	363	368	
act acc cct act cag ccc ctg act ccc tta cat gtg gtg acc cag aat				1269
Thr Thr Pro Thr Gln Pro Leu Thr Pro Leu His Val Val Thr Gln Asn				
369	374	379	384	
gga gct gaa gcc agc tca gtc aaa acc aac agc cct gca tac tct gac				1317
Gly Ala Glu Ala Ser Ser Val Lys Thr Asn Ser Pro Ala Tyr Ser Asp				
385	390	395	400	
atc tct gat gct ggg gag gat ggg gag ggc aag gta gac agt gtc aaa				1365
Ile Ser Asp Ala Gly Glu Asp Gly Glu Gly Lys Val Asp Ser Val Lys				
401	406	411	416	
tca aag gac gcc gaa cag ttg gtt aaa gaa ggg gct aag aaa act ctt				1413
Ser Lys Asp Ala Glu Gln Leu Val Lys Glu Gly Ala Lys Lys Thr Leu				
417	422	427	432	
ttt ccc cct cag cct cag agc aaa gac tca cca tat tac caa ggc ttt				1461
Phe Pro Pro Gln Pro Gln Ser Lys Asp Ser Pro Tyr Tyr Gln Gly Phe				
433	438	443	448	
gag agt tac tat tct cca agt tat gca cag tcc agc cct ggg gct ctg				1509
Glu Ser Tyr Tyr Ser Pro Ser Tyr Ala Gln Ser Ser Pro Gly Ala Leu				
449	454	459	464	
aac ccc agc agc cag gca gga gtg gag agc cag gcc ctg aag aca aaa				1557
Asn Pro Ser Ser Gln Ala Gly Val Glu Ser Gln Ala Leu Lys Thr Lys				
465	470	475	480	
agg gat gag gaa cct gag agc ata gaa ggg aaa gtg aag aac gat atc				1605
Arg Asp Glu Glu Pro Glu Ser Ile Glu Gly Lys Val Lys Asn Asp Ile				
481	486	491	496	
tgt gaa gaa aag aag ccc gag ctg agc agt tcc agt cag cag ccc tcg				1653
Cys Glu Glu Lys Lys Pro Glu Leu Ser Ser Ser Ser Gln Gln Pro Ser				
497	502	507	512	
gtc atc cag cag cgt ccc aat atg tac atg cag tcc ctg tac tac aac				1701
Val Ile Gln Gln Arg Pro Asn Met Tyr Met Gln Ser Leu Tyr Tyr Asn				
513	518	523	528	
cag tat gcc tat gta ccc ccc tat ggc tac agc gac cag agt tac cac				1749
Gln Tyr Ala Tyr Val Pro Pro Tyr Gly Tyr Ser Asp Gln Ser Tyr His				
529	534	539	544	
acc cac ctt ctg agc act aac acg gct tac cgg cag cag tac gaa gaa				1797
Thr His Leu Leu Ser Thr Asn Thr Ala Tyr Arg Gln Gln Tyr Glu Glu				
545	550	555	560	

cag cag aaa cgc cag agc tta gag cag cag cag cgg gga gtg gac aag	1845
Gln Gln Lys Arg Gln Ser Leu Glu Gln Gln Gln Arg Gly Val Asp Lys	
561 566 571 576	
aag gca gag atg ggc ctg aag gag cgg gag gca gca ctc aag gaa gag	1893
Lys Ala Glu Met Gly Leu Lys Glu Arg Glu Ala Ala Leu Lys Glu Glu	
577 582 587 592	
tgg aag caa aag ccg tca att cca cca act ctc acc aag gcc ccc agc	1941
Trp Lys Gln Lys Pro Ser Ile Pro Pro Thr Leu Thr Lys Ala Pro Ser	
593 598 603 608	
ctg aca gac ctg gtg aaa tca gga cct ggc aag gcc aag gag cca ggg	1989
Leu Thr Asp Leu Val Lys Ser Gly Pro Gly Lys Ala Lys Glu Pro Gly	
609 614 619 624	
gct gac cca gcc aaa tca gtc atc att ccc aag tta gat gac tct tca	2037
Ala Asp Pro Ala Lys Ser Val Ile Ile Pro Lys Leu Asp Asp Ser Ser	
625 630 635 640	
aaa ctc ccg ggc cag gcc cct gaa ggc ctt aaa gtg aag ctg agt gat	2085
Lys Leu Pro Gly Gln Ala Pro Glu Gly Leu Lys Val Lys Leu Ser Asp	
641 646 651 656	
gcc agc cac cta agc aag gag gcc tct gag gcc aag aca ggt gct gag	2133
Ala Ser His Leu Ser Lys Glu Ala Ser Glu Ala Lys Thr Gly Ala Glu	
657 662 667 672	
tgt ggt cga cag gca gag atg gat cca ata ctc tgg tac cga cag gag	2181
Cys Gly Arg Gln Ala Glu Met Asp Pro Ile Leu Trp Tyr Arg Gln Glu	
673 678 683 688	
gca gag ccc ccg atg tgg aca tat gtt tat cct gcc aag tac tca gac	2229
Ala Glu Pro Arg Met Trp Thr Tyr Val Tyr Pro Ala Lys Tyr Ser Asp	
689 694 699 704	
atc aag tca gag gat gag ccg tgg aag gag gag ccg gac cgc aaa ttg	2277
Ile Lys Ser Glu Asp Glu Arg Trp Lys Glu Glu Arg Asp Arg Lys Leu	
705 710 715 720	
aag gag gaa agg agt ccg agt aag gac tct gtc ccc aag gaa gat ggg	2325
Lys Glu Glu Arg Ser Arg Ser Lys Asp Ser Val Pro Lys Glu Asp Gly	
721 726 731 736	
aag gaa agc aca agt agt gac tgc aag ctg ccc acg tca gag gag tct	2373
Lys Glu Ser Thr Ser Ser Asp Cys Lys Leu Pro Thr Ser Glu Glu Ser	
737 742 747 752	
cgc ctt ggg agc aag gag ccc ccg cca agt gtc cat gtg cct gtg tcc	2421
Arg Leu Gly Ser Lys Glu Pro Arg Pro Ser Val His Val Pro Val Ser	
753 758 763 768	
tcc cca ctt acc cag cac cag tcc tac atc ccc tac atg cac ggc tat	2469
Ser Pro Leu Thr Gln His Gln Ser Tyr Ile Pro Tyr Met His Gly Tyr	
769 774 779 784	

tcc tac agt cag tcc tac gac ccc aac cac ccc agc tac cgg agc atg 2517
 Ser Tyr Ser Gln Ser Tyr Asp Pro Asn His Pro Ser Tyr Arg Ser Met
 785 790 795 800

cct gct gtg atg atg cag aac tac cca ggt tcc tac ctg cct tcc agc 2565
 Pro Ala Val Met Met Gln Asn Tyr Pro Gly Ser Tyr Leu Pro Ser Ser
 801 806 811 816

tac tct ttt tcc cca tat ggc agc aag gtc tca ggt ggt gaa gat gct 2613
 Tyr Ser Phe Ser Pro Tyr Gly Ser Lys Val Ser Gly Gly Glu Asp Ala
 817 822 827 832

gac aag gca cga gcc agc ccc agt gtg act tgt aaa tcc agc tca gag 2661
 Asp Lys Ala Arg Ala Ser Pro Ser Val Thr Cys Lys Ser Ser Ser Glu
 833 838 843 848

tcc aaa gcc ctg gac atc ttg cag cag cat gcc agt cac tac aag agc 2709
 Ser Lys Ala Leu Asp Ile Leu Gln Gln His Ala Ser His Tyr Lys Ser
 849 854 859 864

aag tct ccc acg ata agt gat aaa act tct cag gag aga gat cga gga 2757
 Lys Ser Pro Thr Ile Ser Asp Lys Thr Ser Gln Glu Arg Asp Arg Gly
 865 870 875 880

ggc tgt ggg gtg gtt ggg ggt ggt ggc agc tgt agc agc gtc ggg gga 2805
 Gly Cys Gly Val Val Gly Gly Gly Gly Ser Cys Ser Ser Val Gly Gly
 881 886 891 896

gca agt ggg ggt gaa cgg agt gtt gac cgg ccc cgc acc tct cct tcc 2853
 Ala Ser Gly Gly Glu Arg Ser Val Asp Arg Pro Arg Thr Ser Pro Ser
 897 902 907 912

cag cgc ctg atg tcc aca cac cac cac cac cac cac ttg ggg tac tca 2901
 Gln Arg Leu Met Ser Thr His His His His His His Leu Gly Tyr Ser
 913 918 923 928

ttg ctc cca gca cag tac aac tta ccc tat gca gca ggg ctt tct tct 2949
 Leu Leu Pro Ala Gln Tyr Asn Leu Pro Tyr Ala Ala Gly Leu Ser Ser
 929 934 939 944

aca gcc att gtt gcc agc caa caa ggc tca act ccc tca ctc tac cca 2997
 Thr Ala Ile Val Ala Ser Gln Gln Gly Ser Thr Pro Ser Leu Tyr Pro
 945 950 955 960

ccc ccc agg agg tga gaatgacacc aagtgcccg ataaagtcag cttcacgggc 3052
 Pro Pro Arg Arg *
 961

ccggactggc ttacccaagg aggtgctgaa ggtgccgttt agacatcagt taaatgggtgt 3112

tgatcatcct gtttgccgtt tccaccatga ctgaaggcag acccttgggt atctcacctc 3172

caccaagacc tccgggacta cctgacccta cctcttcctc aggagctgga gagctgggtac 3232

ttagcaaaaa tattttattct ctcagccaca gttatgacta ttgtggcctc tgtggagatg 3292

aaggcacggg aagcaaccag gggaacatgg cctcagccca gagaagccac tgctctgttc 3352

cccaagccct	tggctctgctg	ctggagcagt	accagcccc	ccgcccacca	gggagggacc	3412
cccaccccc	agcactgggt	aaggtctgaa	gacagcacag	cagccatacc	cctcaccatc	3472
attaccacca	tcaccagatt	ctgcatctcc	ctagtgcctt	gcaccctggg	aattggcagc	3532
atgtggagga	actagaatct	caggaaagaa	attggggggt	gttttctaca	taattgtgaa	3592
aacaaggtct	tcaaagtgtg	agactttctc	ccattttacat	gagcacatat	aaacgctcac	3652
aacctagcct	ggaaaggaag	accaaggcat	ctgccccaac	atggccttga	gctgcctgtg	3712
aggcaggggg	caggggttcc	aacaccagca	cagggctccc	cagggacact	gggagtaagc	3772
tggtgctgga	gcatgaatga	cgtctgtgaa	gtagaacctg	cgtccccact	aagtcctgct	3832
gcttcttatt	ccccaaactc	ttgccctttt	cccttccttc	ctaaccctt	ggtgcctttc	3892
ccagggggat	ccccacactg	gtcttgcttc	ttcttttcca	ctgcttggct	cttaagcctc	3952
aggcagataa	actagtattc	ccccagctt	ggggaacctt	ggagtctgcc	aggtcacctt	4012
agggcaaggc	ccagaaggca	gcccctggga	gcaccagca	gttcttggag	atgtcctgtc	4072
atctagccat	ctgatattct	cctcatttga	ggccacagat	atatacagcc	caattcctct	4132
gtctacaagt	acatgatttt	atatagctca	gtctataacc	tccatgtggg	ccaatataag	4192
ctgtgtttct	tggtaacaca	tattttgttt	gagggggcac	tggccatggg	aggttatttg	4252
ttccttagac	cctggaataa	cacatccaag	ccattactta	ttagagtctc	agaatgtact	4312
cagtggagct	gtgctttgag	gcagccaaca	tttctctgct	ctccttagaa	atgcagtctc	4372
ccaatggaag	ctttatactc	tttgtactgg	gaaagtgagg	atgatttggg	agctttattg	4432
gggtcatgtc	ttccccaagg	tgtggggagc	ttagcttact	tggcttttga	ggtatcatcc	4492
ctctgttctc	ccctcctatc	tttccatgac	cctctggatt	gagagagaga	gataaagact	4552
gacagacacc	agtgtaggct	ggaaaaggga	gtgtgtgacc	agagtgccaa	aagtgactag	4612
gagcaggaac	ttggctccga	ctcagtttgg	aaaatgggaa	ataggggaca	gtaagcacia	4672
tgcccagtag	tagttgattt	ccaaggaccc	tggaaacctc	cacttgagag	gcttagggtc	4732
accatctgct	caagaggatc	ccctctgac	tacaggcctt	ttccctaggt	ttctgcctcc	4792
togtttttgt	tcaagttggg	ttctgagtcc	tccccaaaa	ccattgtttt	agacctcttg	4852
gcagggcccc	aaaacagcct	ccctcatacc	catcattccg	tctgccttct	gctgccttca	4912
tgggcagtgc	tctgagcagt	gacctccctt	tcctccgtgg	aagtagctag	tgcagacacc	4972
gtcatccac	cccacctgag	tcaccccaac	caagagggtg	actgaatttc	agcctgatta	5032

tgccctcctg gggctcctgt gaggtggagc caaggttccc tctctgttcc tgtttgtctt	5092
taaatattgt tgtgtgtttt gtatctgtgg cactggcctg cagcatactc tgtatatatt	5152
gtaaagaaac cgtaggaggt aattttcttt tgcattgggc aggcattggc ctgcattcct	5212
gccctttcca ctcatctgt aacacagagg acgaacttct gtattagctg ggcagccttg	5272
ggttctccag aagagaacag gttttctttt tcttttttaa tttttcttct taaacatttg	5332
gctctttgat cctcatatcc aagtctcccc tgaagagtag gagctgctca gaagagcagg	5392
tgaaagccac catggcagat cctgatgcct gccgggccta gtcttccctc tgaaataaca	5452
tgaagcagca gctgtggaga ttcttgacaa gtgctgagtg aaagatttgc tgcccaacct	5512
tacatgggga ggagaaacac aggtgggagc tacctgtggc atccatgacc tagtcagagg	5572
gatgagatgc tcagcagggg tccccatcct atcccacccc acaaacaag gctggaaaaa	5632
tttgctacca agggccaaga ccaccagacc aagcctgttt atgagccacc cctgccagg	5692
ccctcacaga cattgctcac ggggcttccc atagaggaga agctaaagag ggagggggcc	5752
tcatccccag atagatcagg caaggcttgg agagctgctc tttaggatcc acatcaacta	5812
cttctcatt ttaaggtatg gcagttccct tcatccccct ttcctgcctt gtacatgtac	5872
atgtatgaaa tttccttctc ttaccgaact ctctccacac atcacaaggt caaagaacca	5932
cacgcttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct tgagtctctt	5992
ttttccacgt ttaaggggcc atggcaggac ttagagttgc gagttaagac tgcagagggc	6052
tagagaatta tttcatcacg gctttgaggc caccatgtc acttatcccg tataccctct	6112
caccatcccc ttgtctactc tgatgcccc aagatgcaac tgggcagcta gttggcccca	6172
taattctggg cctttgttgt ttgttttaac tacttgggca tcccaggaag ctttccagt	6232
atctcctacc atgggcccc ctctgggat caagcccctc ccaggccctg tcccagccc	6292
ctctgcccc agcccacccg cttgccttgg tgctcagccc tccattggg agcaggttgg	6352
ggcgagctgg aggcccgggc tggaggggca gtgttgctgt tcatagattt tgttccattg	6412
gcgttgctct gttgaattta atttcagtct tctgattct tcccttctgt aaagtgtaca	6472
ttaccaagtt ccttgttttt ttatatatat atataaatat atatatatat aaactgtact	6532
ctttttgcct ttgtacattc aggcaagaag agaaaataaa tctttttaag agacaatcac	6592
aaatctgtga gggctgctgg ttatttctcc tggagtttgc tgetgagctg cctcttctt	6652
cctccaatt ttctgttct cctcagctc tctgatctt cctggccctg ctccatagc	6712
atcctcagct tcactttccc tggctgatgg caagctgttg aatccagtgt ccagactacc	6772

tgcccttgtaa cccttttctg ccagcattg tttctggct tggccactgg cttagcccag	6832
gagctttact ctgtgccctg gcctcccctc tcttcaacct tagatttcca ttcaccgaag	6892
tggcttttga cccctgggta ctctgggacc tgtttcctgg aggccttggc ttgggacact	6952
cacctgtgaa actatgcagc tgggagctct ctgcctaaga gtttgcacta tttaaacctg	7012
cctgggagtt aggacgatg gttttaggaa tgaccggaaa actacccta aaactcccc	7072
gacattccag cctctagaat gctctgatcc agagctcagt ggatgattcc cagctggtgg	7132
actcctgtgg ctaccccatc agaacaaggg ctaagggttt atgggtcaag agtatttgat	7192
cagaatttta aagggtggta tactctgaaa cacagcccaa ccaaaccatt gtttggccgc	7252
tttctctttt cctctacctt cctcatcccc acttttttcc ctttctctct acttctctt	7312
cttaattggc tttggaattg aaatatattt ttaaattatt tgttgtattt attgaataaa	7372
gtttttaatg tccctgttct t	7393

<210> 373
 <211> 1435
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (215)..(1084)

<400> 373	
ccacttttgta caagaaagct gggtagcgt aagcttgggc ccctcgaggg atactctaga	60
gcggcgcgcg cctcctcctt ctctcctct cctcttctc ctctcctc gctcccacag	120
ccatgtctgc ttagaccaga gcagccccc agccaactag ggcagctgcc gccgccacaa	180
cagcaaggac agccgctgcc gccgcccgtg agcg	232
atg aca gga gtg ttt gac	
Met Thr Gly Val Phe Asp	
1	
aga agg gtc ccc agc atc cga tcc ggc gac ttc caa gct ccg ttc cag	280
Arg Arg Val Pro Ser Ile Arg Ser Gly Asp Phe Gln Ala Pro Phe Gln	
7 12 17 22	
acg tcc gca gct atg cac cat ccg tct cag gaa tcg cca act ttg ccc	328
Thr Ser Ala Ala Met His His Pro Ser Gln Glu Ser Pro Thr Leu Pro	
23 28 33 38	
gag tct tca gct acc gat tct gac tac tac agc cct acg ggg gga gcc	376
Glu Ser Ser Ala Thr Asp Ser Asp Tyr Tyr Ser Pro Thr Gly Gly Ala	
39 44 49 54	

ccg cac ggc tac tgc tct cct acc tcg gct tcc tat ggc aaa gct ctc	424
Pro His Gly Tyr Cys Ser Pro Thr Ser Ala Ser Tyr Gly Lys Ala Leu	
55 60 65 70	
aac ccc tac cag tat cag tat cac ggc gtg aac ggc tcc gcc ggg agc	472
Asn Pro Tyr Gln Tyr Gln Tyr His Gly Val Asn Gly Ser Ala Gly Ser	
71 76 81 86	
tac cca gcc aaa gct tat gcc gac tat agc tac gct agc tcc tac cac	520
Tyr Pro Ala Lys Ala Tyr Ala Asp Tyr Ser Tyr Ala Ser Ser Tyr His	
87 92 97 102	
cag tac ggc ggc gcc tac aac cgc gtc cca agc gcc acc aac cag cca	568
Gln Tyr Gly Gly Ala Tyr Asn Arg Val Pro Ser Ala Thr Asn Gln Pro	
103 108 113 118	
gag aaa gaa gtg acc gag ccc gag gtg aga atg gtg aat ggc aaa cca	616
Glu Lys Glu Val Thr Glu Pro Glu Val Arg Met Val Asn Gly Lys Pro	
119 124 129 134	
aag aaa gtt cgt aaa ccc agg act att tat tcc agc ttt cag ctg gcc	664
Lys Lys Val Arg Lys Pro Arg Thr Ile Tyr Ser Ser Phe Gln Leu Ala	
135 140 145 150	
gca tta cag aga agg ttt cag aag act cag tac ctc gcc ttg ccg gaa	712
Ala Leu Gln Arg Arg Phe Gln Lys Thr Gln Tyr Leu Ala Leu Pro Glu	
151 156 161 166	
cgc gcc gag ctg gcc gcc tcg ctg gga ttg aca caa aca cag gtg aaa	760
Arg Ala Glu Leu Ala Ala Ser Leu Gly Leu Thr Gln Thr Gln Val Lys	
167 172 177 182	
atc tgg ttt cag aac aaa aga tcc aag atc aag aag atc atg aaa aac	808
Ile Trp Phe Gln Asn Lys Arg Ser Lys Ile Lys Lys Ile Met Lys Asn	
183 188 193 198	
ggg gag atg ccc ccg gag cac agt ccc agc tcc agc gac cca atg gcg	856
Gly Glu Met Pro Pro Glu His Ser Pro Ser Ser Ser Asp Pro Met Ala	
199 204 209 214	
tgt aac tcg ccg cag tct cca gcg gtg tgg gag ccc cag ggc tcg tcc	904
Cys Asn Ser Pro Gln Ser Pro Ala Val Trp Glu Pro Gln Gly Ser Ser	
215 220 225 230	
cgc tcg ctc agc cac cac cct cat gcc cac cct ccg acc tcc aac cag	952
Arg Ser Leu Ser His His Pro His Ala His Pro Pro Thr Ser Asn Gln	
231 236 241 246	
tcc cca gcg tcc agc tac ctg gag aac tct gca tcc tgg tac aca agt	1000
Ser Pro Ala Ser Ser Tyr Leu Glu Asn Ser Ala Ser Trp Tyr Thr Ser	
247 252 257 262	
gca gcc agc tca atc aat tcc cac ctg ccg ccg ccg ggc tcc tta cag	1048
Ala Ala Ser Ser Ile Asn Ser His Leu Pro Pro Pro Gly Ser Leu Gln	
263 268 273 278	

cac ccg ctg gcg ctg gcc tcc ggg aca ctc tat tag atgg gctgctctct 1098
 His Pro Leu Ala Leu Ala Ser Gly Thr Leu Tyr *
 279 284 289
 cttactctct tttttgggac tactgtgttt tgctgttcta gaaaatcata aagaaaggaa 1158
 ttcatatggg gaagttcgga aaactgaaaa agattcatgt gtaaagcttt tttttgcatg 1218
 taagttattg catttcaaaa gacccccccc tttttttaca gaggactttt tttgcgcaac 1278
 tgtggacact ttcaatggtg ccttgaaatc tatgacctca actttttcaa agactttttt 1338
 caatgttatt ttagccatgt aaataagtgt agatagagga attaaactgt atattctgga 1398
 taaataaaat tatttggacc atgaaaaaaaa aaaaaaa 1435

<210> 374
 <211> 2148
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (610)..(1734)

<400> 374
 gtaccgctcc ggaattcccg ggtcgacgat ttctgtccac gtgatcctgg cctgcagttg 60
 ggtggctgcg gtgagatacc tgggttctctg aagggcgggg ggtaggtcg taactactgc 120
 ccccgccggc tgagtctccg agcggccggg ctcggaagcc acgagccagc tgaggcggtc 180
 tccgcttagt gcctacggca tgggtcagct ctttctgcc cctccgcctt cgcggtcctc 240
 acctctttgc ggggtgaagt acctttgggt ttccagacct tgggggcctg aggcccaaac 300
 tcgggacgaa cccctaacc acctctctt tctgtcatt ctccaactct tactttgtac 360
 cacggaatca cttggcctta aagctagcca gctcgccgt gccttgaggc caggttcgag 420
 agataaaggt aaccgtgggg aaagcggccc ccagtgagc aaaggcggag gcaagaatag 480
 agcaggcctg agggccatag gcgatgagaa taggcagttg aggggtgaaa aagaaaacaa 540
 acaacaaca acaacaaacc ctgaagagta ctgaagattt agaagggact ggaaaggact 600
 tgttgcgca atg gaa gaa tct gac tct gag aaa acg acg gag aaa gaa 648
 Met Glu Glu Ser Asp Ser Glu Lys Thr Thr Glu Lys Glu
 1 5 10
 aat ctg ggg ccg aga atg gat cca cca cta ggg gaa ccg gaa gga tcg 696
 Asn Leu Gly Pro Arg Met Asp Pro Pro Leu Gly Glu Pro Glu Gly Ser
 14 19 24 29

ctt ggg tgg gtg cta cca aat aca gcc atg aag aaa aag gtg ctg ttg	744
Leu Gly Trp Val Leu Pro Asn Thr Ala Met Lys Lys Lys Val Leu Leu	
30 35 40 45	
atg ggt aaa agt ggg tct ggt aag acc agc atg agg tct att atc ttt	792
Met Gly Lys Ser Gly Ser Gly Lys Thr Ser Met Arg Ser Ile Ile Phe	
46 51 56 61	
gca aat tat att gcc aga gac aca cgt cgc ctt ggc gca aca ata cta	840
Ala Asn Tyr Ile Ala Arg Asp Thr Arg Arg Leu Gly Ala Thr Ile Leu	
62 67 72 77	
gac cgt ata cat agt ctt caa att aat agc agt ttg agc acc tac tct	888
Asp Arg Ile His Ser Leu Gln Ile Asn Ser Ser Leu Ser Thr Tyr Ser	
78 83 88 93	
ctc gta gac tct gtt gga aat aca aag aca ttt gat gta gaa cat tct	936
Leu Val Asp Ser Val Gly Asn Thr Lys Thr Phe Asp Val Glu His Ser	
94 99 104 109	
cat gtt cga ttt ctg gga aac ctg gta ttg aac ctg tgg gat tgt ggt	984
His Val Arg Phe Leu Gly Asn Leu Val Leu Asn Leu Trp Asp Cys Gly	
110 115 120 125	
ggg caa gac acc ttc atg gaa aat tat ttc act agc caa cgg gac aac	1032
Gly Gln Asp Thr Phe Met Glu Asn Tyr Phe Thr Ser Gln Arg Asp Asn	
126 131 136 141	
atc ttc cga aat gtg gag gtt ctg att tat gtc ttt gat gtg gag agc	1080
Ile Phe Arg Asn Val Glu Val Leu Ile Tyr Val Phe Asp Val Glu Ser	
142 147 152 157	
cgc gaa ctg gaa aag gac atg cac tat tac caa tca tgc ctg gag gcc	1128
Arg Glu Leu Glu Lys Asp Met His Tyr Tyr Gln Ser Cys Leu Glu Ala	
158 163 168 173	
att ctg cag aat tct cca gat gcc aaa ata ttt tgc ttg gta cac aaa	1176
Ile Leu Gln Asn Ser Pro Asp Ala Lys Ile Phe Cys Leu Val His Lys	
174 179 184 189	
atg gat ctg gta cag gag gat caa cgg gac ctg att ttt aaa gag cga	1224
Met Asp Leu Val Gln Glu Asp Gln Arg Asp Leu Ile Phe Lys Glu Arg	
190 195 200 205	
gaa gaa gat ttg agg cgt ttg tct cgc cca ttg gaa tgt tct tgt ttc	1272
Glu Glu Asp Leu Arg Arg Leu Ser Arg Pro Leu Glu Cys Ser Cys Phe	
206 211 216 221	
cga aca tct atc tgg gat gaa acc ctc tat aag gct tgg tcc agc ata	1320
Arg Thr Ser Ile Trp Asp Glu Thr Leu Tyr Lys Ala Trp Ser Ser Ile	
222 227 232 237	
gtt tat cag ctg att ccc aat gtt cag cag ctg gaa atg aac cta agg	1368
Val Tyr Gln Leu Ile Pro Asn Val Gln Gln Leu Glu Met Asn Leu Arg	
238 243 248 253	
aat ttt gct gaa att atc gaa gct gat gaa gta ctt ctt ttt gag aga	1416

Asn Phe Ala Glu Ile Ile Glu Ala Asp Glu Val Leu Leu Phe Glu Arg	
254 259 264 269	
gct act ttt ctg gta att tct cac tat cag tgt aaa gag cag cgt gat	1464
Ala Thr Phe Leu Val Ile Ser His Tyr Gln Cys Lys Glu Gln Arg Asp	
270 275 280 285	
gcc cat aga ttt gag aaa ata agc aac att att aag cag ttc aag ctg	1512
Ala His Arg Phe Glu Lys Ile Ser Asn Ile Ile Lys Gln Phe Lys Leu	
286 291 296 301	
agc tgc agc aag ctg gct gcc tct ttc cag agt atg gaa gtc agg aac	1560
Ser Cys Ser Lys Leu Ala Ala Ser Phe Gln Ser Met Glu Val Arg Asn	
302 307 312 317	
tct aac ttc gct gct ttc att gac atc ttt aca tcc aac act tat gtg	1608
Ser Asn Phe Ala Ala Phe Ile Asp Ile Phe Thr Ser Asn Thr Tyr Val	
318 323 328 333	
atg gtt gtg atg tct gat ccg tcc att cct tct gca gct act ctg atc	1656
Met Val Val Met Ser Asp Pro Ser Ile Pro Ser Ala Ala Thr Leu Ile	
334 339 344 349	
aac atc cgc aat gcc agg aaa cac ttt gaa aag ctg gaa aga gtg gat	1704
Asn Ile Arg Asn Ala Arg Lys His Phe Glu Lys Leu Glu Arg Val Asp	
350 355 360 365	
gga cca aag cag tgt ctt ctc atg cgc taa a cattgatgaa tattgtttca	1755
Gly Pro Lys Gln Cys Leu Leu Met Arg *	
366 371	
cacaaaaaatt aaaagtttcc taattaatgt tgtattcata tatgtaggct ctgaaatggt	1815
gtgatgctta ttgcttctgt atttcttctc tactccctag tcttaatggt taaccttgaa	1875
tgctattaac ttaaatagcc attgaggagt tagaagatga attgttcattg aagtcgggtgt	1935
tacataaaaag taggtgatat gtaagttttc tgataacaag gttctaatag tgtttaaatg	1995
tactggtaac ctggttccaa tagttgtgtt tgcccaagcc tttctcggca tcattcttgta	2055
ttccttatca gatagtaagt aacctgtaag tttggagtat tactgttttc tcagcatgca	2115
ttaaaaatat tccttaactt caaaaaaaaaaaa aaa	2148

<210> 375

<211> 2064

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (610)..(1650)

[illegible][illegible]

tgc ctg gag gcc att ctg cag aat tct cca gat gcc aaa ata ttt tgc	1080
Cys Leu Glu Ala Ile Leu Gln Asn Ser Pro Asp Ala Lys Ile Phe Cys	
142 147 152 157	
ttg gta cac aaa atg gat ctg gta cag gag gat caa cgg gac ctg att	1128
Leu Val His Lys Met Asp Leu Val Gln Glu Asp Gln Arg Asp Leu Ile	
158 163 168 173	
ttt aaa gag cga gaa gaa gat ttg agg cgt ttg tct cgc cca ttg gaa	1176
Phe Lys Glu Arg Glu Glu Asp Leu Arg Arg Leu Ser Arg Pro Leu Glu	
174 179 184 189	
tgt tct tgt ttc cga aca tct atc tgg gat gaa acc ctc tat aag gct	1224
Cys Ser Cys Phe Arg Thr Ser Ile Trp Asp Glu Thr Leu Tyr Lys Ala	
190 195 200 205	
tgg tcc agc ata gtt tat cag ctg att ccc aat gtt cag cag ctg gaa	1272
Trp Ser Ser Ile Val Tyr Gln Leu Ile Pro Asn Val Gln Gln Leu Glu	
206 211 216 221	
atg aac cta agg aat ttt gct gaa att atc gaa gct gat gaa gta ctt	1320
Met Asn Leu Arg Asn Phe Ala Glu Ile Ile Glu Ala Asp Glu Val Leu	
222 227 232 237	
ctt ttt gag aga gct act ttt ctg gta att tct cac tat cag tgt aaa	1368
Leu Phe Glu Arg Ala Thr Phe Leu Val Ile Ser His Tyr Gln Cys Lys	
238 243 248 253	
gag cag cgt gat gcc cat aga ttt gag aaa ata agc aac att att aag	1416
Glu Gln Arg Asp Ala His Arg Phe Glu Lys Ile Ser Asn Ile Ile Lys	
254 259 264 269	
cag ttc aag ctg agc tgc agc aag ctg gct gcc tct ttc cag agt atg	1464
Gln Phe Lys Leu Ser Cys Ser Lys Leu Ala Ala Ser Phe Gln Ser Met	
270 275 280 285	
gaa gtc agg aac tct aac ttc gct gct ttc att gac atc ttt aca tcc	1512
Glu Val Arg Asn Ser Asn Phe Ala Ala Phe Ile Asp Ile Phe Thr Ser	
286 291 296 301	
aac act tat gtg atg gtt gtg atg tct gat ccg tcc att cct tct gca	1560
Asn Thr Tyr Val Met Val Val Met Ser Asp Pro Ser Ile Pro Ser Ala	
302 307 312 317	
gct act ctg atc aac atc cgc aat gcc agg aaa cac ttt gaa aag ctg	1608
Ala Thr Leu Ile Asn Ile Arg Asn Ala Arg Lys His Phe Glu Lys Leu	
318 323 328 333	
gaa aga gtg gat gga cca aag cag tgt ctt ctc atg cgc taa acattga	1657
Glu Arg Val Asp Gly Pro Lys Gln Cys Leu Leu Met Arg *	
334 339 344	
tgaatattgt ttcacacaaa aattaaaagt ttcctaatta atgttgtatt catatatgta	1717
ggctctgaaa tgttgtgatg cttattgctt ctgtatttct tctctactcc ctagtcttaa	1777
tgtttaacct tgaatgctat taacttaaata agccattgag gagttagaag atgaattggt	1837

catgaagtcg gtgttacata aaagtaggtg atatgtaagt tttctgataa caaggttcta 1897
 atagtgttta aatgtactgg taacctgggt ccaatagttg tgtttgcca agcctttctc 1957
 ggcatcatct tgtattcctt atcagatagt aagtaacctg taagtttgga gtattactgt 2017
 tttctcagca tgcattaaaa atattcctta acttcaaaaa aaaaaaa 2064

<210> 376
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (610)..(1689)

<400> 376
 gtaccgctcc ggaattcccg ggtcgacgat ttcgcccac gtgatcctgg cctgcagttg 60
 ggtggctgcg gtgagatacc tgggttcctg aagggcgggt ggtaggtcg taactactgc 120
 ccccgccggc tgagtctccg agcggccggg ctcggaagcc acgagccagc tgaggcgctc 180
 tccgcttagt gcctacggca tgggtcagct ctttctgcca cctccgcctt cgcggctctc 240
 acctctttgc ggggtgaagtt acctttgggt ttccagacct tgggggcctg aggcccaaac 300
 tcgggaagaa cccctaacc acctctctt tctgtcatt ctccaactct tactttgtac 360
 cacggaatca cttggcctta aagctagcca gctcgccgt gccttgaggc caggttcgag 420
 agataaaggt aaccgtgggg aaagcggccc ccagtgagc aaaggcggag gcaagaatag 480
 agcaggcctg agggccatag gcgatgagaa taggcagttg aggggtgaaa aagaaaacaa 540
 acaacaaca acaacaacc ctgaagagta ctgaagattt agaagggact ggaaaggact 600
 tgttgcgca atg gaa gaa tct gac tct gag aaa acg acg gag aaa gaa 648
 Met Glu Glu Ser Asp Ser Glu Lys Thr Thr Glu Lys Glu
 1 5 10
 aat ctg ggg ccg aga atg gat cca cca cta ggg gaa ccg gaa gga tcg 696
 Asn Leu Gly Pro Arg Met Asp Pro Pro Leu Gly Glu Pro Glu Gly Ser
 14 19 24 29
 ctt ggg tgg gtg cta cca aat aca gcc atg aag aaa aag gta aga cgt 744
 Leu Gly Trp Val Leu Pro Asn Thr Ala Met Lys Lys Lys Val Arg Arg
 30 35 40 45
 gtt aga tac gtc aaa acc atg aag aaa aag gtg ctg ttg atg ggt aaa 792
 Val Arg Tyr Val Lys Thr Met Lys Lys Lys Val Leu Leu Met Gly Lys
 46 51 56 61

agt ggg tct ggt aag acc agc atg agg tct att atc ttt gca aat tat	840
Ser Gly Ser Gly Lys Thr Ser Met Arg Ser Ile Ile Phe Ala Asn Tyr	
62 67 72 77	
att gcc aga gac aca cgt cgc ctt ggc gca aca att gat gta gaa cat	888
Ile Ala Arg Asp Thr Arg Arg Leu Gly Ala Thr Ile Asp Val Glu His	
78 83 88 93	
tct cat gtt cga ttt ctg gga aac ctg gta ttg aac ctg tgg gat tgt	936
Ser His Val Arg Phe Leu Gly Asn Leu Val Leu Asn Leu Trp Asp Cys	
94 99 104 109	
ggg ggg caa gac acc ttc atg gaa aat tat ttc act agc caa cgg gac	984
Gly Gly Gln Asp Thr Phe Met Glu Asn Tyr Phe Thr Ser Gln Arg Asp	
110 115 120 125	
aac atc ttc cga aat gtg gag gtt ctg att tat gtc ttt gat gtg gag	1032
Asn Ile Phe Arg Asn Val Glu Val Leu Ile Tyr Val Phe Asp Val Glu	
126 131 136 141	
agc cgc gaa ctg gaa aag gac atg cac tat tac caa tca tgc ctg gag	1080
Ser Arg Glu Leu Glu Lys Asp Met His Tyr Tyr Gln Ser Cys Leu Glu	
142 147 152 157	
gcc att ctg cag aat tct cca gat gcc aaa ata ttt tgc ttg gta cac	1128
Ala Ile Leu Gln Asn Ser Pro Asp Ala Lys Ile Phe Cys Leu Val His	
158 163 168 173	
aaa atg gat ctg gta cag gag gat caa cgg gac ctg att ttt aaa gag	1176
Lys Met Asp Leu Val Gln Glu Asp Gln Arg Asp Leu Ile Phe Lys Glu	
174 179 184 189	
cga gaa gaa gat ttg agg cgt ttg tct cgc cca ttg gaa tgt tct tgt	1224
Arg Glu Glu Asp Leu Arg Arg Leu Ser Arg Pro Leu Glu Cys Ser Cys	
190 195 200 205	
ttc cga aca tct atc tgg gat gaa acc ctc tat aag gct tgg tcc agc	1272
Phe Arg Thr Ser Ile Trp Asp Glu Thr Leu Tyr Lys Ala Trp Ser Ser	
206 211 216 221	
ata gtt tat cag ctg att ccc aat gtt cag cag ctg gaa atg aac cta	1320
Ile Val Tyr Gln Leu Ile Pro Asn Val Gln Gln Leu Glu Met Asn Leu	
222 227 232 237	
agg aat ttt gct gaa att atc gaa gct gat gaa gta ctt ctt ttt gag	1368
Arg Asn Phe Ala Glu Ile Ile Glu Ala Asp Glu Val Leu Leu Phe Glu	
238 243 248 253	
aga gct act ttt ctg gta att tct cac tat cag tgt aaa gag cag cgt	1416
Arg Ala Thr Phe Leu Val Ile Ser His Tyr Gln Cys Lys Glu Gln Arg	
254 259 264 269	
gat gcc cat aga ttt gag aaa ata agc aac att att aag cag ttc aag	1464
Asp Ala His Arg Phe Glu Lys Ile Ser Asn Ile Ile Lys Gln Phe Lys	
270 275 280 285	

ctg agc tgc agc aag ctg gct gcc tct ttc cag agt atg gaa gtc agg	1512
Leu Ser Cys Ser Lys Leu Ala Ala Ser Phe Gln Ser Met Glu Val Arg	
286 291 296 301	
aac tct aac ttc gct gct ttc att gac atc ttt aca tcc aac act tat	1560
Asn Ser Asn Phe Ala Ala Phe Ile Asp Ile Phe Thr Ser Asn Thr Tyr	
302 307 312 317	
gtg atg gtt gtg atg tct gat ccg tcc att cct tct gca gct act ctg	1608
Val Met Val Val Met Ser Asp Pro Ser Ile Pro Ser Ala Ala Thr Leu	
318 323 328 333	
atc aac atc cgc aat gcc agg aaa cac ttt gaa aag ctg gaa aga gtg	1656
Ile Asn Ile Arg Asn Ala Arg Lys His Phe Glu Lys Leu Glu Arg Val	
334 339 344 349	
gat gga cca aag cag tgt ctt ctc atg cgc taa acattgat gaatattgtt	1707
Asp Gly Pro Lys Gln Cys Leu Leu Met Arg *	
350 355 360	
tcacacaaaa attaaaagtt tcctaattaa tgttgatttc atatatgtag gctctgaaat	1767
gttgatgagc ttattgcttc tgtatttctt ctctactccc tagtcttaat gtttaacott	1827
gaatgctatt aacttaaata gccattgagg agttagaaga tgaattgttc atgaagtcgg	1887
tggtacataa aagtaggtga tatgtaagtt ttctgataac aaggttctaa tagtgtttaa	1947
atgtactggt aacctgggtc caatagttgt gtttgcccaa gcctttctcg gcatcatctt	2007
gtattcctta tcagatagta agtaacctgt aagtttgag tattactgtt ttctcagcat	2067
gcattaaaaa tattccttaa cttcaaaaaa aaaaaa	2103

<210> 377
 <211> 2554
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (213)..(1703)

<400> 377	
tgcccgctg ctgaattogg cagcaggaca cgctgaacag aattcacctc acgtccagta	60
tgagatggga gtatgaacaa acagtcatgc agagtgatga gtgcaaacaat ggactataaa	120
gcggccatag agaatgaact gcacgagtcg ctccaactcc tgcagagctg agccggaggg	180
aatccggaag gacacgctga acaggaacag aa atg aat aaa agt cgc tgg cag	233
Met Asn Lys Ser Arg Trp Gln	
1 5	

agt aga aga cga cat ggg aga aga agc cac cag cag aac cct tgg ttc	281
Ser Arg Arg Arg His Gly Arg Arg Ser His Gln Gln Asn Pro Trp Phe	
8 13 18 23	
aga ctc cgt gat tct gaa gac agg tct gac tcc cgg gca gca cag ccc	329
Arg Leu Arg Asp Ser Glu Asp Arg Ser Asp Ser Arg Ala Ala Gln Pro	
24 29 34 39	
gct cac gat tcc ggc cac ggt gat gac gag tct ccg tca acc tcg tct	377
Ala His Asp Ser Gly His Gly Asp Asp Glu Ser Pro Ser Thr Ser Ser	
40 45 50 55	
ggc aca gct ggg acc tcc tct gtg cca gag cta cct ggg ttt tac ttt	425
Gly Thr Ala Gly Thr Ser Ser Val Pro Glu Leu Pro Gly Phe Tyr Phe	
56 61 66 71	
gac cct gaa aag aaa cgc tac ttc cgc ttg ctc cct gga cat aac aac	473
Asp Pro Glu Lys Lys Arg Tyr Phe Arg Leu Leu Pro Gly His Asn Asn	
72 77 82 87	
tgc aac ccc ctg acg aaa gag agc atc cgg cag aag gag atg gag agc	521
Cys Asn Pro Leu Thr Lys Glu Ser Ile Arg Gln Lys Glu Met Glu Ser	
88 93 98 103	
aag aga ctg cgg ctg ctc cag gaa gaa gac aga cgg aaa aag att gcc	569
Lys Arg Leu Arg Leu Leu Gln Glu Glu Asp Arg Arg Lys Lys Ile Ala	
104 109 114 119	
agg atg gga ttt aat gca tct tcc atg cta cga aaa agc cag ctg ggt	617
Arg Met Gly Phe Asn Ala Ser Ser Met Leu Arg Lys Ser Gln Leu Gly	
120 125 130 135	
ttt ctc aac gtc acc aat tac tgc cat tta gcc cac gag ctg cgt ctc	665
Phe Leu Asn Val Thr Asn Tyr Cys His Leu Ala His Glu Leu Arg Leu	
136 141 146 151	
agc tgc atg gag agg aaa aag gtc cag att cga agc atg gat ccc tcc	713
Ser Cys Met Glu Arg Lys Lys Val Gln Ile Arg Ser Met Asp Pro Ser	
152 157 162 167	
gcc ttg gca agc gac cga ttt aac ctc ata ctg gca gat acc aac agt	761
Ala Leu Ala Ser Asp Arg Phe Asn Leu Ile Leu Ala Asp Thr Asn Ser	
168 173 178 183	
gac cgg ctc ttc aca gtg aac gat gtt aca gtt gga ggc tcc aag tat	809
Asp Arg Leu Phe Thr Val Asn Asp Val Thr Val Gly Gly Ser Lys Tyr	
184 189 194 199	
ggg atc atc aac ctg caa agt ctg aag acc cct acg ctc aag gtg ttc	857
Gly Ile Ile Asn Leu Gln Ser Leu Lys Thr Pro Thr Leu Lys Val Phe	
200 205 210 215	
atg cac gaa aac ctc tac ttc acc aac cgg aag gtg aga ttc ggt gtg	905
Met His Glu Asn Leu Tyr Phe Thr Asn Arg Lys Val Arg Phe Gly Val	
216 221 226 231	
ctg ggc ctc gct gaa tca ctt gga ttc cca cat tct gct atg cct cat	953

Leu Gly Leu Ala Glu Ser Leu Gly Phe Pro His Ser Ala Met Pro His	
232 237 242 247	
ggg act cgc agg act cca ggc tgt gcc acc ctg ctc cca gca tca ctg	1001
Gly Thr Arg Arg Thr Pro Gly Cys Ala Thr Leu Leu Pro Ala Ser Leu	
248 253 258 263	
ttc gtc aat agt cac cca gca gga ata gac cgg cct ggc atg ctc tgc	1049
Phe Val Asn Ser His Pro Ala Gly Ile Asp Arg Pro Gly Met Leu Cys	
264 269 274 279	
agt ttc cgg atc cct ggt gcc tgg tcc tgt gcc tgg tcc ctg aat atc	1097
Ser Phe Arg Ile Pro Gly Ala Trp Ser Cys Ala Trp Ser Leu Asn Ile	
280 285 290 295	
caa gca aat aac tgc ttc agt aca ggc ttg tct cgg cgg gtc ctg ttg	1145
Gln Ala Asn Asn Cys Phe Ser Thr Gly Leu Ser Arg Arg Val Leu Leu	
296 301 306 311	
acc aac gtg gtg acg gga cac cgg cag tcc ttt ggg acc aac agt gat	1193
Thr Asn Val Val Thr Gly His Arg Gln Ser Phe Gly Thr Asn Ser Asp	
312 317 322 327	
gtc ttg gcc cag cag ttt gct ctc atg gct cct ctg ctg ttt aat ggc	1241
Val Leu Ala Gln Gln Phe Ala Leu Met Ala Pro Leu Leu Phe Asn Gly	
328 333 338 343	
tgc cgc tct ggg gaa atc ttt gcc att gat ctg cgt tgt gga aat caa	1289
Cys Arg Ser Gly Glu Ile Phe Ala Ile Asp Leu Arg Cys Gly Asn Gln	
344 349 354 359	
ggc aag gga tgg aag gcc acc cgc ctg ttt cat gat tca gca gtg acc	1337
Gly Lys Gly Trp Lys Ala Thr Arg Leu Phe His Asp Ser Ala Val Thr	
360 365 370 375	
tct gtg cgg atc ctc caa gat gag caa tac ctg atg gct tca gac atg	1385
Ser Val Arg Ile Leu Gln Asp Glu Gln Tyr Leu Met Ala Ser Asp Met	
376 381 386 391	
gct gga aag atc aag ctg tgg gac ctg agg acc acg aag tgc gta agg	1433
Ala Gly Lys Ile Lys Leu Trp Asp Leu Arg Thr Thr Lys Cys Val Arg	
392 397 402 407	
cag tac gaa ggc cac gtg aat gag tac gcc tac ctg ccc ctg cat gtg	1481
Gln Tyr Glu Gly His Val Asn Glu Tyr Ala Tyr Leu Pro Leu His Val	
408 413 418 423	
cac gag gaa gaa gga atc ctg gtg gca gtg ggc cag gac tgc tac acg	1529
His Glu Glu Glu Gly Ile Leu Val Ala Val Gly Gln Asp Cys Tyr Thr	
424 429 434 439	
aga atc tgg agc ctc cac gat gcc cgc cta ctg aga acc ata ccc tcc	1577
Arg Ile Trp Ser Leu His Asp Ala Arg Leu Leu Arg Thr Ile Pro Ser	
440 445 450 455	
ccg tac cct gcc tcc aag gcc gac att ccc agt gtg gcc ttc tcg tcg	1625
Pro Tyr Pro Ala Ser Lys Ala Asp Ile Pro Ser Val Ala Phe Ser Ser	

456	461	466	471	
cgg ctg ggg ggc tcc cgg ggc gcg ccg ggg ctg ctc atg gct gtc ggg				1673
Arg Leu Gly Gly Ser Arg Gly Ala Pro Gly Leu Leu Met Ala Val Gly				
472	477	482	487	
cag gac ctt tac tgt tac tcc tac agc taa t tctgcagggc acagcccaga				1724
Gln Asp Leu Tyr Cys Tyr Ser Tyr Ser *				
488	493			
gccatgtgga tttgacttac gggagtaaag cgtaactttt tactgcatct aatgaggggtg				1784
ttttaagtga cactcagtgt acacagatcc catcctctgg ctgctaggag agaagtgctg				1844
aatgttccgt gtggagatgc tcaggaaagt tatttgagtt aaattgctgg ctgagagagc				1904
ttggaagtcc ttttcataaa aggtacctct ttccttttct tattgaattc ttagaactta				1964
gttaaccctc cctgcctttt cttaacaaaa aggacttttc taaggactga agattggcaa				2024
aaacgaaaag cttcttcctc caagagccca ttgaagaagc ccagtgatga gacggtgaga				2084
tggtttgagt cctcgggtgcc tgggtagcag gaagaaagac ctgcatcctg catctgtact				2144
tggggaagcc agcggagagg acggggaggt tactttctcta agtttctgca gaaatattga				2204
aggctggagt ttggaatcct taaacttggc cttctcaaac tcagcagcag atctccggga				2264
ttctgctggt attatccaaa ggcgttggaa ggaaagatgg atcttcttac atgctagaag				2324
ttttaaacgg tccttaacat gcctttgttc aagcaccctc cagaatgtaa ggttcagcag				2384
ctctggtttc tattacggtg acttgaatgt cagattcaag ggcccggcgt caaaggaaat				2444
tggttttgac tttttgtaat ctaggagcga cagttcgtga gatgtttatt cagtgttaaa				2504
gagcctgttt ttctacccaaa caataaaacc aagagaagaa aaaaaaaaaa				2554

<210> 378
 <211> 1678
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (33) .. (992)

<400> 378		
cgccctgagga attcggcacg agccgacgcc ac	atg gcg gcg ccc agt ggc gtc	53
	Met Ala Ala Pro Ser Gly Val	
	1 5	

cac ctg ctc gtc cgc aga ggt tct cat aga att ttc tct tca cca ctc	101
His Leu Leu Val Arg Arg Gly Ser His Arg Ile Phe Ser Ser Pro Leu	

8	13	18	23	
aat cat atc tac tta cac aag cag tca agc agt caa caa aga aga aat				149
Asn His Ile Tyr Leu His Lys Gln Ser Ser Ser Gln Gln Arg Arg Asn				
24	29	34	39	
ttc ttt ttt cgg aga caa aga gat att tca cac agt ata gtt ttg ccg				197
Phe Phe Phe Arg Arg Gln Arg Asp Ile Ser His Ser Ile Val Leu Pro				
40	45	50	55	
gct gca gtt tct tca gct cat ccg gtt cct aag cac ata aag aag cca				245
Ala Ala Val Ser Ser Ala His Pro Val Pro Lys His Ile Lys Lys Pro				
56	61	66	71	
gac tat gtg acg aca ggc att gta cca gac tgg gga gac agc ata gaa				293
Asp Tyr Val Thr Thr Gly Ile Val Pro Asp Trp Gly Asp Ser Ile Glu				
72	77	82	87	
gtt aag aat gaa gat cag att caa ggg ctt cat cag gct tgt cag ctg				341
Val Lys Asn Glu Asp Gln Ile Gln Gly Leu His Gln Ala Cys Gln Leu				
88	93	98	103	
gcc cgc cac gtc ctc ctc ttg gct ggg aag agt tta aag gtt gac atg				389
Ala Arg His Val Leu Leu Leu Ala Gly Lys Ser Leu Lys Val Asp Met				
104	109	114	119	
aca act gaa gag ata gat gct ctt gtt cat ccg gaa atc atc agt cat				437
Thr Thr Glu Glu Ile Asp Ala Leu Val His Arg Glu Ile Ile Ser His				
120	125	130	135	
aat gcc tat ccc tca cct cta ggc tat gga ggt ttt cca aaa tct gtt				485
Asn Ala Tyr Pro Ser Pro Leu Gly Tyr Gly Gly Phe Pro Lys Ser Val				
136	141	146	151	
tgt acc tct gta aac aac gtg ctc tgt cat ggt att cct gac agt cga				533
Cys Thr Ser Val Asn Asn Val Leu Cys His Gly Ile Pro Asp Ser Arg				
152	157	162	167	
cct ctt cag gat gga gat att atc aac att gat gtc aca gtc tat tac				581
Pro Leu Gln Asp Gly Asp Ile Ile Asn Ile Asp Val Thr Val Tyr Tyr				
168	173	178	183	
aat ggc tac cat gga gac acc tct gaa aca ttt ttg gtg ggc aat gtg				629
Asn Gly Tyr His Gly Asp Thr Ser Glu Thr Phe Leu Val Gly Asn Val				
184	189	194	199	
gac gaa tgt ggt aaa aag tta gtg gag gtt gcc agg agg tgt aga gat				677
Asp Glu Cys Gly Lys Lys Leu Val Glu Val Ala Arg Arg Cys Arg Asp				
200	205	210	215	
gaa gca att gca gct tgc aga gca ggg gct ccc ttc tct gta att gga				725
Glu Ala Ile Ala Ala Cys Arg Ala Gly Ala Pro Phe Ser Val Ile Gly				
216	221	226	231	
aac aca atc agc cac ata act cat cag aat ggt ttt caa gtc tgt cca				773
Asn Thr Ile Ser His Ile Thr His Gln Asn Gly Phe Gln Val Cys Pro				
232	237	242	247	

cat ttt gtg gga cat gga ata gga tct tac ttt cat gga cat cca gaa	821
His Phe Val Gly His Gly Ile Gly Ser Tyr Phe His Gly His Pro Glu	
248 253 258 263	
att tgg cat cat gca aac gac agt gat cta ccc atg gag gag ggc atg	869
Ile Trp His His Ala Asn Asp Ser Asp Leu Pro Met Glu Glu Gly Met	
264 269 274 279	
gca ttc act ata gag cca atc atc acg gag gga tcc cct gaa ttt aaa	917
Ala Phe Thr Ile Glu Pro Ile Ile Thr Glu Gly Ser Pro Glu Phe Lys	
280 285 290 295	
gtc ctg gag gat gca tgg act gtg gtc tcc cta gac aat caa agg tgt	965
Val Leu Glu Asp Ala Trp Thr Val Val Ser Leu Asp Asn Gln Arg Cys	
296 301 306 311	
cgg cgc agt tcg agc aca cgg ttc tga tcacg tcgaggggcg cgcagatcct	1017
Arg Arg Ser Ser Ser Thr Arg Phe *	
312 317	
gaccaaacta ccccatgagg cctgaggagc cgcccgaagg tcgcggtgac ctggtgcctt	1077
tttaaataaa ttgctgaaat ttggctggag aactttttaga agaaacaggg aaatgaccgg	1137
tggtgcggta acctgcgtgg ctccctgatag cgtttggaag aacgcggggg agactgaaga	1197
gcaactggga actcggatct gaagccctgc tggggtcgcg cggcttttga aaaacaaatc	1257
ctggccctgg actcggtttc ccagcgcggt caacgcattt ggaggggact ggaggaaacc	1317
cccttgttgg aagagattcc aagagaagca cggttttctc tttcccttgc cctgactgtt	1377
ggagtaaaaa acctcttaaa tccattgtat cagaggtcct tacctctctg acagttacaa	1437
tgatctttgt atttgaactt tgcacgtctg ccgaaaaatc cgaacctgtt gactgggatt	1497
tttaaaaaatc cttttcccc ttttgtgtat tcaatattgg ccggcccca ggatgctcgc	1557
agaagccagc ccccaacccc agcccttcg tatctttccc ctccatcgcg gctttgcgat	1617
gaaagattag cccgcgaaca gaggcattga ttacaaacat gtccttggca aaaaaaaaaa	1677
a	1678

<210> 379
 <211> 4695
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (52) .. (1623)

<400> 379

gcacaactcg cgccaaacgg ggcctaagag aagccggact tcgcaagcac c atg cag	57
Met Gln	
1	
tgg ata agg ggc gga tcg gga atg ctg atc act gga gat tcc atc gtt	105
Trp Ile Arg Gly Gly Ser Gly Met Leu Ile Thr Gly Asp Ser Ile Val	
3 8 13 18	
agt gct gag gca gta tgg gat cac gtc acc atg gcc aac cgg gag ttg	153
Ser Ala Glu Ala Val Trp Asp His Val Thr Met Ala Asn Arg Glu Leu	
19 24 29 34	
gca ttt aaa gct ggc gac gtc atc aaa gtc ttg gat gct tcc aac aag	201
Ala Phe Lys Ala Gly Asp Val Ile Lys Val Leu Asp Ala Ser Asn Lys	
35 40 45 50	
gat tgg tgg tgg ggc cag atc gac gat gag gag gga tgg ttt cct gcc	249
Asp Trp Trp Trp Gly Gln Ile Asp Asp Glu Glu Gly Trp Phe Pro Ala	
51 56 61 66	
agc ttt gtg agg ctc tgg gtg aac cag gag gat gag gtg gag gag ggg	297
Ser Phe Val Arg Leu Trp Val Asn Gln Glu Asp Glu Val Glu Glu Gly	
67 72 77 82	
ccc agc gat gtg cag aac gga cac ctg gac ccc aat tca gac tgc ctc	345
Pro Ser Asp Val Gln Asn Gly His Leu Asp Pro Asn Ser Asp Cys Leu	
83 88 93 98	
tgt ctg ggg cgg cca cta cag aac cgg gac cag atg cgg gcc aat gtc	393
Cys Leu Gly Arg Pro Leu Gln Asn Arg Asp Gln Met Arg Ala Asn Val	
99 104 109 114	
atc aat gag ata atg agc act gag cgt cac tac atc aag cac ctc aag	441
Ile Asn Glu Ile Met Ser Thr Glu Arg His Tyr Ile Lys His Leu Lys	
115 120 125 130	
gat att tgt gag ggc tat ctg aag cag tgc cgg aag aga agg gac atg	489
Asp Ile Cys Glu Gly Tyr Leu Lys Gln Cys Arg Lys Arg Arg Asp Met	
131 136 141 146	
ttc agt gac gag caa ctg aag gta atc ttt ggg aac att gaa gat atc	537
Phe Ser Asp Glu Gln Leu Lys Val Ile Phe Gly Asn Ile Glu Asp Ile	
147 152 157 162	
tac aga ttt cag atg ggc ttt gtg aga gac ctg gag aaa cag tat aac	585
Tyr Arg Phe Gln Met Gly Phe Val Arg Asp Leu Glu Lys Gln Tyr Asn	
163 168 173 178	
aat gat gac ccc cac ctc agc gag ata gga ccc tgc ttc cta gag cac	633
Asn Asp Asp Pro His Leu Ser Glu Ile Gly Pro Cys Phe Leu Glu His	
179 184 189 194	
caa gat gga ttc tgg ata tac tct gag tat tgt aac aac cac ctg gat	681
Gln Asp Gly Phe Trp Ile Tyr Ser Glu Tyr Cys Asn Asn His Leu Asp	
195 200 205 210	

gct tgc atg gag ctc tcc aaa ctg atg aag gac agc cgc tac cag cac	729
Ala Cys Met Glu Leu Ser Lys Leu Met Lys Asp Ser Arg Tyr Gln His	
211 216 221 226	
ttc ttt gag gcc tgt cgc ctc ttg cag cag atg att gac att gct atc	777
Phe Phe Glu Ala Cys Arg Leu Leu Gln Gln Met Ile Asp Ile Ala Ile	
227 232 237 242	
gat ggt ttc ctt ttg act cca gtg cag aag atc tgc aag tat ccc tta	825
Asp Gly Phe Leu Leu Thr Pro Val Gln Lys Ile Cys Lys Tyr Pro Leu	
243 248 253 258	
cag ttg gct gag ctc cta aag tat act gcc caa gac cac agt gac tac	873
Gln Leu Ala Glu Leu Leu Lys Tyr Thr Ala Gln Asp His Ser Asp Tyr	
259 264 269 274	
agg tat gtg gca gct gct ttg gct gtc atg aga aat gtg act cag cag	921
Arg Tyr Val Ala Ala Ala Leu Ala Val Met Arg Asn Val Thr Gln Gln	
275 280 285 290	
atc aac gaa cgc aag cga cgt tta gag aat att gac aag att gct cag	969
Ile Asn Glu Arg Lys Arg Arg Leu Glu Asn Ile Asp Lys Ile Ala Gln	
291 296 301 306	
tgg cag gct tct gtc cta gac tgg gag ggc gag gac atc cta gac agg	1017
Trp Gln Ala Ser Val Leu Asp Trp Glu Gly Glu Asp Ile Leu Asp Arg	
307 312 317 322	
agc tgc gag ctg atc tac act ggg gag atg gcc tgg atc tac cag ccc	1065
Ser Ser Glu Leu Ile Tyr Thr Gly Glu Met Ala Trp Ile Tyr Gln Pro	
323 328 333 338	
tac ggc cgc aac cag cag cgg gtc ttc ttc ctg ttt gac cac cag atg	1113
Tyr Gly Arg Asn Gln Gln Arg Val Phe Phe Leu Phe Asp His Gln Met	
339 344 349 354	
gtc ctc tgc aag aag gac cta atc cgg aga gac atc ctg tac tac aaa	1161
Val Leu Cys Lys Lys Asp Leu Ile Arg Arg Asp Ile Leu Tyr Tyr Lys	
355 360 365 370	
ggc cgc att gac atg gat aaa tat gag gta gtt gac att gag gat ggc	1209
Gly Arg Ile Asp Met Asp Lys Tyr Glu Val Val Asp Ile Glu Asp Gly	
371 376 381 386	
aga gat gat gac ttc aat gtc agc atg aag aat gcc ttt aag ctt cac	1257
Arg Asp Asp Asp Phe Asn Val Ser Met Lys Asn Ala Phe Lys Leu His	
387 392 397 402	
aac aag gag act gag gag ata cat ctg ttc ttt gcc aag aag ctg gag	1305
Asn Lys Glu Thr Glu Glu Ile His Leu Phe Phe Ala Lys Lys Leu Glu	
403 408 413 418	
gaa aaa ata cgc tgg ctc agg gct ttc aga gaa gag agg aaa atg gta	1353
Glu Lys Ile Arg Trp Leu Arg Ala Phe Arg Glu Glu Arg Lys Met Val	
419 424 429 434	
cag gaa gat gaa aaa att ggc ttt gaa att tct gaa aac cag aag agg	1401

Gln Glu Asp Glu Lys Ile Gly Phe Glu Ile Ser Glu Asn Gln Lys Arg	
435 440 445 450	
cag gct gca atg act gtg aga aaa gtc cct aag caa aaa ggt gtc aac	1449
Gln Ala Ala Met Thr Val Arg Lys Val Pro Lys Gln Lys Gly Val Asn	
451 456 461 466	
tct gcc cgc tca gtt cct cct tcc tac cca cca ccg cag gac ccg tta	1497
Ser Ala Arg Ser Val Pro Pro Ser Tyr Pro Pro Pro Gln Asp Pro Leu	
467 472 477 482	
aac cac ggc cag tac ctg gtc ccc gac ggc atc gct cag tcg cag gtc	1545
Asn His Gly Gln Tyr Leu Val Pro Asp Gly Ile Ala Gln Ser Gln Val	
483 488 493 498	
ttt gag ttc acc gaa ccc aag cgc agc cag tca cca ttc tgg caa aac	1593
Phe Glu Phe Thr Glu Pro Lys Arg Ser Gln Ser Pro Phe Trp Gln Asn	
499 504 509 514	
ttc agc agg tta acc ccc ttc aaa aaa tga t acctacaggg aggcagataa	1644
Phe Ser Arg Leu Thr Pro Phe Lys Lys *	
515 520	
ttttaaaata aagtaaataa aattatattt atagatggac cttttttcgg agaagcactg	1704
ttgaaattta tacacacaca cacacacaga gacccttgag tacacatata cacacacaca	1764
cacagacaca cacacacaca cacacacaca cacacacaca gagagataag gaacaaaagt	1824
gttttctgtt gttttgggga agtgaaatat gtggttggtta ggaagaggta ccaatgactt	1884
ccaaacatgt gattccgtct taaaagtttt ccattttttac cctgtccccc ttccctttgc	1944
tttcagaagt tgacatttct attcattgct tttcttggtta agataatctc ttactcccc	2004
tgtgagtgat tctactgcctt gtcattatta cgatagatgt gtttgtattg ttttttttct	2064
gatgatactg atgttgatga atttttaatt ttatttgatg tggtagagtt gggaggtttc	2124
agggtttttt cccctctttt actttccatt gaggaaggga atgagctcct ttctcctctc	2184
cttcagccaa tcattatcaa atgttccttc agccctgcag ttgccccaaa taaccttttt	2244
tcagcatcct ctgtcctcag tcatgccagt ctggacatgc tctgttggtc cctgtgacaa	2304
aactgctcag tattcctatt gcttttactg tgtttttaggt actgtgaagg gatcaaaaaa	2364
ccaaacagaa gcaaggaggat atcagactat gatgatgctg gaggaggactt ctgttcaggg	2424
aacattttgc attcaggctg tttcttctat cactgggggtt tcccatgttg cagcacttct	2484
gggtcgttgc aattttgcat ctaggaggtta gtttgatoga gttattctct tttttcaagt	2544
cacttttggt ataggtctcc ccctaggcct gtctctccct tagccccaaa gatctgaact	2604
ggaagcagag gttgagattc tgccctccag gagagggtt tacctgcccc ctagtaccag	2664

ataggttttag	ggcagtgatc	tctacagcaa	tcagttcagt	gtcctgggtg	tcctgctcc	2724
catttacaga	tgtttgggca	gcattgatag	aagtatggag	gggttcaaga	cagagcccac	2784
ctgatcaaga	tcacagcta	ccttcaaatt	attgacctgg	acagggcca	agtctgatag	2844
taacctttta	caagaaagaa	cagggatggg	aatggaaaga	gatagccttg	atccacagta	2904
ttgtacctgc	atcttctacc	accctaaaat	tgtgtgagac	ttctccatt	gttaacagat	2964
tgcatggaca	atcttccctg	gcttctttct	ttccctctct	ctttcttctt	tctcctgcca	3024
tcctagcaca	ggaggatttt	tggtattgat	atagttaaag	ctgttctggc	actcaaagaa	3084
ggccgtgttt	ccaacatcct	ctcatcccag	gacatttggg	gcaagtgagt	taggggcccc	3144
ggggcaattt	tcctctgaa	taacgtgtct	gaggcagga	tgctaccctc	aggctcgctt	3204
ttggccagct	ttttgcttgg	gaaaatctaa	cttctttcac	aaggaggcag	gcttcctatg	3264
gatgttggag	tacctgtttt	tcctccacac	atagcccttt	tcatggatag	accttgaaca	3324
acaaaaaggg	tataagggaa	taaggatgaa	ctctgctgtg	aagagcaagc	cactgtagtg	3384
aggaatgtgg	agactgggag	tctgtcctaa	accccatggg	agaagacttc	atcatgacag	3444
gacttcagct	taccaagcag	cagccatagc	tgtgtggagg	cttcagcata	gctagcatgt	3504
ttactgctct	atgcctcctg	atccagacca	ggcattgcc	agcctgggaa	tcttttcttt	3564
gtgggaatca	aattacaagc	tatttaagtt	tatattccat	cacaaccaag	tcagacttgt	3624
attataagtc	aaggatgagc	ctgatctggg	gagagggccg	gggctcggga	ctggccacca	3684
ctgttcagca	catgacctaa	ctacgtaagc	ctctttggca	agggtcctgg	tgcccagcac	3744
ccaggctaaa	atatcctgtc	tggcagagtg	ttttggtagc	tatgcaggcc	tccttccagt	3804
gtacctcttt	ttccaacttc	tcactcctcc	ttactaggct	tggccttgac	atgcttcttc	3864
gagggttggc	agcacaccgg	gaggggatgc	ttggacaagt	ttctgggcct	acatttcttg	3924
actaggccct	ctcatttctc	cctccttgg	ggcttctgcc	cagggctcca	ggatcaggga	3984
tattacttct	caaccgcac	ttctcctcta	ctgaaccac	tggcatcacc	tgatgccact	4044
aatttgtgaa	caacaagaaa	tcatttcccc	attggttggg	gtattccctc	agcctatagc	4104
atcaaagcag	accagtggcc	aacagcccca	aggggagccc	aattaaatac	ctgggttcag	4164
tatcctaacc	tgttatgtcc	tgacagcaat	ggtaacccca	gtaattctgt	aatgttgtaa	4224
ttccgcagtg	gccctgagct	cccttttctc	caactcagtg	aggccaggat	ttgctctcca	4284
aaaggctttg	ctagtgtgtt	caatgggacc	tgctgtgggg	agtcctaaga	cagacatcta	4344
attattctct	ctttttcccc	ccctctctat	gtgtatat	ctaattggatc	tataagaaca	4404

aac agt ggc aaa tat tgt act cca aga tac ttg gat tac gaa gat ttg	570
Asn Ser Gly Lys Tyr Cys Thr Pro Arg Tyr Leu Asp Tyr Glu Asp Leu	
104 109 114 119	
gag cgc aag tac tgg aag aac tta act ttt gtg gca cct atc tat ggt	618
Glu Arg Lys Tyr Trp Lys Asn Leu Thr Phe Val Ala Pro Ile Tyr Gly	
120 125 130 135	
gca gat att aat ggg agc ata tat gat gag ggt gtg gat gaa tgg aac	666
Ala Asp Ile Asn Gly Ser Ile Tyr Asp Glu Gly Val Asp Glu Trp Asn	
136 141 146 151	
ata gct cgc ctc aat aca gtc ttg gat gtg gtt gaa gaa gag tgt ggc	714
Ile Ala Arg Leu Asn Thr Val Leu Asp Val Val Glu Glu Glu Cys Gly	
152 157 162 167	
att tct att gag ggt gta aat acc cca tat ctc tat ttt ggc atg tgg	762
Ile Ser Ile Glu Gly Val Asn Thr Pro Tyr Leu Tyr Phe Gly Met Trp	
168 173 178 183	
aag acc acg ttt gca tgg cac acc gaa gac atg gac ctc tat agc att	810
Lys Thr Thr Phe Ala Trp His Thr Glu Asp Met Asp Leu Tyr Ser Ile	
184 189 194 199	
aat tat ctc cac ttt gga gag ccc aag tct tgg tat gct ata cct ccg	858
Asn Tyr Leu His Phe Gly Glu Pro Lys Ser Trp Tyr Ala Ile Pro Pro	
200 205 210 215	
gag cat gga aaa cga ctt gaa aga cta gct caa ggt ttt ttc cca agc	906
Glu His Gly Lys Arg Leu Glu Arg Leu Ala Gln Gly Phe Phe Pro Ser	
216 221 226 231	
agc tcc caa ggg tgt gat gca ttt ctt cgc cac aag atg aca ttg att	954
Ser Ser Gln Gly Cys Asp Ala Phe Leu Arg His Lys Met Thr Leu Ile	
232 237 242 247	
tct cca tca gta ttg aag aaa tat ggt att ccc ttt gac aag ata acc	1002
Ser Pro Ser Val Leu Lys Lys Tyr Gly Ile Pro Phe Asp Lys Ile Thr	
248 253 258 263	
cag gag gct gga gaa ttc atg atc act ttc cca tat ggc tac cat gct	1050
Gln Glu Ala Gly Glu Phe Met Ile Thr Phe Pro Tyr Gly Tyr His Ala	
264 269 274 279	
ggt ttt aat cat ggt ttc aac tgt gca gaa tct aca aat ttt gct act	1098
Gly Phe Asn His Gly Phe Asn Cys Ala Glu Ser Thr Asn Phe Ala Thr	
280 285 290 295	
gtc aga tgg att gac tat gga aaa gtt gcc aaa ttg tgc act tgc agg	1146
Val Arg Trp Ile Asp Tyr Gly Lys Val Ala Lys Leu Cys Thr Cys Arg	
296 301 306 311	
aaa gac atg gtg aag att tca atg gat atc ttt gtg agg aaa ttt cag	1194
Lys Asp Met Val Lys Ile Ser Met Asp Ile Phe Val Arg Lys Phe Gln	
312 317 322 327	

cca gac aga tat cag ctt tgg aaa caa gga aag gat ata tac acc att	1242
Pro Asp Arg Tyr Gln Leu Trp Lys Gln Gly Lys Asp Ile Tyr Thr Ile	
328 333 338 343	
gat cac acg aag cct act cca gca tcc acc cct gaa gta aaa gca tgg	1290
Asp His Thr Lys Pro Thr Pro Ala Ser Thr Pro Glu Val Lys Ala Trp	
344 349 354 359	
ctg cag agg agg agg aaa gta aga aaa gca tcc cga agc ttc cag tgt	1338
Leu Gln Arg Arg Arg Lys Val Arg Lys Ala Ser Arg Ser Phe Gln Cys	
360 365 370 375	
gct agg tct acc tct aaa agg cct aag gct gat gag gaa gag gaa gtg	1386
Ala Arg Ser Thr Ser Lys Arg Pro Lys Ala Asp Glu Glu Glu Glu Val	
376 381 386 391	
tca gat gaa gtc gat ggg gca gag gtc cct aac ccc gac tca gtc aca	1434
Ser Asp Glu Val Asp Gly Ala Glu Val Pro Asn Pro Asp Ser Val Thr	
392 397 402 407	
gat gac ctc aag gtc agt gaa aag tca gaa gca gca gtg aag ctg agg	1482
Asp Asp Leu Lys Val Ser Glu Lys Ser Glu Ala Ala Val Lys Leu Arg	
408 413 418 423	
aac aca gaa gca tct tca gaa gaa gag tca tct gct agc agg atg cag	1530
Asn Thr Glu Ala Ser Ser Glu Glu Glu Ser Ser Ala Ser Arg Met Gln	
424 429 434 439	
gtg gag cag aat tta tca gat cat atc aaa ctc tca gga aac agc tgc	1578
Val Glu Gln Asn Leu Ser Asp His Ile Lys Leu Ser Gly Asn Ser Cys	
440 445 450 455	
tta agt aca tct gta aca gaa gac ata aaa act gag gat gac aaa gct	1626
Leu Ser Thr Ser Val Thr Glu Asp Ile Lys Thr Glu Asp Asp Lys Ala	
456 461 466 471	
tat gca tat aga agt gta cct tct ata tcc agt gag gct gat gat tcc	1674
Tyr Ala Tyr Arg Ser Val Pro Ser Ile Ser Ser Glu Ala Asp Asp Ser	
472 477 482 487	
att cca ttg tct act ggc tat gag aag ccc gag aaa tca gac cca tcc	1722
Ile Pro Leu Ser Thr Gly Tyr Glu Lys Pro Glu Lys Ser Asp Pro Ser	
488 493 498 503	
gag ctt tca tgg cca aag tca cct gag tca tgc tca tca gtg gca gag	1770
Glu Leu Ser Trp Pro Lys Ser Pro Glu Ser Cys Ser Ser Val Ala Glu	
504 509 514 519	
agt aat ggt gtg tta aca gag gga gaa gag agt gat gtg gag agc cat	1818
Ser Asn Gly Val Leu Thr Glu Gly Glu Glu Ser Asp Val Glu Ser His	
520 525 530 535	
ggg aat ggc ctt gaa cct ggg gaa atc cca ggc gtc ccc agt gga gag	1866
Gly Asn Gly Leu Glu Pro Gly Glu Ile Pro Ala Val Pro Ser Gly Glu	
536 541 546 551	
aga aat agc ttc aaa gtc ccc agt ata gca gag gga gag aac aaa acc	1914

Arg	Asn	Ser	Phe	Lys	Val	Pro	Ser	Ile	Ala	Glu	Gly	Glu	Asn	Lys	Thr	
552					557					562					567	
tct	aag	agt	tgg	cgc	cat	cca	ctt	agc	agg	cct	cca	gca	aga	tct	ccg	1962
Ser	Lys	Ser	Trp	Arg	His	Pro	Leu	Ser	Arg	Pro	Pro	Ala	Arg	Ser	Pro	
568					573					578					583	
atg	act	ctt	gtg	aag	cag	cag	gcg	cca	agt	gat	gaa	gaa	ttg	cct	gag	2010
Met	Thr	Leu	Val	Lys	Gln	Gln	Ala	Pro	Ser	Asp	Glu	Glu	Leu	Pro	Glu	
584					589					594					599	
gtt	ctg	tcc	att	gag	gag	gaa	gtg	gaa	gaa	aca	gag	tct	tgg	gcg	aaa	2058
Val	Leu	Ser	Ile	Glu	Glu	Glu	Val	Glu	Glu	Thr	Glu	Ser	Trp	Ala	Lys	
600					605					610					615	
cct	ctc	atc	cac	ctt	tgg	cag	acg	aag	tcc	cct	aac	ttc	gca	gct	gag	2106
Pro	Leu	Ile	His	Leu	Trp	Gln	Thr	Lys	Ser	Pro	Asn	Phe	Ala	Ala	Glu	
616					621					626					631	
caa	gag	tat	aat	gca	aca	gtg	gcc	agg	atg	aag	cca	cac	tgt	gcc	atc	2154
Gln	Glu	Tyr	Asn	Ala	Thr	Val	Ala	Arg	Met	Lys	Pro	His	Cys	Ala	Ile	
632					637					642					647	
tgc	act	ctg	ctc	atg	ccg	tac	cac	aag	cca	gat	agc	agc	aat	gaa	gaa	2202
Cys	Thr	Leu	Leu	Met	Pro	Tyr	His	Lys	Pro	Asp	Ser	Ser	Asn	Glu	Glu	
648					653					658					663	
aat	gat	gct	aga	tgg	gag	aca	aaa	tta	gat	gaa	gtc	gtt	aca	tcg	gag	2250
Asn	Asp	Ala	Arg	Trp	Glu	Thr	Lys	Leu	Asp	Glu	Val	Val	Thr	Ser	Glu	
664					669					674					679	
gga	aag	act	aag	ccc	ctc	ata	cca	gag	atg	tgt	ttt	att	tat	agt	gaa	2298
Gly	Lys	Thr	Lys	Pro	Leu	Ile	Pro	Glu	Met	Cys	Phe	Ile	Tyr	Ser	Glu	
680					685					690					695	
gaa	aat	ata	gaa	tat	tct	cca	ccc	aat	gcc	ttc	ctt	gaa	gag	gat	gga	2346
Glu	Asn	Ile	Glu	Tyr	Ser	Pro	Pro	Asn	Ala	Phe	Leu	Glu	Glu	Asp	Gly	
696					701					706					711	
aca	agt	ctc	ctt	att	tcc	tgt	gca	aag	tgc	tgc	gta	cgg	gtt	cat	gca	2394
Thr	Ser	Leu	Leu	Ile	Ser	Cys	Ala	Lys	Cys	Cys	Val	Arg	Val	His	Ala	
712					717					722					727	
agt	tgt	tat	ggt	att	cct	tct	cat	gag	atc	tgt	gat	gga	tgg	ctg	tgt	2442
Ser	Cys	Tyr	Gly	Ile	Pro	Ser	His	Glu	Ile	Cys	Asp	Gly	Trp	Leu	Cys	
728					733					738					743	
gcc	cgg	tgc	aaa	aga	aat	gcg	tgg	aca	gca	gaa	tgc	tgt	ctc	tgc	aat	2490
Ala	Arg	Cys	Lys	Arg	Asn	Ala	Trp	Thr	Ala	Glu	Cys	Cys	Leu	Cys	Asn	
744					749					754					759	
ttg	aga	gga	ggt	gct	ctt	aag	caa	acg	aag	aac	aat	aag	tgg	gcc	cat	2538
Leu	Arg	Gly	Gly	Ala	Leu	Lys	Gln	Thr	Lys	Asn	Asn	Lys	Trp	Ala	His	
760					765					770					775	
gtc	atg	tgc	gcc	gtt	gcg	gtc	cca	gaa	gtt	cga	ttc	act	aat	gtc	cca	2586
Val	Met	Cys	Ala	Val	Ala	Val	Pro	Glu	Val	Arg	Phe	Thr	Asn	Val	Pro	

776	781	786	791	
gaa agg aca caa ata gat gta ggc aga ata cct tta cag agg tta aaa				2634
Glu Arg Thr Gln Ile Asp Val Gly Arg Ile Pro Leu Gln Arg Leu Lys				
792	797	802	807	
ttg aaa tgc atc ttc tgc aga cac cgg gtt aag agg gtc tct gga gcc				2682
Leu Lys Cys Ile Phe Cys Arg His Arg Val Lys Arg Val Ser Gly Ala				
808	813	818	823	
tgc atc cag tgt tcc tac ggt cgc tgc ccg gcc tcc ttc cat gtc act				2730
Cys Ile Gln Cys Ser Tyr Gly Arg Cys Pro Ala Ser Phe His Val Thr				
824	829	834	839	
tgt gcc cat gct gct ggg gta ctg atg gag cct gat gat tgg cct tat				2778
Cys Ala His Ala Ala Gly Val Leu Met Glu Pro Asp Asp Trp Pro Tyr				
840	845	850	855	
gtg gtg aac att aca tgc ttt cga cat aag gtc aac ccc aac gtg aag				2826
Val Val Asn Ile Thr Cys Phe Arg His Lys Val Asn Pro Asn Val Lys				
856	861	866	871	
tcc aag gct tgc gag aag gtc att tcc gtg ggt caa acg gtc atc acg				2874
Ser Lys Ala Cys Glu Lys Val Ile Ser Val Gly Gln Thr Val Ile Thr				
872	877	882	887	
aag cat cgg aac acc cgg tat tac agt tgc aga gtg atg gct gtg aca				2922
Lys His Arg Asn Thr Arg Tyr Tyr Ser Cys Arg Val Met Ala Val Thr				
888	893	898	903	
tcg cag acc ttc tat gag gtc atg ttt gat gat ggc tcc ttt agc aga				2970
Ser Gln Thr Phe Tyr Glu Val Met Phe Asp Asp Gly Ser Phe Ser Arg				
904	909	914	919	
gac aca ttt cct gag gat atc gtg agc cga gac tgt ctg aag ctg ggc				3018
Asp Thr Phe Pro Glu Asp Ile Val Ser Arg Asp Cys Leu Lys Leu Gly				
920	925	930	935	
cca cct gct gag gga gaa gtc gtc caa gtc aag tgg ccc gat ggc aaa				3066
Pro Pro Ala Glu Gly Glu Val Val Gln Val Lys Trp Pro Asp Gly Lys				
936	941	946	951	
ctc tat gga gca aaa tat ttt gga tca aat att gcc cac atg tac cag				3114
Leu Tyr Gly Ala Lys Tyr Phe Gly Ser Asn Ile Ala His Met Tyr Gln				
952	957	962	967	
gtt gag ttt gaa gat gga tcc cag ata gca atg aag aga gag gac atc				3162
Val Glu Phe Glu Asp Gly Ser Gln Ile Ala Met Lys Arg Glu Asp Ile				
968	973	978	983	
tac act tta gat gaa gag tta ccc aag aga gtg aaa gct cga ttt gta				3210
Tyr Thr Leu Asp Glu Glu Leu Pro Lys Arg Val Lys Ala Arg Phe Val				
984	989	994	999	
agt gct ggc aga tgc cac ttg ggg acc tgc caa gtg aat tcc ttg tcc				3258
Ser Ala Gly Arg Cys His Leu Gly Thr Cys Gln Val Asn Ser Leu Ser				
1000	1005	1010	1015	

atg caa ctg act cgc tgc tgc ttc gtg ttc ctg gtg cag ggt agc ctc	168
Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser Leu	
1 5 10 15	
tat ctg gtc atc tgt ggc cag gat gat ggt cct ccc ggc tca gag gac	216
Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser Glu Asp	
17 22 27 32	
cct gag cgt gat gac cac gag ggc cag ccc cgg ccc cgg gtg cct cgg	264
Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg Val Pro Arg	
33 38 43 48	
aag cgg ggc cac atc tca cct aag tcc cgc ccc atg gcc aat tcc act	312
Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met Ala Asn Ser Thr	
49 54 59 64	
ctc cta ggg ctg ctg gcc ccg cct ggg gag gct tgg ggc att ctt ggg	360
Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala Trp Gly Ile Leu Gly	
65 70 75 80	
cag ccc ccc aac cgc ccg aac cac agc ccc cca ccc tca gcc aag gtg	408
Gln Pro Pro Asn Arg Pro Asn His Ser Pro Pro Pro Ser Ala Lys Val	
81 86 91 96	
aag aaa atc ttt ggc tgg ggc gac ttc tac tcc aac atc aag acg gtg	456
Lys Lys Ile Phe Gly Trp Gly Asp Phe Tyr Ser Asn Ile Lys Thr Val	
97 102 107 112	
gcc ctg aac ctg ctc gtc aca ggg aag att gtg gac cat ggc aat ggg	504
Ala Leu Asn Leu Leu Val Thr Gly Lys Ile Val Asp His Gly Asn Gly	
113 118 123 128	
acc ttc agc gtc cac ttc caa cac aat gcc aca ggc cag gga aac atc	552
Thr Phe Ser Val His Phe Gln His Asn Ala Thr Gly Gln Gly Asn Ile	
129 134 139 144	
tcc atc agc ctc gtg ccc ccc agt aaa gct gta gag ttc cac cag gaa	600
Ser Ile Ser Leu Val Pro Pro Ser Lys Ala Val Glu Phe His Gln Glu	
145 150 155 160	
cag cag atc ttc atc gaa gcc aag gcc tcc aaa atc ttc aac tgc cgg	648
Gln Gln Ile Phe Ile Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg	
161 166 171 176	
atg gag tgg gag aag gta gaa cgg ggc cgc cgg acc tcg ctt tgc acc	696
Met Glu Trp Glu Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr	
177 182 187 192	
cac gac cca gcc aag atc tgc tcc cga gac cac gct cag agc tca gcc	744
His Asp Pro Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala	
193 198 203 208	
acc tgg agc tgc tcc cag ccc ttc aaa gtc gtc tgt gtc tac atc gcc	792
Thr Trp Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala	
209 214 219 224	

cttgatcccc tgcggtaccg gtccggaatt cccgggtcga cccacgcgtc cgcacccgct 60
 tccgtcagcc tcactggggc ttccttccgt ctcgctcgga gtttccctct gcgttcgctc 120
 cgcgctgctg gaggtgtcg tccca atg ctc ccc aaa cgg cgg cga gcg cgg 172
 Met Leu Pro Lys Arg Arg Arg Ala Arg
 1 5
 gtc ggg tcc cct agc ggc gat gcc gct tcc tcc acg ccg ccc tcg acg 220
 Val Gly Ser Pro Ser Gly Asp Ala Ala Ser Ser Thr Pro Pro Ser Thr
 10 15 20 25
 cgc ttc ccg gga gtc gcc atc tac ctg gtc gag cct cgc atg ggt cgc 268
 Arg Phe Pro Gly Val Ala Ile Tyr Leu Val Glu Pro Arg Met Gly Arg
 26 31 36 41
 agc cgc cgg gcc ttc ctc aca ggc ctg gcg cgc tcc aaa ggc ttc cgc 316
 Ser Arg Arg Ala Phe Leu Thr Gly Leu Ala Arg Ser Lys Gly Phe Arg
 42 47 52 57
 gtc ctt gac gcc tgc agc tcc gaa gcg aca cat gtt gtg atg gaa gag 364
 Val Leu Asp Ala Cys Ser Ser Glu Ala Thr His Val Val Met Glu Glu
 58 63 68 73
 acc tca gca gag gag gcc gtc agc tgg cag gag cgc agg atg gca gct 412
 Thr Ser Ala Glu Glu Ala Val Ser Trp Gln Glu Arg Arg Met Ala Ala
 74 79 84 89
 gct ccc ccg ggt tgc acc ccc cca gct ctg ctg gac ata agc tgg tta 460
 Ala Pro Pro Gly Cys Thr Pro Pro Ala Leu Leu Asp Ile Ser Trp Leu
 90 95 100 105
 aca gag agc ctg gga gct ggg cag cct gta cct gtg gag tgc cgg cac 508
 Thr Glu Ser Leu Gly Ala Gly Gln Pro Val Pro Val Glu Cys Arg His
 106 111 116 121
 cgc ctg gag gtg gct ggg cca agg aag ggg cct ctg agc cca gca tgg 556
 Arg Leu Glu Val Ala Gly Pro Arg Lys Gly Pro Leu Ser Pro Ala Trp
 122 127 132 137
 atg cct gcc tat gcc tgc cag cgc cct acg ccc ctc aca cac cac aac 604
 Met Pro Ala Tyr Ala Cys Gln Arg Pro Thr Pro Leu Thr His His Asn
 138 143 148 153
 act ggc ctc tcc gag gct ctg gag ata ctg gcc gag gca gca ggc ttt 652
 Thr Gly Leu Ser Glu Ala Leu Glu Ile Leu Ala Glu Ala Ala Gly Phe
 154 159 164 169
 gaa ggc agt gag ggc cgc ctc ctc acc ttc tgc aga gca gcc tcg gtg 700
 Glu Gly Ser Glu Gly Arg Leu Leu Thr Phe Cys Arg Ala Ala Ser Val
 170 175 180 185
 ctc aag gcc ctt ccc agc cct gtc aca acc ctg agc cag ctg cag ggg 748
 Leu Lys Ala Leu Pro Ser Pro Val Thr Thr Leu Ser Gln Leu Gln Gly
 186 191 196 201
 ctt ccc cac ttt gga gaa cac tcc tct agg gtt gtc cag gag ctg ctg 796

Leu Pro His Phe Gly Glu His Ser Ser Arg Val Val Gln Glu Leu Leu	
202 207 212 217	
gag cat gga gtg tgt gag gag gtg gag aga gtt cgg cgc tca gag agg	844
Glu His Gly Val Cys Glu Glu Val Glu Arg Val Arg Arg Ser Glu Arg	
218 223 228 233	
tac cag acc atg aag ctc ttc acc cag atc ttc ggg gtc ggt gtg aag	892
Tyr Gln Thr Met Lys Leu Phe Thr Gln Ile Phe Gly Val Gly Val Lys	
234 239 244 249	
act gct gac cgg tgg tac cgg gaa gga ctg cga acc tta gat gac ctc	940
Thr Ala Asp Arg Trp Tyr Arg Glu Gly Leu Arg Thr Leu Asp Asp Leu	
250 255 260 265	
cga gag cag ccc cag aaa cta acc caa cag cag aaa gcg ggt gag ccc	988
Arg Glu Gln Pro Gln Lys Leu Thr Gln Gln Gln Lys Ala Gly Glu Pro	
266 271 276 281	
tcc aga gag gct ggg ccc tgg gct tcc cta aac tgc acc ctg gat ccc	1036
Ser Arg Glu Ala Gly Pro Trp Ala Ser Leu Asn Cys Thr Leu Asp Pro	
282 287 292 297	
tca gca tca act ccc tag agggaa gggagcagtc tgggtgcagag ggtttggtgg	1090
Ser Ala Ser Thr Pro *	
298 303	
cagctttgtg tgggtgggctt cctgggggtct ccacccagtg cagtcaggat ctatcaaagc	1150
cttttctcag tggacgatgc tgaccacagc aacttccatg atatgccagg ggcttgtgtc	1210
tgccactactgg ttagactttg accagtgacc agggacagcc tgggccttgg gcacactgcc	1270
cagtgtggtg cttggtacat ggaggcctgc agaggtggca ctgagcagca gaaagaacat	1330
cagctttcaa gtttggttagg cctggggttg agtcttatct accatttgcc aggtaggtga	1390
ccattgccca agaaataacc tctctgagtc tgttacattt tctgtaaaat ggagaaggaa	1450
ggctgggcat ggtgactcac acctgtaatc ccagcacttt gggaggtcaa ggtgggtaga	1510
tcgcttgagc tcagcagttc aagaccagtc tgggcaacag ggtgaaacc tgtctctacg	1570
agaaatacaa gagttagcca ggcgtgatgg tggatgcccg tagtaccagc tactcatgag	1630
gccgaggtac aaggatcgct cgagcccggg aggtcaagcc ttgaggccaa ggtggaagtt	1690
gcaatgagct gagattgagc cactgcactc cagcctgagt gacagagcaa gaccctatct	1750
caaaaaaaaaaaa aaa	1763

<210> 383
 <211> 4352
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(3675)

<400> 383

atg gag gat gaa tca att tac acc tgc gat cac tgt cag cag gac ttc	48
Met Glu Asp Glu Ser Ile Tyr Thr Cys Asp His Cys Gln Gln Asp Phe	
1 5 10	
gag tct ctg gca gac ctg acg gac cac cgg gcc cac cgc tgt cct gga	96
Glu Ser Leu Ala Asp Leu Thr Asp His Arg Ala His Arg Cys Pro Gly	
17 22 27 32	
gat ggt gat gac gac cca caa ctc tcc tgg gtg gcc tcg tct ccc tcc	144
Asp Gly Asp Asp Asp Pro Gln Leu Ser Trp Val Ala Ser Ser Pro Ser	
33 38 43 48	
agc aag gat gtt gcg tca ccc acg cag atg atc gga gat ggt tgt gac	192
Ser Lys Asp Val Ala Ser Pro Thr Gln Met Ile Gly Asp Gly Cys Asp	
49 54 59 64	
ctc ggc ctc ggc gag gag gaa ggg ggc acg ggc ctg cca tac cct tgc	240
Leu Gly Leu Gly Glu Glu Glu Gly Gly Thr Gly Leu Pro Tyr Pro Cys	
65 70 75 80	
cag ttc tgc gac aag tcc ttc atc cgc ttg agc tac ttg aag agg cac	288
Gln Phe Cys Asp Lys Ser Phe Ile Arg Leu Ser Tyr Leu Lys Arg His	
81 86 91 96	
gag cag atc cac agc gac aag ctg cgg ttc aag tgc acc tac tgc agc	336
Glu Gln Ile His Ser Asp Lys Leu Pro Phe Lys Cys Thr Tyr Cys Ser	
97 102 107 112	
cgc ctc ttc aag cac aag agg agc cgt gac cgg cac atc aag ctg cat	384
Arg Leu Phe Lys His Lys Arg Ser Arg Asp Arg His Ile Lys Leu His	
113 118 123 128	
acg ggc gac aag aag tat cac tgc cac gag tgc gag gca gcc ttc tcc	432
Thr Gly Asp Lys Lys Tyr His Cys His Glu Cys Glu Ala Ala Phe Ser	
129 134 139 144	
cgc agc gac cac ctc aag atc cac ctg aag acc cac agc tcc agc aag	480
Arg Ser Asp His Leu Lys Ile His Leu Lys Thr His Ser Ser Ser Lys	
145 150 155 160	
ccc ttc aag tgc act gtg tgc aag cgc ggc ttc tcc tcc acc agc tcg	528
Pro Phe Lys Cys Thr Val Cys Lys Arg Gly Phe Ser Ser Thr Ser Ser	
161 166 171 176	
ctg cag agc cac atg cag gcc cac aaa aag aac aag gag cat ctg gcc	576
Leu Gln Ser His Met Gln Ala His Lys Lys Asn Lys Glu His Leu Ala	
177 182 187 192	
aag tcg gag aag gaa gcc aag aag gac gac ttc atg tgc gac tac tgc	624
Lys Ser Glu Lys Glu Ala Lys Lys Asp Asp Phe Met Cys Asp Tyr Cys	

193	198	203	208	
gag gac acc ttc agc	cag acg gag gag ctg	gag aag cac gtg ctc acc		672
Glu Asp Thr Phe Ser	Gln Thr Glu Glu Leu	Glu Lys His Val Leu Thr		
209	214	219	224	
cgc cac ccg cag ctg	tcc gag aag gcg gac	ctg cag tgc att cac tgc		720
Arg His Pro Gln Leu	Ser Glu Lys Ala Asp	Leu Gln Cys Ile His Cys		
225	230	235	240	
cct gag gtc ttc gtc	gac gag aac aca ctg	ctc gcc cat atc cac caa		768
Pro Glu Val Phe Val	Asp Glu Asn Thr Leu	Leu Ala His Ile His Gln		
241	246	251	256	
gcc cac gcc aac cag	aaa cac aag tgc ccc	atg tgc cct gag cag ttc		816
Ala His Ala Asn Gln	Lys His Lys Cys Pro	Met Cys Pro Glu Gln Phe		
257	262	267	272	
tcc tca gtg gaa ggt	gtc tac tgc cac ctg	gac agc cac cgg cag ccc		864
Ser Ser Val Glu Gly	Val Tyr Cys His Leu	Asp Ser His Arg Gln Pro		
273	278	283	288	
gac tcc agc aac cac	agt gtc agt ccc gac	cct gta ctg ggc agc gtg		912
Asp Ser Ser Asn His	Ser Val Ser Pro Asp	Pro Val Leu Gly Ser Val		
289	294	299	304	
gcc tcc atg agc agc	gcc aca ccc gac tcc	agc gcc tct gtg gag cgt		960
Ala Ser Met Ser Ser	Ala Thr Pro Asp Ser	Ser Ala Ser Val Glu Arg		
305	310	315	320	
ggc tcc acc ccg gac	tcc acc ttg aag ccg	ctg cgg ggg cag aag aag		1008
Gly Ser Thr Pro Asp	Ser Thr Leu Lys Pro	Leu Arg Gly Gln Lys Lys		
321	326	331	336	
atg cgg gat gac ggg	cag ggc tgg acc aag	gtg gtc tat agc tgc ccc		1056
Met Arg Asp Asp Gly	Gln Gly Trp Thr Lys	Val Val Tyr Ser Cys Pro		
337	342	347	352	
tat tgt tcc aag cgg	gac ttt aac agc ctg	gcc gtg ctg gag atc cac		1104
Tyr Cys Ser Lys Arg	Asp Phe Asn Ser Leu	Ala Val Leu Glu Ile His		
353	358	363	368	
ctg aag acc atc cac	gcg gac aag ccc cag	cag agc cac aca tgt cag		1152
Leu Lys Thr Ile His	Ala Asp Lys Pro Gln	Gln Ser His Thr Cys Gln		
369	374	379	384	
atc tgc ctg gac tcc	atg ccc acc ctc tac	aac ctc aac gag cac gtt		1200
Ile Cys Leu Asp Ser	Met Pro Thr Leu Tyr	Asn Leu Asn Glu His Val		
385	390	395	400	
cgc aag ctg cac aag	aac cat gcc tac cct	gtg atg cag ttt ggc aac		1248
Arg Lys Leu His Lys	Asn His Ala Tyr Pro	Val Met Gln Phe Gly Asn		
401	406	411	416	
atc tct gcc ttc cac	tgc aac tac tgc ccc	gag atg ttc gcc gac atc		1296
Ile Ser Ala Phe His	Cys Asn Tyr Cys Pro	Glu Met Phe Ala Asp Ile		
417	422	427	432	

aat agc ctg cag gag cac atc cgc gtc tcc cac tgc ggc ccc aac gcc	1344
Asn Ser Leu Gln Glu His Ile Arg Val Ser His Cys Gly Pro Asn Ala	
433 438 443 448	
aac ccc tct gac ggt aat aat gct ttc ttc tgc aac cag tgc tcc atg	1392
Asn Pro Ser Asp Gly Asn Asn Ala Phe Phe Cys Asn Gln Cys Ser Met	
449 454 459 464	
ggt ttc ctt act gag tcc tcc ctc acc gag cac atc cag cag gcc cac	1440
Gly Phe Leu Thr Glu Ser Ser Leu Thr Glu His Ile Gln Gln Ala His	
465 470 475 480	
tgc agt gtg ggc agt gcc aaa cta gag tct ccg gtg gtg cag ccc acg	1488
Cys Ser Val Gly Ser Ala Lys Leu Glu Ser Pro Val Val Gln Pro Thr	
481 486 491 496	
cag tcc ttc atg gag gtc tat tcc tgc ccc tac tgc acc aac tcc ccc	1536
Gln Ser Phe Met Glu Val Tyr Ser Cys Pro Tyr Cys Thr Asn Ser Pro	
497 502 507 512	
atc ttt ggc tcc atc ctg aaa ctc acc aag cac atc aag gag aac cac	1584
Ile Phe Gly Ser Ile Leu Lys Leu Thr Lys His Ile Lys Glu Asn His	
513 518 523 528	
aag aac att cca ctg gcc cac agc aag aag tcc aag gcc gag cag agc	1632
Lys Asn Ile Pro Leu Ala His Ser Lys Lys Ser Lys Ala Glu Gln Ser	
529 534 539 544	
cca gtc tcg tcc gat gtg gag gtg tct tcc ccg aag cgg cag cgg ctc	1680
Pro Val Ser Ser Asp Val Glu Val Ser Ser Pro Lys Arg Gln Arg Leu	
545 550 555 560	
tca gca agc gcc aac tcc atc tcc aat ggg gag tat cct tgc aat caa	1728
Ser Ala Ser Ala Asn Ser Ile Ser Asn Gly Glu Tyr Pro Cys Asn Gln	
561 566 571 576	
tgc gac ctc aag ttc tcc aac ttt gag agc ttc cag acc cac ctg aag	1776
Cys Asp Leu Lys Phe Ser Asn Phe Glu Ser Phe Gln Thr His Leu Lys	
577 582 587 592	
ctg cac ctg gag ctg ctg ctg cgg aag caa gcg tgc ccc cag tgc aaa	1824
Leu His Leu Glu Leu Leu Leu Arg Lys Gln Ala Cys Pro Gln Cys Lys	
593 598 603 608	
gag gac ttt gac tcc cag gag tcc ctc ctg cag cac ctg aca gtg cat	1872
Glu Asp Phe Asp Ser Gln Glu Ser Leu Leu Gln His Leu Thr Val His	
609 614 619 624	
tac atg acc acg tcg acc cac tat gtg tgc gag agc tgc gac aag caa	1920
Tyr Met Thr Thr Ser Thr His Tyr Val Cys Glu Ser Cys Asp Lys Gln	
625 630 635 640	
ttt tcc tcg gtg gat gac ctg cag aag cac ctg ctg gac atg cac acc	1968
Phe Ser Ser Val Asp Asp Leu Gln Lys His Leu Leu Asp Met His Thr	
641 646 651 656	

ttt gtg ttg tac cac tgc acc ctg tgt cag gag gtc ttc gac tcc aag	2016
Phe Val Leu Tyr His Cys Thr Leu Cys Gln Glu Val Phe Asp Ser Lys	
657 662 667 672	
gtg tcc atc cag gtg cac ctg gcg gtg aag cac agc aat gag aag aag	2064
Val Ser Ile Gln Val His Leu Ala Val Lys His Ser Asn Glu Lys Lys	
673 678 683 688	
atg tac cgc tgc acg gcc tgc aac tgg gac ttc cgc aag gag gct gac	2112
Met Tyr Arg Cys Thr Ala Cys Asn Trp Asp Phe Arg Lys Glu Ala Asp	
689 694 699 704	
ctg cag gtg cac gtc aaa cac agc cac ctg ggc aac ccg gcc aag gct	2160
Leu Gln Val His Val Lys His Ser His Leu Gly Asn Pro Ala Lys Ala	
705 710 715 720	
cac aag tgc atc ttc tgt ggg gag acc ttc agc acc gag gtg gag ctg	2208
His Lys Cys Ile Phe Cys Gly Glu Thr Phe Ser Thr Glu Val Glu Leu	
721 726 731 736	
cag tgc cac atc acc aca cac agc aag aag tat aac tgt aag ttc tgc	2256
Gln Cys His Ile Thr Thr His Ser Lys Lys Tyr Asn Cys Lys Phe Cys	
737 742 747 752	
agc aag gcc ttc cac gcc atc atc ctg ctg gag aag cac ctg cgg gag	2304
Ser Lys Ala Phe His Ala Ile Ile Leu Leu Glu Lys His Leu Arg Glu	
753 758 763 768	
aag cac tgt gtg ttt gat gct gcg acc gag aac ggc acg gcc aat ggg	2352
Lys His Cys Val Phe Asp Ala Ala Thr Glu Asn Gly Thr Ala Asn Gly	
769 774 779 784	
gta ccc cca atg gcc acc aag aaa gct gag cct gct gac ctg cag gcc	2400
Val Pro Pro Met Ala Thr Lys Lys Ala Glu Pro Ala Asp Leu Gln Gly	
785 790 795 800	
atg ctg ctt aag aac cct gag gca cct aac agc cat gag gcc agc gag	2448
Met Leu Leu Lys Asn Pro Glu Ala Pro Asn Ser His Glu Ala Ser Glu	
801 806 811 816	
gat gac gtg gac gcg tgc gag ccc atg tac ggc tgt gac atc tgc ggg	2496
Asp Asp Val Asp Ala Ser Glu Pro Met Tyr Gly Cys Asp Ile Cys Gly	
817 822 827 832	
gcg gcc tac acc atg gag gtg ctg ctg cag aat cac cgg ctg cgg gac	2544
Ala Ala Tyr Thr Met Glu Val Leu Leu Gln Asn His Arg Leu Arg Asp	
833 838 843 848	
cac aat atc cgg ccg ggc gag gat gat ggc tca cgc aag aag gct gag	2592
His Asn Ile Arg Pro Gly Glu Asp Asp Gly Ser Arg Lys Lys Ala Glu	
849 854 859 864	
ttt atc aag ggc agt cac aag tgc aac gtt tgt tca cgg act ttc ttc	2640
Phe Ile Lys Gly Ser His Lys Cys Asn Val Cys Ser Arg Thr Phe Phe	
865 870 875 880	
tcg gag aac ggg cta cgg gag cac ctg cag acg cac cgg ggc cct gcc	2688

Ser	Glu	Asn	Gly	Leu	Arg	Glu	His	Leu	Gln	Thr	His	Arg	Gly	Pro	Ala		
881					886					891					896		
aag	cac	tac	atg	tgt	ccc	atc	tgt	ggg	gag	cgc	ttc	cct	tcg	ctg	ctg	2736	
Lys	His	Tyr	Met	Cys	Pro	Ile	Cys	Gly	Glu	Arg	Phe	Pro	Ser	Leu	Leu		
897					902					907					912		
acg	ctc	acc	gaa	cac	aag	gtg	acc	cac	agc	aag	agc	ctg	gac	acg	ggc	2784	
Thr	Leu	Thr	Glu	His	Lys	Val	Thr	His	Ser	Lys	Ser	Leu	Asp	Thr	Gly		
913					918					923					928		
acc	tgt	cgc	atc	tgc	aag	atg	ccc	ctg	cag	agc	gag	gag	gag	ttt	att	2832	
Thr	Cys	Arg	Ile	Cys	Lys	Met	Pro	Leu	Gln	Ser	Glu	Glu	Glu	Phe	Ile		
929					934					939					944		
gag	cac	tgc	cag	atg	cac	cct	gac	ctg	cgc	aac	tca	ctc	acg	ggc	ttc	2880	
Glu	His	Cys	Gln	Met	His	Pro	Asp	Leu	Arg	Asn	Ser	Leu	Thr	Gly	Phe		
945					950					955					960		
cgc	tgt	gtg	gtc	tgc	atg	cag	aca	gtc	act	tcc	acg	ctt	gag	ctc	aag	2928	
Arg	Cys	Val	Val	Cys	Met	Gln	Thr	Val	Thr	Ser	Thr	Leu	Glu	Leu	Lys		
961					966					971					976		
atc	cat	ggc	acc	ttc	cac	atg	cag	aag	ctg	gcg	ggc	agc	tca	gcg	gcg	2976	
Ile	His	Gly	Thr	Phe	His	Met	Gln	Lys	Leu	Ala	Gly	Ser	Ser	Ala	Ala		
977					982					987					992		
tcc	tcc	ccc	aat	ggc	cag	ggg	ctg	cag	aag	ctc	tac	aag	tgc	gcc	ctg	3024	
Ser	Ser	Pro	Asn	Gly	Gln	Gly	Leu	Gln	Lys	Leu	Tyr	Lys	Cys	Ala	Leu		
993					998					1003					1008		
tgc	ctc	aag	gag	ttc	cgc	agc	aag	cag	gac	ctg	gtg	aag	ctt	gac	gtc	3072	
Cys	Leu	Lys	Glu	Phe	Arg	Ser	Lys	Gln	Asp	Leu	Val	Lys	Leu	Asp	Val		
1009					1014					1019					1024		
aat	ggg	ctg	ccc	tac	ggc	ctc	tgc	gcc	ggc	tgc	atg	gcc	cgc	agc	gcc	3120	
Asn	Gly	Leu	Pro	Tyr	Gly	Leu	Cys	Ala	Gly	Cys	Met	Ala	Arg	Ser	Ala		
1025					1030					1035					1040		
aac	gga	cag	gtg	ggg	ggc	ctg	gcc	ccg	ccc	gag	ccc	gcc	gac	cgg	ccc	3168	
Asn	Gly	Gln	Val	Gly	Gly	Leu	Ala	Pro	Pro	Glu	Pro	Ala	Asp	Arg	Pro		
1041					1046					1051					1056		
tgt	gcc	ggc	ctc	cgt	tgc	ccc	gag	tgc	agt	gtc	aag	ttt	gag	agt	gcc	3216	
Cys	Ala	Gly	Leu	Arg	Cys	Pro	Glu	Cys	Ser	Val	Lys	Phe	Glu	Ser	Ala		
1057					1062					1067					1072		
gaa	gac	ctg	gag	agc	cac	atg	cag	gtg	gac	cac	cgt	gac	ctc	acg	ccg	3264	
Glu	Asp	Leu	Glu	Ser	His	Met	Gln	Val	Asp	His	Arg	Asp	Leu	Thr	Pro		
1073					1078					1083					1088		
gag	acc	agt	ggg	ccc	cgg	aaa	ggc	acc	cag	aca	tcg	cca	gtg	ccc	cgg	3312	
Glu	Thr	Ser	Gly	Pro	Arg	Lys	Gly	Thr	Gln	Thr	Ser	Pro	Val	Pro	Arg		
1089					1094					1099					1104		
aaa	aag	aca	tac	cag	tgc	atc	aag	tgc	cag	atg	acc	ttc	gag	aac	gag	3360	
Lys	Lys	Thr	Tyr	Gln	Cys	Ile	Lys	Cys	Gln	Met	Thr	Phe	Glu	Asn	Glu		

1105	1110	1115	1120	
aga gag atc caa atc cac gtt gcc aac cac atg att gag gaa ggc atc				3408
Arg Glu Ile Gln Ile His Val Ala Asn His Met Ile Glu Glu Gly Ile				
1121	1126	1131	1136	
aac cac gag tgt aag ctg tgc aac cag atg ttc gac tcc ccg gcc aag				3456
Asn His Glu Cys Lys Leu Cys Asn Gln Met Phe Asp Ser Pro Ala Lys				
1137	1142	1147	1152	
ctc ctc tgt cac ctc att gag cac agc ttc gag ggc atg ggc ggc acc				3504
Leu Leu Cys His Leu Ile Glu His Ser Phe Glu Gly Met Gly Gly Thr				
1153	1158	1163	1168	
ttc aaa tgc ccc gtg tgt ttc aca gtc ttc gtc cag gcc aac aag ttg				3552
Phe Lys Cys Pro Val Cys Phe Thr Val Phe Val Gln Ala Asn Lys Leu				
1169	1174	1179	1184	
cag cag cac atc ttt gcc gtg cac ggg cag gag gac aag atc tac gac				3600
Gln Gln His Ile Phe Ala Val His Gly Gln Glu Asp Lys Ile Tyr Asp				
1185	1190	1195	1200	
tgc tca cag tgc cct cag aag ttc ttc ttc cag acc gag ctg cag aac				3648
Cys Ser Gln Cys Pro Gln Lys Phe Phe Phe Gln Thr Glu Leu Gln Asn				
1201	1206	1211	1216	
cac acg atg agc cag cac gca cag tga gggat cgctcaacag gacacctctc				3700
His Thr Met Ser Gln His Ala Gln *				
1217	1222			
cgcagaaggc ttgccggaga cgccgtgggg agggccattt gaacattaca tccaatcaaa				3760
gtgtcatttg caaccagat gtaaaactct aatgatttgg ccatgaggcg ctgctattat				3820
aagcagctgg aaatgaatat taatggcaga gattaaaagt attccatgct cagtattttt				3880
tattgtcctg ctacagctag tgtgtcttta gactttccgc cgcagactac atttctagag				3940
ttagagaaac ctgcttttta aggcatttgt cctttgttcc ttcattgtatt atattgatag				4000
tttttaaaaa agaattagtg tgattttttt tctttgtctc ttttttttct ttcttgtttt				4060
tcttcccccc cccccccca ccccttcgg ttaactactt ttaattgca attctaggta				4120
attgtgcac gtgatgtgat tgcttggtta ttgtctgaat atttcctttt aattttttta				4180
ttaaagacta atgctttgat tggatttgcc agttcaccgg acagtgatta aaactatgta				4240
atgaatataa tcggtttcag tgcaactgga tggctctgctt ttaaagtga cttaatctga				4300
ctgcagtaac tagtacagtt caataaaggg aatccatgcg aaaaaaaaaa aa				4352

<210> 384
<211> 2008

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (217)..(1986)

<400> 384

gctgttcgcc tgcggtaccg gtccggaatt cccgggtcga cgatttcgta cgaaatcgta 60

gggaaaaaca aactcgaagt taatcattcc cagctcaaag ccttgtgcaa gtgctctctg 120

ccttcacgct tgcttccttt gggagagaac cttcctcttc ttgatcgggg attcaggaag 180

gagcccagga gcagaggaag tagagagaga gacaac atg tta cat ctg cac cat 234
Met Leu His Leu His His
1

tct tgt ttg tgt ttc agg agc tgg ctg cca gcg atg ctc gct gta ctg 282
Ser Cys Leu Cys Phe Arg Ser Trp Leu Pro Ala Met Leu Ala Val Leu
7 12 17 22

cta agt ttg gca cca tca gct tcc agc gac att tcc gcc tcc cga ccg 330
Leu Ser Leu Ala Pro Ser Ala Ser Ser Asp Ile Ser Ala Ser Arg Pro
23 28 33 38

aac atc ctt ctt ctg atg gcg gac gac ctt ggc att ggg gac att ggc 378
Asn Ile Leu Leu Leu Met Ala Asp Asp Leu Gly Ile Gly Asp Ile Gly
39 44 49 54

tgc tat ggc aac aac acc atg agg act ccg aat att gac cgc ctt gca 426
Cys Tyr Gly Asn Asn Thr Met Arg Thr Pro Asn Ile Asp Arg Leu Ala
55 60 65 70

gag gac ggc gtg aag ctg acc caa cac atc tct gcc gca tct ttg tgc 474
Glu Asp Gly Val Lys Leu Thr Gln His Ile Ser Ala Ala Ser Leu Cys
71 76 81 86

acc cca agc aga gcc gcc ttc ctc acg ggc aga tac cct gtg cga tca 522
Thr Pro Ser Arg Ala Ala Phe Leu Thr Gly Arg Tyr Pro Val Arg Ser
87 92 97 102

ggg atg gtt tcc agc att ggt tac cgt gtt ctt cag tgg acc gga gca 570
Gly Met Val Ser Ser Ile Gly Tyr Arg Val Leu Gln Trp Thr Gly Ala
103 108 113 118

tct gga ggt ctt cca aca aat gag aca act ttt gca aaa ata ctg gaa 618
Ser Gly Gly Leu Pro Thr Asn Glu Thr Thr Phe Ala Lys Ile Leu Glu
119 124 129 134

gag aaa ggc tat gcc act gga ctc att gga aaa tgg cat ctg ggt ctc 666
Glu Lys Gly Tyr Ala Thr Gly Leu Ile Gly Lys Trp His Leu Gly Leu
135 140 145 150

aac tgt gag tca gcc agt gat cat tgc cac cac cct ctc cat cat ggc 714
Asn Cys Glu Ser Ala Ser Asp His Cys His His Pro Leu His His Gly
151 156 161 166

ttt gac cat ttc tac gga atg cct ttc tcc ttg atg ggt gat tgc gcc	762
Phe Asp His Phe Tyr Gly Met Pro Phe Ser Leu Met Gly Asp Cys Ala	
167 172 177 182	
cgc tgg gaa ctc tca gag aag cgt gtc aac ctg gaa caa aaa ctc aac	810
Arg Trp Glu Leu Ser Glu Lys Arg Val Asn Leu Glu Gln Lys Leu Asn	
183 188 193 198	
ttc ctc ttc caa gtc ctg gcc ttg gtt gcc ctc aca ctg gta gca ggg	858
Phe Leu Phe Gln Val Leu Ala Leu Val Ala Leu Thr Leu Val Ala Gly	
199 204 209 214	
aag ctc aca cac ctg ata ccc gtc tcg tgg atg ccg gtc atc tgg tca	906
Lys Leu Thr His Leu Ile Pro Val Ser Trp Met Pro Val Ile Trp Ser	
215 220 225 230	
gcc ctt tcg gcc gtc ctc ctc ctc gca agc tcc tat ttt gtg ggt gct	954
Ala Leu Ser Ala Val Leu Leu Leu Ala Ser Ser Tyr Phe Val Gly Ala	
231 236 241 246	
ctg att gtc cat gcc gat tgc ttt ctg atg aga aac cac acc atc acg	1002
Leu Ile Val His Ala Asp Cys Phe Leu Met Arg Asn His Thr Ile Thr	
247 252 257 262	
gag cag ccc atg tgc ttc caa aga acg aca ccc ctt att ctg cag gag	1050
Glu Gln Pro Met Cys Phe Gln Arg Thr Thr Pro Leu Ile Leu Gln Glu	
263 268 273 278	
gtt gcg tcc ttt ctc aaa agg aat aag cat ggg cct ttc ctc ctc ttt	1098
Val Ala Ser Phe Leu Lys Arg Asn Lys His Gly Pro Phe Leu Leu Phe	
279 284 289 294	
gtt tcc ttt cta cac gtt cac atc cct ctt atc act atg gag aac ttc	1146
Val Ser Phe Leu His Val His Ile Pro Leu Ile Thr Met Glu Asn Phe	
295 300 305 310	
ctc ggg aag agt ctc cac ggg ctg tat ggg gac aac gta aag gag atg	1194
Leu Gly Lys Ser Leu His Gly Leu Tyr Gly Asp Asn Val Lys Glu Met	
311 316 321 326	
gac tgg atg gta gga cgg atc ctt gac act ttg gac gtg gag ggt ttg	1242
Asp Trp Met Val Gly Arg Ile Leu Asp Thr Leu Asp Val Glu Gly Leu	
327 332 337 342	
agc aac agc acc ctc att tat ttt acg tcg gat cac ggc ggt tcc cta	1290
Ser Asn Ser Thr Leu Ile Tyr Phe Thr Ser Asp His Gly Gly Ser Leu	
343 348 353 358	
gag aat caa ctt gga aac acc cag tat ggt ggc tgg aat gga att tat	1338
Glu Asn Gln Leu Gly Asn Thr Gln Tyr Gly Gly Trp Asn Gly Ile Tyr	
359 364 369 374	
aaa ggt ggg aag ggc atg gga gga tgg gaa ggt ggg atc cgc gtg ccc	1386
Lys Gly Gly Lys Gly Met Gly Gly Trp Glu Gly Gly Ile Arg Val Pro	
375 380 385 390	

ggg atc ttc cgc tgg ccc ggg gtg ctc ccg gcc ggc cga gtg att ggc	1434
Gly Ile Phe Arg Trp Pro Gly Val Leu Pro Ala Gly Arg Val Ile Gly	
391 396 401 406	
gag ccc acg agt ctg atg gac gtg ttc ccc acc gtg ggc cgg ctg gcg	1482
Glu Pro Thr Ser Leu Met Asp Val Phe Pro Thr Val Gly Arg Leu Ala	
407 412 417 422	
ggc agc gag gtg ccc cag gac aga gtg att gac ggc caa gac ctt ctg	1530
Gly Ser Glu Val Pro Gln Asp Arg Val Ile Asp Gly Gln Asp Leu Leu	
423 428 433 438	
ccc ttg ctc ctg ggg aca gcc caa cac tca gac cac gag ttc ctg atg	1578
Pro Leu Leu Leu Gly Thr Ala Gln His Ser Asp His Glu Phe Leu Met	
439 444 449 454	
cat tat tgt gag agg ttt ctg cac gca gcc agg tgg cat caa cgg gac	1626
His Tyr Cys Glu Arg Phe Leu His Ala Ala Arg Trp His Gln Arg Asp	
455 460 465 470	
aga gga aca atg tgg aaa gtc cac ttt gtg acg cct gtg ttc cag cca	1674
Arg Gly Thr Met Trp Lys Val His Phe Val Thr Pro Val Phe Gln Pro	
471 476 481 486	
gag gga gcc ggt gcc tgc tat gga aga aag gtc tgc ccg tgc ttt ggg	1722
Glu Gly Ala Gly Ala Cys Tyr Gly Arg Lys Val Cys Pro Cys Phe Gly	
487 492 497 502	
gaa aaa gta gtc cac cac gat cca cct ttg ctc ttt gac ctc tca aga	1770
Glu Lys Val Val His His Asp Pro Pro Leu Leu Phe Asp Leu Ser Arg	
503 508 513 518	
gac cct tct gag acc cac atc ctc aca cca gcc tca gag ccc gtg ttc	1818
Asp Pro Ser Glu Thr His Ile Leu Thr Pro Ala Ser Glu Pro Val Phe	
519 524 529 534	
tat cag gtg atg gaa cga gtc cag cag gcg gtg tgg gaa cac cag cgg	1866
Tyr Gln Val Met Glu Arg Val Gln Gln Ala Val Trp Glu His Gln Arg	
535 540 545 550	
aca ctc agc cca gtt cct ctg cag ctg gac agg ctg ggc aac atc tgg	1914
Thr Leu Ser Pro Val Pro Leu Gln Leu Asp Arg Leu Gly Asn Ile Trp	
551 556 561 566	
aga ccg tgg ctg cag ccc tgc tgt ggc ccg ttc ccc ctc tgc tgg tgc	1962
Arg Pro Trp Leu Gln Pro Cys Cys Gly Pro Phe Pro Leu Cys Trp Cys	
567 572 577 582	
ctt agg gaa gat gac cca caa taa atgtctgcag tgaaaaaaaa aa	2008
Leu Arg Glu Asp Asp Pro Gln *	
583 588	

<210> 385

<211> 1325
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (117)..(1325)

<400> 385

```

tcgacgattt cgtaagggag agagagaggg ggactctgtg tgaggggaaag aaaacaatgt      60

ctcctgctct gcagcttctg ttcaggatca atgtgactct aagaacaaat ggatga      116
atg aat atc cat atg aag aga aaa aca ata aag aat atc aac acc ttt      164
Met Asn Ile His Met Lys Arg Lys Thr Ile Lys Asn Ile Asn Thr Phe
  1             5             10             15

gag aac aga atg tta atg ctt gat ggg atg ccg gca gtc aga gtc aaa      212
Glu Asn Arg Met Leu Met Leu Asp Gly Met Pro Ala Val Arg Val Lys
 17             22             27             32

aca gag ctt ttg gaa tct gaa caa ggg tct cca aac gtc cac aac tat      260
Thr Glu Leu Leu Glu Ser Glu Gln Gly Ser Pro Asn Val His Asn Tyr
 33             38             43             48

ccc gat atg gaa gcc gtt ccc ctg ttg cta aat aat gtg aaa ggg gag      308
Pro Asp Met Glu Ala Val Pro Leu Leu Leu Asn Asn Val Lys Gly Glu
 49             54             59             64

ccc ccg gag gac tcg tta tct gta gat cac ttc caa aca caa act gag      356
Pro Pro Glu Asp Ser Leu Ser Val Asp His Phe Gln Thr Gln Thr Glu
 65             70             75             80

cca gtg gac ttg tca ata aac aaa gcc agg acg tcc cct act gcc gtt      404
Pro Val Asp Leu Ser Ile Asn Lys Ala Arg Thr Ser Pro Thr Ala Val
 81             86             91             96

tca tcc tcc cca gtt tcc atg aca gca tct gcc tcc tca cct tct tca      452
Ser Ser Ser Pro Val Ser Met Thr Ala Ser Ala Ser Ser Pro Ser Ser
 97             102            107            112

act tca acc tct tca tcg tct tct agt cgt cta gcc tca tcc cca act      500
Thr Ser Thr Ser Ser Ser Ser Ser Ser Arg Leu Ala Ser Ser Pro Thr
113             118            123            128

gtt atc aca tca gta tct tca gcg tca tct tcg tca aca gta tta act      548
Val Ile Thr Ser Val Ser Ser Ala Ser Ser Ser Ser Thr Val Leu Thr
129             134            139            144

cca ggg ccc ctt gtg gcc tct gca tct ggt gtt gga ggc cag cag ttt      596
Pro Gly Pro Leu Val Ala Ser Ala Ser Gly Val Gly Gly Gln Gln Phe
145             150            155            160

ttg cac att atc cat ccc gta ccg cct tca agt ccc atg aat tta cag      644
Leu His Ile Ile His Pro Val Pro Pro Ser Ser Pro Met Asn Leu Gln
161             166            171            176

tct aac aaa ctg agt cat gtt cac cgc atc ccc gtg gtg gta cag tcg      692

```


Ser Asn Lys Leu Ser His Val His Arg Ile Pro Val Val Val Gln Ser	
177 182 187 192	
gtg cct gtt gtc tac aca gct gta agg tca cct gga aat gtg aac aac	740
Val Pro Val Val Tyr Thr Ala Val Arg Ser Pro Gly Asn Val Asn Asn	
193 198 203 208	
act att gtc gtg ccg ctt ttg gag gat ggg aga ggc cat ggc aaa gca	788
Thr Ile Val Val Pro Leu Leu Glu Asp Gly Arg Gly His Gly Lys Ala	
209 214 219 224	
caa atg gac ccc cga ggc cta tct ccc aga caa agt aaa agt gac agt	836
Gln Met Asp Pro Arg Gly Leu Ser Pro Arg Gln Ser Lys Ser Asp Ser	
225 230 235 240	
gat gat gat gac ctg cca aat gtg acc tta gat agc gtt aat gaa act	884
Asp Asp Asp Asp Leu Pro Asn Val Thr Leu Asp Ser Val Asn Glu Thr	
241 246 251 256	
gga tct acg gcc ctt tcc ata gcc aga gca gta caa gag gta cat ccg	932
Gly Ser Thr Ala Leu Ser Ile Ala Arg Ala Val Gln Glu Val His Pro	
257 262 267 272	
tcc cca gta tca agg gtc cgg ggc aat cga atg aat aat caa aag ttt	980
Ser Pro Val Ser Arg Val Arg Gly Asn Arg Met Asn Asn Gln Lys Phe	
273 278 283 288	
cct tgt tca att tca cca ttt agt att gag agc aca aga cgc cag aga	1028
Pro Cys Ser Ile Ser Pro Phe Ser Ile Glu Ser Thr Arg Arg Gln Arg	
289 294 299 304	
cgg tct gaa tcc cca gac tcc aga aaa cgg cgt atc cac aga tgt gat	1076
Arg Ser Glu Ser Pro Asp Ser Arg Lys Arg Arg Ile His Arg Cys Asp	
305 310 315 320	
ttt gag gga tgc aac aaa gtg tac aca aaa agt tct cac ctg aag gct	1124
Phe Glu Gly Cys Asn Lys Val Tyr Thr Lys Ser Ser His Leu Lys Ala	
321 326 331 336	
cac cgg agg aca cat aca gga gag aaa cct tac aag tgt acc tgg gaa	1172
His Arg Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Thr Trp Glu	
337 342 347 352	
ggc tgc acc tgg aag ttc gct cgt tca gat gaa ctg acg agg cat tac	1220
Gly Cys Thr Trp Lys Phe Ala Arg Ser Asp Glu Leu Thr Arg His Tyr	
353 358 363 368	
cgc aaa cat acg gga gtg aag cca ttc aag tgc gcg gac tgt gat cgc	1268
Arg Lys His Thr Gly Val Lys Pro Phe Lys Cys Ala Asp Cys Asp Arg	
369 374 379 384	
agc ttt tcc cgg tca gat cat ttg gcc ctg cac cgc cgg agg cat atg	1316
Ser Phe Ser Arg Ser Asp His Leu Ala Leu His Arg Arg Arg His Met	
385 390 395 400	
ttg gtg tga	1325
Leu Val *	

<210> 386
 <211> 1428
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (131)..(1132)

<400> 386

```

atgaggcctg acgcactgtc gaccggaccg gaattcccg gacgagccac gcgtgcgctt      60
gcaactccac ctcagcaggg gtctctcagt cctctcaaag caaggaaaga gtactgtgtg      120
ctgagagacc  atg gca aag aat ggt cca gag aat tgt gaa gac tgt cac      169
              Met Ala Lys Asn Gly Pro Glu Asn Cys Glu Asp Cys His
              1          5          10

att cta aat gca gaa gct ttt aaa tcc aag aaa ata tgt aaa tca ctt      217
Ile Leu Asn Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu
  14          19          24          29

aag att tgt gga ctg gtg ttt ggt atc ctg gcc cta act cta att gtc      265
Lys Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val
  30          35          40          45

ctg ttt tgg ggg agc aag cac ttc tgg ccg gag gta ccc aaa aaa gcc      313
Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys Ala
  46          51          56          61

tat gac atg gag cac act ttc tac agc aat gga gag aag aag aag att      361
Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys Lys Ile
  62          67          72          77

tac atg gaa att gat cct gtg acc aga act gaa ata ttc aga agc gga      409
Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe Arg Ser Gly
  78          83          88          93

aat ggc act gat gaa aca ttg gaa gta cac gac ttt aaa aac gga tac      457
Asn Gly Thr Asp Glu Thr Leu Glu Val His Asp Phe Lys Asn Gly Tyr
  94          99          104          109

act ggc atc tac ttc gtg ggt ctt caa aaa tgt ttt atc aaa act cag      505
Thr Gly Ile Tyr Phe Val Gly Leu Gln Lys Cys Phe Ile Lys Thr Gln
  110          115          120          125

att aaa gtg att cct gaa ttt tct gaa cca gaa gag gaa ata gat gag      553
Ile Lys Val Ile Pro Glu Phe Ser Glu Pro Glu Glu Glu Ile Asp Glu
  126          131          136          141

aat gaa gaa att acc aca act ttc ttt gaa cag tca gtg att tgg gtc      601

```

Asn Glu Glu Ile Thr Thr Thr Phe Phe Glu Gln Ser Val Ile Trp Val	
142 147 152 157	
cca gca gaa aag cct att gaa aac cga gat ttt ctt aaa aat tcc aaa	649
Pro Ala Glu Lys Pro Ile Glu Asn Arg Asp Phe Leu Lys Asn Ser Lys	
158 163 168 173	
att ctg gag att tgt gat aac gtg acc atg tat tgg atc aat ccc act	697
Ile Leu Glu Ile Cys Asp Asn Val Thr Met Tyr Trp Ile Asn Pro Thr	
174 179 184 189	
cta ata tca gga aca ttt gca aag cag ttg cat cac aac ttt gca ttt	745
Leu Ile Ser Gly Thr Phe Ala Lys Gln Leu His His Asn Phe Ala Phe	
190 195 200 205	
att atc tta gtt tct gag tta caa gac ttt gag gag gag gga gaa gat	793
Ile Ile Leu Val Ser Glu Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp	
206 211 216 221	
ctt cac ttt cct gcc aac gaa aaa aaa ggg att gaa caa aat gaa cag	841
Leu His Phe Pro Ala Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln	
222 227 232 237	
tgg gtg gtc cct caa gtg aaa gta gag aag acc cgt cac gcc aga caa	889
Trp Val Val Pro Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln	
238 243 248 253	
gca agt gag gaa gaa ctt cca ata aat gac tat act gaa aat gga ata	937
Ala Ser Glu Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile	
254 259 264 269	
gaa ttt gat ccc atg ctg gat gag aga ggt tat tgt tgt att tac tgc	985
Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys	
270 275 280 285	
cgt cga ggc aac cgc tat tgc cgc cgc gtc tgt gaa cct tta cta ggc	1033
Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly	
286 291 296 301	
tac tac cca tat cca tac tgc tac caa gga gga cga gtc atc tgt cgt	1081
Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys Arg	
302 307 312 317	
gtc atc atg cct tgt aac tgg tgg gtg gcc cgc atg ctg ggg agg gtc	1129
Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg Val	
318 323 328 333	
taa tagg aggtttgagc tcaaatgctt aaactgctgg caacatataa taaatgcatg	1186
* 334	
ctattcaatg aatttctgcc tatgaggcat ctggcccctg gtagccagct ctccagaatt	1246
acttgtaggt aattcctctc ttcattgttct aataaacttc tacattatca ccaacagcct	1306
gattgctgct gaacacactg ggtaagtgtt tgctgagaat attcacagca actgaaatgg	1366

agcagacccg tcaaacatag atgactatgc tgaggctcag aaaacaatgc cccaaaatga 1426

aa 1428

<210> 387

<211> 1380

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (131)..(1084)

<400> 387

atgaggcctg acgcactgtc gaccggaccg gaattcccg gacgagccac gcgtgcgctt 60

gcaactccac ctcagcaggg gtctctcagt cctctcaaag caaggaaaga gtactgtgtg 120

ctgagagacc atg gca aag aat ggt cca gag aat tgt gaa gac tgt cac 169
Met Ala Lys Asn Gly Pro Glu Asn Cys Glu Asp Cys His
1 5 10

att cta aat gca gaa gct ttt aaa tcc aag aaa ata tgt aaa tca ctt 217
Ile Leu Asn Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu
14 19 24 29

aag att tgt gga ctg gtg ttt ggt atc ctg gcc cta act cta att gtc 265
Lys Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val
30 35 40 45

ctg ttt tgg ggg agc aag cac ttc tgg ccg gag gta ccc aaa aaa gcc 313
Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys Ala
46 51 56 61

tat gac atg gag cac act ttc tac agc aat gga gag aag aag aag att 361
Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys Lys Ile
62 67 72 77

tac atg gaa att gat cct gtg acc aga act gaa ata ttc aga agc gga 409
Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe Arg Ser Gly
78 83 88 93

aat ggc act gat gaa aca ttg gaa gta cac gac ttt aaa aac gga tac 457
Asn Gly Thr Asp Glu Thr Leu Glu Val His Asp Phe Lys Asn Gly Tyr
94 99 104 109

act ggc atc tac ttc gtg ggt ctt caa aaa tgt ttt atc aaa act cag 505
Thr Gly Ile Tyr Phe Val Gly Leu Gln Lys Cys Phe Ile Lys Thr Gln
110 115 120 125

att aaa gtg att cct gaa ttt tct gaa cca gaa gag gaa ata gat gag 553
Ile Lys Val Ile Pro Glu Phe Ser Glu Pro Glu Glu Glu Ile Asp Glu
126 131 136 141

aat gaa gaa att acc aca act ttc ttt gaa cag tca gtg att tgg gtc	601
Asn Glu Glu Ile Thr Thr Thr Phe Phe Glu Gln Ser Val Ile Trp Val	
142 147 152 157	
cca gca gaa aag cct att gaa aac cga gat ttt ctt aaa aat tcc aaa	649
Pro Ala Glu Lys Pro Ile Glu Asn Arg Asp Phe Leu Lys Asn Ser Lys	
158 163 168 173	
att ctg gag att tgt gat aac gtg acc atg tat tgg atc aat ccc act	697
Ile Leu Glu Ile Cys Asp Asn Val Thr Met Tyr Trp Ile Asn Pro Thr	
174 179 184 189	
cta ata tca gtt tct gag tta caa gac ttt gag gag gag gga gaa gat	745
Leu Ile Ser Val Ser Glu Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp	
190 195 200 205	
ctt cac ttt cct gcc aac gaa aaa aaa ggg att gaa caa aat gaa cag	793
Leu His Phe Pro Ala Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln	
206 211 216 221	
tgg gtg gtc cct caa gtg aaa gta gag aag acc cgt cac gcc aga caa	841
Trp Val Val Pro Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln	
222 227 232 237	
gca agt gag gaa gaa ctt cca ata aat gac tat act gaa aat gga ata	889
Ala Ser Glu Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile	
238 243 248 253	
gaa ttt gat ccc atg ctg gat gag aga ggt tat tgt tgt att tac tgc	937
Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys	
254 259 264 269	
cgt cga ggc aac cgc tat tgc cgc cgc gtc tgt gaa cct tta cta ggc	985
Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly	
270 275 280 285	
tac tac cca tat cca tac tgc tac caa gga gga cga gtc atc tgt cgt	1033
Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys Arg	
286 291 296 301	
gtc atc atg cct tgt aac tgg tgg gtg gcc cgc atg ctg ggg agg gtc	1081
Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg Val	
302 307 312 317	
taa tagg aggtttgagc tcaaattgctt aaactgctgg caacatataa taaatgcatg	1138
*	
318	
ctattcaatg aatttctgcc tatgaggcat ctggcccttg gtagccagct ctccagaatt	1198
acttgtaggt aattcctctc ttcatgttct aataaaacttc tacattatca ccaacagcct	1258
gattgctgct gaacacactg ggtaagtgtt tgctgagaat attcacagca actgaaatgg	1318
agcagaccog tcaaacatag atgactatgc tgaggctcag aaaacaatgc cccaaatga	1378
aa	1380

<210> 388
 <211> 1239
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (332) .. (937)

<400> 388

```

ggcacgagct ggggttggggc tgaggaaggc ctatgcgcgg aggggtgcggc cttcggtga      60
ggcagaggac cagggttggg tccgtggcgg cgggaggggt ggcctcctgc gctggtcgcc      120
ccaggggacc tgagaggcgc gacaaacagt cggcgcgttt ggtactcgcg cctgcagagc      180
tttcaacctc cgcgccggct gcgctgttt ctcggccagg ggagcaaggc cacgcggcct      240
agcgcagccg agtcggaacc aaccggttgt ttggtgaaac ctaccccaga gcctcccgcg      300
gccacagag cacagactgt ttttgccaac c   atg_gca tct gga gat gac agt      352
                                   Met Ala Ser Gly Asp Asp Ser
                                   1               5

cct atc ttt gaa gat gat gag agc cct cct tac agc cta gaa aaa atg      400
Pro Ile Phe Glu Asp Asp Glu Ser Pro Pro Tyr Ser Leu Glu Lys Met
   8               13               18               23

aca gat ctc gta gct gtt tgg gat gtt gct tta agt gac gga gtc cac      448
Thr Asp Leu Val Ala Val Trp Asp Val Ala Leu Ser Asp Gly Val His
  24               29               34               39

aag atc gaa ttt gaa cat ggg act aca tca ggc aaa cga gta gta tat      496
Lys Ile Glu Phe Glu His Gly Thr Thr Ser Gly Lys Arg Val Val Tyr
  40               45               50               55

gta gat gga aag gaa gag ata aga aaa gag tgg atg ttc aaa tta gtg      544
Val Asp Gly Lys Glu Glu Ile Arg Lys Glu Trp Met Phe Lys Leu Val
  56               61               66               71

ggc aaa gaa aca ttc tat gtt gga gct gca aag aca aaa gcg acc ata      592
Gly Lys Glu Thr Phe Tyr Val Gly Ala Ala Lys Thr Lys Ala Thr Ile
  72               77               82               87

aat ata gac gct atc agt ggt ttt gct tat gaa tat act ctg gaa att      640
Asn Ile Asp Ala Ile Ser Gly Phe Ala Tyr Glu Tyr Thr Leu Glu Ile
  88               93               98              103

aat ggg aaa agt ctc aag aag tat atg gag gac aga tca aaa acc acc      688
Asn Gly Lys Ser Leu Lys Lys Tyr Met Glu Asp Arg Ser Lys Thr Thr
 104               109               114              119

aat act tgg gta tta cac atg gat ggt gag aac ttt aga att gtt ttg      736

```

[illegible]

```
<220>
<221> CDS
<222> (25) .. (1197)
```

1406

gcg acc ggg gcg gag gag gag gcg ccc tgg gcg gcg acg gag cgg cga	195
Ala Thr Gly Ala Glu Glu Glu Ala Pro Trp Ala Ala Thr Glu Arg Arg	
42 47 52 57	
atg ccg ggc cag tgc tcc gtg ctg ctc ttc ccg ggc cag ggc agc cag	243
Met Pro Gly Gln Cys Ser Val Leu Leu Phe Pro Gly Gln Gly Ser Gln	
58 63 68 73	
gtg gtg ggc atg ggc cgc ggt ctg ctc aac tac ccg cgc gtc cgc gaa	291
Val Val Gly Met Gly Arg Gly Leu Leu Asn Tyr Pro Arg Val Arg Glu	
74 79 84 89	
ctc tac gcc gcc gcc cgc cgc gtg ctg ggc tac gac ctg ctg gaa ctg	339
Leu Tyr Ala Ala Ala Arg Arg Val Leu Gly Tyr Asp Leu Leu Glu Leu	
90 95 100 105	
agc ctg cac ggg ccg cag gag acc ctg gac cgc acc gtg cac tgt cag	387
Ser Leu His Gly Pro Gln Glu Thr Leu Asp Arg Thr Val His Cys Gln	
106 111 116 121	
ccc gcg atc ttc gtg gca tcc ctg gcc gct gtc gag aaa cta cat cac	435
Pro Ala Ile Phe Val Ala Ser Leu Ala Ala Val Glu Lys Leu His His	
122 127 132 137	
ctg cag ccc tcc gtg att gag aac tgt gtt gct gct gct gga ttc agt	483
Leu Gln Pro Ser Val Ile Glu Asn Cys Val Ala Ala Ala Gly Phe Ser	
138 143 148 153	
gtg gga gag ttt gca gcc cta gtg ttt gcc gga gcc atg gaa ttt gct	531
Val Gly Glu Phe Ala Ala Leu Val Phe Ala Gly Ala Met Glu Phe Ala	
154 159 164 169	
gaa ggt ttg tat gca gtg aaa atc cga gct gag gcc atg cag gaa gct	579
Glu Gly Leu Tyr Ala Val Lys Ile Arg Ala Glu Ala Met Gln Glu Ala	
170 175 180 185	
tca gaa gct gtc ccc agt ggg atg ctg tct gtc ctc ggc cag cct cag	627
Ser Glu Ala Val Pro Ser Gly Met Leu Ser Val Leu Gly Gln Pro Gln	
186 191 196 201	
tcc aag ttc aac ttc gcc tgt ttg gaa gcc ccg gaa cac tgc aag tct	675
Ser Lys Phe Asn Phe Ala Cys Leu Glu Ala Arg Glu His Cys Lys Ser	
202 207 212 217	
tta ggc ata gag aac ccc gta tgt gaa gtg tcc aac tac ctc ttt cca	723
Leu Gly Ile Glu Asn Pro Val Cys Glu Val Ser Asn Tyr Leu Phe Pro	
218 223 228 233	
gat tgc agg gtg att tca gga cac caa gag gct cta ccg ttt ctc cag	771
Asp Cys Arg Val Ile Ser Gly His Gln Glu Ala Leu Arg Phe Leu Gln	
234 239 244 249	
aag aat tcc tct aag ttt cat ttc aga cgc acc agg atg ttg ccg gtt	819
Lys Asn Ser Ser Lys Phe His Phe Arg Arg Thr Arg Met Leu Pro Val	
250 255 260 265	

agt ggc gca ttc cac acc cgc ctc atg gag cca gcc gtg gag ccc ctg	867
Ser Gly Ala Phe His Thr Arg Leu Met Glu Pro Ala Val Glu Pro Leu	
266 271 276 281	
acg caa gct tta aag gca gtc gac att aag aag cct ctg gtt tct gtc	915
Thr Gln Ala Leu Lys Ala Val Asp Ile Lys Lys Pro Leu Val Ser Val	
282 287 292 297	
tac tcc aac gtc cac gcg cat aga tac agg cat ccc ggg cac atc cac	963
Tyr Ser Asn Val His Ala His Arg Tyr Arg His Pro Gly His Ile His	
298 303 308 313	
aag ctg ctg gcc cag cag ctg gtc tcc cca gtg aag tgg gag cag acg	1011
Lys Leu Leu Ala Gln Gln Leu Val Ser Pro Val Lys Trp Glu Gln Thr	
314 319 324 329	
atg cat gcc ata tac gaa agg aaa aag ggc agg ggg ttc ccc caa act	1059
Met His Ala Ile Tyr Glu Arg Lys Lys Gly Arg Gly Phe Pro Gln Thr	
330 335 340 345	
ttc gaa gta ggc cct ggc agg cag ctg gga gcc atc ctg aag agc tgt	1107
Phe Glu Val Gly Pro Gly Arg Gln Leu Gly Ala Ile Leu Lys Ser Cys	
346 351 356 361	
aac atg cag gcc tgg aag tcc tac agc gcc gtg gat gtg ctg cag acc	1155
Asn Met Gln Ala Trp Lys Ser Tyr Ser Ala Val Asp Val Leu Gln Thr	
362 367 372 377	
ctc gaa cat gtg gac ctg gac cct cag gag ccc ccg aga tga ctgcagg	1204
Leu Glu His Val Asp Leu Asp Pro Gln Glu Pro Pro Arg *	
378 383 388	
gggctcaaat gcgatgaccc cctctgtcct cctgaggaga ggctgtaggc tgtgcctgtc	1264
gccccctacc ttctaatgg ctccctcctct gaggagtgaaggaggatttgt ttgcaacgtg	1324
ctttgaaggc cacataaaaa gccctaaaaa tgagtatttc ttacatgac ccagtccatt	1384
tctccccctt ggaaaaacgt ttggacgttg ggaagaatga tgccacaggc ctggtgtgtg	1444
gggaagctag aatcctggcc ccgcctctgc cagccctgca ccataggcag gtgtgccatc	1504
tcagcgggaa ggggaggact ggctgctgca gcctgtcctg ctctgtgagt gctgagaaca	1564
tgctggtgtg gcctcaattt cagccagtgc caggggagcc cctccaccac cccagcctg	1624
ccccccaggc ctccctttgtc acaaattctga aagggttttag aacccaaaaa aaaaaaaaa	1682

<210> 390
 <211> 4103
 <212> DNA
 <213> Homo sapiens

 <220>

<221> CDS

<222> (104)..(3493)

<400> 390

gttccggaat tccccgggtcg acgatttcgt ccgaagcgcg ggaagcagct cttgtggatc 60

ctcagtggcg gtggctcggc caccgggata ggtaaaggaa aac atg cct gcc aca 115
Met Pro Ala Thr
1

cgg aag cca atg aga tat ggg cat aca gag gga cac acg gag gtc tgt 163
Arg Lys Pro Met Arg Tyr Gly His Thr Glu Gly His Thr Glu Val Cys
5 10 15 20

ttt gat gat tct ggg agt ttt att gtg act tgt gga agt gat ggt gat 211
Phe Asp Asp Ser Gly Ser Phe Ile Val Thr Cys Gly Ser Asp Gly Asp
21 26 31 36

gtg agg att tgg gaa gac ttg gat gat gat gat cct aag ttc att aat 259
Val Arg Ile Trp Glu Asp Leu Asp Asp Asp Asp Pro Lys Phe Ile Asn
37 42 47 52

gtt gga gaa aag gca tat tca tgt gct ttg aag agt gga aaa ctg gtc 307
Val Gly Glu Lys Ala Tyr Ser Cys Ala Leu Lys Ser Gly Lys Leu Val
53 58 63 68

act gca gtt tct aat aat act att caa gtc cac aca ttt cct gaa gga 355
Thr Ala Val Ser Asn Asn Thr Ile Gln Val His Thr Phe Pro Glu Gly
69 74 79 84

gtt cca gat ggt ata ttg act cgc ttc act aca aat gca aac cat gtg 403
Val Pro Asp Gly Ile Leu Thr Arg Phe Thr Thr Asn Ala Asn His Val
85 90 95 100

gtc ttt aat ggg gat ggt act aaa att gct gct gga tct agt gat ttt 451
Val Phe Asn Gly Asp Gly Thr Lys Ile Ala Ala Gly Ser Ser Asp Phe
101 106 111 116

cta gtc aaa att gtg gat gtg atg gat agc agc caa cag aaa aca ttt 499
Leu Val Lys Ile Val Asp Val Met Asp Ser Ser Gln Gln Lys Thr Phe
117 122 127 132

cga gga cat gat gcc cct gtt tta agt ctt tcc ttt gat cct aag gac 547
Arg Gly His Asp Ala Pro Val Leu Ser Leu Ser Phe Asp Pro Lys Asp
133 138 143 148

atc ttt ctg gca tca gct agt tgt gat gga tct gtc aga gtg tgg caa 595
Ile Phe Leu Ala Ser Ala Ser Cys Asp Gly Ser Val Arg Val Trp Gln
149 154 159 164

att tca gat cag aca tgt gct att agt tgg cca ctg cta caa aaa tgc 643
Ile Ser Asp Gln Thr Cys Ala Ile Ser Trp Pro Leu Leu Gln Lys Cys
165 170 175 180

aac gat gtg ata aat gca aaa tca atc tgc aga ctt gct tgg cag cca 691
Asn Asp Val Ile Asn Ala Lys Ser Ile Cys Arg Leu Ala Trp Gln Pro
181 186 191 196

aaa agt ggg aag tta ctg gca att cct gtg gaa aaa tct gtt aag cta	739
Lys Ser Gly Lys Leu Leu Ala Ile Pro Val Glu Lys Ser Val Lys Leu	
197 202 207 212	
tat aga aga gaa tct tgg agt cat caa ttt gat ctt tca gat aat ttc	787
Tyr Arg Arg Glu Ser Trp Ser His Gln Phe Asp Leu Ser Asp Asn Phe	
213 218 223 228	
atc tct cag acc ctc aat ata gta acc tgg tct ccc tgt ggg caa tat	835
Ile Ser Gln Thr Leu Asn Ile Val Thr Trp Ser Pro Cys Gly Gln Tyr	
229 234 239 244	
tta gct gca ggt agt att aat ggt cta atc ata gtt tgg aat gtg gaa	883
Leu Ala Ala Gly Ser Ile Asn Gly Leu Ile Ile Val Trp Asn Val Glu	
245 250 255 260	
acc aaa gac tgc atg gaa agg gtg aaa cat gag aaa ggt tat gca att	931
Thr Lys Asp Cys Met Glu Arg Val Lys His Glu Lys Gly Tyr Ala Ile	
261 266 271 276	
tgt ggt ctg gca tgg cat cct act tgt ggt cga ata tcg tat act gat	979
Cys Gly Leu Ala Trp His Pro Thr Cys Gly Arg Ile Ser Tyr Thr Asp	
277 282 287 292	
gcg gaa gga aat cta ggg ctt cta gag aat gtt tgt gac ccc agt gga	1027
Ala Glu Gly Asn Leu Gly Leu Leu Glu Asn Val Cys Asp Pro Ser Gly	
293 298 303 308	
aag aca tca agc agt aag gta tct agc aga gtg gaa aag gat tat aat	1075
Lys Thr Ser Ser Ser Lys Val Ser Ser Arg Val Glu Lys Asp Tyr Asn	
309 314 319 324	
gat ctt ttt gat gga gat gat atg agt aat gct ggt gat ttt cta aat	1123
Asp Leu Phe Asp Gly Asp Asp Met Ser Asn Ala Gly Asp Phe Leu Asn	
325 330 335 340	
gac aat gca gtt gag atc cct tct ttt tca aaa ggg att ata aat gat	1171
Asp Asn Ala Val Glu Ile Pro Ser Phe Ser Lys Gly Ile Ile Asn Asp	
341 346 351 356	
gat gag gat gat gaa gac ctc atg atg gct tca ggt cgt cct aga cag	1219
Asp Glu Asp Asp Glu Asp Leu Met Met Ala Ser Gly Arg Pro Arg Gln	
357 362 367 372	
cga agt cac atc cta gaa gat gat gaa aac tca gtt gat att tca atg	1267
Arg Ser His Ile Leu Glu Asp Asp Glu Asn Ser Val Asp Ile Ser Met	
373 378 383 388	
cta aaa act ggt tct agt ctt ctc aaa gag gag gag gaa gat ggt caa	1315
Leu Lys Thr Gly Ser Ser Leu Leu Lys Glu Glu Glu Glu Asp Gly Gln	
389 394 399 404	
gaa ggc agc att cac aat cta cca ctt gta aca tcc caa agg cca ttt	1363
Glu Gly Ser Ile His Asn Leu Pro Leu Val Thr Ser Gln Arg Pro Phe	
405 410 415 420	

tat gat gga ccc atg cca act ccc cgg caa aag cca ttt cag tca ggt	1411
Tyr Asp Gly Pro Met Pro Thr Pro Arg Gln Lys Pro Phe Gln Ser Gly	
421 426 431 436	
tct aca ccg ttg cat ctc act cac aga ttc atg gtg tgg aac tct att	1459
Ser Thr Pro Leu His Leu Thr His Arg Phe Met Val Trp Asn Ser Ile	
437 442 447 452	
gga att att cgc tgc tat aat gat gag caa gac aat gcc ata gat gtg	1507
Gly Ile Ile Arg Cys Tyr Asn Asp Glu Gln Asp Asn Ala Ile Asp Val	
453 458 463 468	
gag ttc cat gat acc tcc ata cac cat gca aca cac tta tca aac act	1555
Glu Phe His Asp Thr Ser Ile His His Ala Thr His Leu Ser Asn Thr	
469 474 479 484	
ttg aat tat aca ata gca gat ctt tcc cac gaa gct att ttg ttg gca	1603
Leu Asn Tyr Thr Ile Ala Asp Leu Ser His Glu Ala Ile Leu Leu Ala	
485 490 495 500	
tgt gaa agc act gat gaa cta gca agc aag ctt cac tgc ctg cac ttt	1651
Cys Glu Ser Thr Asp Glu Leu Ala Ser Lys Leu His Cys Leu His Phe	
501 506 511 516	
agt tct tgg gat tca agc aaa gag tgg ata ata gac ttg cct cag aat	1699
Ser Ser Trp Asp Ser Ser Lys Glu Trp Ile Ile Asp Leu Pro Gln Asn	
517 522 527 532	
gag gat att gaa gcc ata tgt ctc ggt caa gga tgg gct gct gcc gct	1747
Glu Asp Ile Glu Ala Ile Cys Leu Gly Gln Gly Trp Ala Ala Ala Ala	
533 538 543 548	
act agt gcc ctg ctt ctt cga ttg ttt act att gga ggg gtt caa aaa	1795
Thr Ser Ala Leu Leu Leu Arg Leu Phe Thr Ile Gly Gly Val Gln Lys	
549 554 559 564	
gag gta ttc agc ctt gct gga cct gtg gtg tca atg gca gga cat gga	1843
Glu Val Phe Ser Leu Ala Gly Pro Val Val Ser Met Ala Gly His Gly	
565 570 575 580	
gaa cag ctt ttc att gtt tat cac aga ggt aca gga ttt gat ggg gat	1891
Glu Gln Leu Phe Ile Val Tyr His Arg Gly Thr Gly Phe Asp Gly Asp	
581 586 591 596	
cag tgc ctt gga gtt caa ctg cta gag ctg ggg aaa aag aaa aaa caa	1939
Gln Cys Leu Gly Val Gln Leu Leu Glu Leu Gly Lys Lys Lys Lys Gln	
597 602 607 612	
att ttg cat ggt gac cct ctt cct ctt aca agg aaa tcc tac ctt gca	1987
Ile Leu His Gly Asp Pro Leu Pro Leu Thr Arg Lys Ser Tyr Leu Ala	
613 618 623 628	
tgg att ggg ttt tca gct gaa ggt acc cct tgt tac gtg gat tca gaa	2035
Trp Ile Gly Phe Ser Ala Glu Gly Thr Pro Cys Tyr Val Asp Ser Glu	
629 634 639 644	
gga att gtt cga atg ctt aac aga gga ctt ggt aat acg tgg act cct	2083

NAME	AGE	SEX	REL	DATE	TIME	PLACE	REMARKS
JOHN	15	M	S	1900	10	100	100
MARY	12	F	D	1900	10	100	100
JOHN	10	M	S	1900	10	100	100
MARY	8	F	D	1900	10	100	100
JOHN	6	M	S	1900	10	100	100
MARY	4	F	D	1900	10	100	100
JOHN	2	M	S	1900	10	100	100
MARY	1	F	D	1900	10	100	100

gga gaa gct gat gat gaa gaa aaa cca gaa ata cat aag cct gga cag 2755
Gly Glu Ala Asp Asp Glu Glu Lys Pro Glu Ile His Lys Pro Gly Gln

869	874	879	884	
aac tcg ttt tcc aaa agt aca aat tcc tct gat gtt tca gct aag tca				2803
Asn Ser Phe Ser Lys Ser Thr Asn Ser Ser Asp Val Ser Ala Lys Ser				
885	890	895	900	
ggg gca gtt acc ttt agc agc caa gga cga gta aat ccc ttt aag gta				2851
Gly Ala Val Thr Phe Ser Ser Gln Gly Arg Val Asn Pro Phe Lys Val				
901	906	911	916	
tca gcc agt tcc aaa gaa cca gcc atg tca atg aat tca gca cgt tca				2899
Ser Ala Ser Ser Lys Glu Pro Ala Met Ser Met Asn Ser Ala Arg Ser				
917	922	927	932	
act aat att tta gac aat atg ggc aaa tca tcc aag aaa tcc act gca				2947
Thr Asn Ile Leu Asp Asn Met Gly Lys Ser Ser Lys Lys Ser Thr Ala				
933	938	943	948	
ctt agt cga act aca aat aat gaa aag tct ccc att ata aag cct ctg				2995
Leu Ser Arg Thr Thr Asn Asn Glu Lys Ser Pro Ile Ile Lys Pro Leu				
949	954	959	964	
att cca aag ccg aag cct aag cag gca tct gca gca tcc tat ttc cag				3043
Ile Pro Lys Pro Lys Pro Lys Gln Ala Ser Ala Ala Ser Tyr Phe Gln				
965	970	975	980	
aaa aga aat tct caa act aat aaa act gag gaa gtg aaa gaa gaa aat				3091
Lys Arg Asn Ser Gln Thr Asn Lys Thr Glu Glu Val Lys Glu Glu Asn				
981	986	991	996	
ctt aaa aat gta tta tct gaa acc cca gct ata tgt cct cct caa aac				3139
Leu Lys Asn Val Leu Ser Glu Thr Pro Ala Ile Cys Pro Pro Gln Asn				
997	1002	1007	1012	
act gaa aac caa agg cca aag acc ggg ttc cag atg tgg tta gaa gaa				3187
Thr Glu Asn Gln Arg Pro Lys Thr Gly Phe Gln Met Trp Leu Glu Glu				
1013	1018	1023	1028	
aat aga agt aat att ttg tct gac aat cct gac ttt tca gat gaa gca				3235
Asn Arg Ser Asn Ile Leu Ser Asp Asn Pro Asp Phe Ser Asp Glu Ala				
1029	1034	1039	1044	
gac ata ata aaa gaa gga atg att cga ttt aga gta ttg tca act gaa				3283
Asp Ile Ile Lys Glu Gly Met Ile Arg Phe Arg Val Leu Ser Thr Glu				
1045	1050	1055	1060	
gaa aga aag gtg tgg gct aac aaa gcc aaa gga gaa acg gca agt gaa				3331
Glu Arg Lys Val Trp Ala Asn Lys Ala Lys Gly Glu Thr Ala Ser Glu				
1061	1066	1071	1076	
gga act gaa gca aag aag cga aaa cgt gtg gtt gat gaa agt gat gaa				3379
Gly Thr Glu Ala Lys Lys Arg Lys Arg Val Val Asp Glu Ser Asp Glu				
1077	1082	1087	1092	
aca gaa aac cag gaa gaa aaa gca aaa gag aac ctg aat ttg tct aaa				3427
Thr Glu Asn Gln Glu Glu Lys Ala Lys Glu Asn Leu Asn Leu Ser Lys				
1093	1098	1103	1108	

aag cag aaa cct tta gat ttt tct aca aat cag aaa cta tca gct ttt 3475
 Lys Gln Lys Pro Leu Asp Phe Ser Thr Asn Gln Lys Leu Ser Ala Phe
 1109 1114 1119 1124

gca ttt aag cag gag taa aggaag aaagtgaccc tagggaagta atggatTTTT 3529
 Ala Phe Lys Gln Glu *
 1125 1130

ttttactcat ctttgaatat agactcgagt ctttgggaaa ctcattatat atatattttt 3589

taaagagttt gaagcaactg tttgtcttta taagataatg tagtaattat attggtgtag 3649

gtaacaggac atatgtaaaa actatcatct ttgcagatta ctctgcctcc aaatgcaggg 3709

cctttcagag atgcattgtg attgtaatta ctgagttgaa gctccaacca atttgaattt 3769

gtttcttaac cttgaaaaat cattaaagcc aaggatttaa aacctttgtg cattaatacc 3829

ttctaggggt ttggttcatt tggtttttgt catgtgcaag gaaggacaat agtctctttt 3889

ccaagtgtgt tagcatagac ttctctatat gtttctacta gacctagggg atgacgtctt 3949

ttaataatac tggccctaaa catgtaaata atcttgtagg tgagactttt tcttttgtgt 4009

ttcggaaatt tcctatgtgg ctttcagttg tctgtttgta tagcctggat ttttttgagg 4069

taaatgaaac tttctcattt gtaaaaaaaaaaaaa 4103

<210> 391
 <211> 857
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (44)..(655)

<400> 391
 atttggccct cgaggccaag aattcggcac gagcggcacg agg atg gcg gtg acg 55
 Met Ala Val Thr
 1

ggc tgg ttg gag agt ctg cgg aca gcc cag aag act gcg ctg ctg cag 103
 Gly Trp Leu Glu Ser Leu Arg Thr Ala Gln Lys Thr Ala Leu Leu Gln
 5 10 15 20

gac ggg aga agg aag gtt cac tat tta ttc cca gac ggc aag gaa atg 151
 Asp Gly Arg Arg Lys Val His Tyr Leu Phe Pro Asp Gly Lys Glu Met
 21 26 31 36

gct gaa gaa tat gac gag aag acg agt gaa cta ctt gtg aga aag tgg 199
 Ala Glu Glu Tyr Asp Glu Lys Thr Ser Glu Leu Leu Val Arg Lys Trp
 37 42 47 52

cgt gtg aaa agt gcc ctg gga gcc atg ggc cag tgg cag ctt gaa gta	247
Arg Val Lys Ser Ala Leu Gly Ala Met Gly Gln Trp Gln Leu Glu Val	
53 58 63 68	
gga gac cca gcg ccc cta gga gca ggg aac ctg ggg cct gaa ctc atc	295
Gly Asp Pro Ala Pro Leu Gly Ala Gly Asn Leu Gly Pro Glu Leu Ile	
69 74 79 84	
aag gaa agc aat gcc aat cct atc ttc atg cgc aag gac acc aag atg	343
Lys Glu Ser Asn Ala Asn Pro Ile Phe Met Arg Lys Asp Thr Lys Met	
85 90 95 100	
agt ttc cag tgg cgg att cga aac ctc ccc tat cct aag gat gtc tat	391
Ser Phe Gln Trp Arg Ile Arg Asn Leu Pro Tyr Pro Lys Asp Val Tyr	
101 106 111 116	
agt gtc tct gtg gac cag aag gag cgc tgc atc att gtc aga aca acc	439
Ser Val Ser Val Asp Gln Lys Glu Arg Cys Ile Ile Val Arg Thr Thr	
117 122 127 132	
aac aag aag tac tac aag aag ttc tcc att cct gat cta gat aga cac	487
Asn Lys Lys Tyr Tyr Lys Lys Phe Ser Ile Pro Asp Leu Asp Arg His	
133 138 143 148	
cag cta cct ctg gat gac gcc ttg ctg agc ttt gcc cac gcc aac tgc	535
Gln Leu Pro Leu Asp Asp Ala Leu Leu Ser Phe Ala His Ala Asn Cys	
149 154 159 164	
acc ctg atc atc tct tac cag aag cca aag gag gtt gtg gtg gcc gag	583
Thr Leu Ile Ile Ser Tyr Gln Lys Pro Lys Glu Val Val Val Ala Glu	
165 170 175 180	
tct gag cta cag aag gaa cta aag aag gtg aag aca gcc cac agc aac	631
Ser Glu Leu Gln Lys Glu Leu Lys Lys Val Lys Thr Ala His Ser Asn	
181 186 191 196	
gat ggg gac tgc aag acc cag tag ttggcccctg agccttatac ctccaccaca	685
Asp Gly Asp Cys Lys Thr Gln *	
197 202	
gggggtgccg tgagaattca aggcttggcc cttcttgacc acggcagcct cctgtcttct	745
aggagctatc aagggtctct aagaactggg catggggcac tctagccag tgagtcatgg	805
tcatatattcc tgagtaaagt cattctgagt tacttactgc aaaaaaaaaa aa	857

<210> 392
 <211> 3256
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (74)..(1777)

<400> 392

ggaattcccc ggtcgacgat ttcgtcgagc ctgggccggc gcggggcctt gtgggagggc 60

ttaaggaagt aaa atg gcg gac ctg gcg aac gaa gaa aag cct gcc att 109
Met Ala Asp Leu Ala Asn Glu Glu Lys Pro Ala Ile
1 5 10

gct ccg ccc gtc ttt gtg ttt cag aag gat aaa gga caa aag tcc cct 157
Ala Pro Pro Val Phe Val Phe Gln Lys Asp Lys Gly Gln Lys Ser Pro
13 18 23 28

gca gag caa aaa aac ttg tcg gat tcg gga gag gag cct cgg ggg gag 205
Ala Glu Gln Lys Asn Leu Ser Asp Ser Gly Glu Glu Pro Arg Gly Glu
29 34 39 44

gct gag gcc ccc cac cat ggc acg ggt cac ccc gag tca gct ggc gag 253
Ala Glu Ala Pro His His Gly Thr Gly His Pro Glu Ser Ala Gly Glu
45 50 55 60

cat gcc cta gaa cct cct gcc cct gct ggc gcc tca gcc agc act cct 301
His Ala Leu Glu Pro Pro Ala Pro Ala Gly Ala Ser Ala Ser Thr Pro
61 66 71 76

ccg cct ccc gct cct gaa gcc cag ctt cct cct ttt ccg cga gaa ctg 349
Pro Pro Pro Ala Pro Glu Ala Gln Leu Pro Pro Phe Pro Arg Glu Leu
77 82 87 92

gca ggg agg tca gct ggc gcc tcc agt cct gaa ggc gga gaa gat tct 397
Ala Gly Arg Ser Ala Gly Gly Ser Ser Pro Glu Gly Gly Glu Asp Ser
93 98 103 108

gac aga gaa gat gga aat tac tgc cct cct gtc aag cga gaa aga aca 445
Asp Arg Glu Asp Gly Asn Tyr Cys Pro Pro Val Lys Arg Glu Arg Thr
109 114 119 124

tcc tct tta acc cag ttc cca ccc tca cag tca gag gaa agg agc agt 493
Ser Ser Leu Thr Gln Phe Pro Pro Ser Gln Ser Glu Glu Arg Ser Ser
125 130 135 140

ggc ttc cgg ttg aag cca cca acg ctg atc cac ggc caa gcc ccc agc 541
Gly Phe Arg Leu Lys Pro Pro Thr Leu Ile His Gly Gln Ala Pro Ser
141 146 151 156

gca ggt ctg cca agc cag aag ccc aag gag cag cag cgg agc gtg ctt 589
Ala Gly Leu Pro Ser Gln Lys Pro Lys Glu Gln Gln Arg Ser Val Leu
157 162 167 172

cgc ccg gca gtg tta caa gct ccg cag cca aag gcg ctg tcc cag act 637
Arg Pro Ala Val Leu Gln Ala Pro Gln Pro Lys Ala Leu Ser Gln Thr
173 178 183 188

gtc ccc agc agt ggc acc aac ggg gtc agc ctc cca gca gac tgc acg 685
Val Pro Ser Ser Gly Thr Asn Gly Val Ser Leu Pro Ala Asp Cys Thr
189 194 199 204

ggg gca gtg ccc gca gca tcc cct gac act gct gca tgg aga agt cct	733
Gly Ala Val Pro Ala Ala Ser Pro Asp Thr Ala Ala Trp Arg Ser Pro	
205 210 215 220	
tcc gaa gct gcc gat gag gtg tgt gca ctt gag gag aaa gag ccc cag	781
Ser Glu Ala Ala Asp Glu Val Cys Ala Leu Glu Glu Lys Glu Pro Gln	
221 226 231 236	
aaa aat gag tcc agc aat gcc tct gaa gag gaa gcc tgt gag aaa aaa	829
Lys Asn Glu Ser Ser Asn Ala Ser Glu Glu Ala Cys Glu Lys Lys	
237 242 247 252	
gac ccc gcc aca cag caa gcc ttt gta ttt ggg cag aac ttg agg gac	877
Asp Pro Ala Thr Gln Gln Ala Phe Val Phe Gly Gln Asn Leu Arg Asp	
253 258 263 268	
aga gtt aag ctg ata aat gag agc gtg gac gaa gcc gac atg gag aat	925
Arg Val Lys Leu Ile Asn Glu Ser Val Asp Glu Ala Asp Met Glu Asn	
269 274 279 284	
gct gga cac ccc agc gca gac acg cca acc gca acg aac tat ttc ctc	973
Ala Gly His Pro Ser Ala Asp Thr Pro Thr Ala Thr Asn Tyr Phe Leu	
285 290 295 300	
cag tat atc agt tcc agt tta gag aac tca acc aat agt gcc gac gcc	1021
Gln Tyr Ile Ser Ser Ser Leu Glu Asn Ser Thr Asn Ser Ala Asp Ala	
301 306 311 316	
tcc agc aac aaa ttt gta ttt ggc cag aac atg agc gag cga gtt ttg	1069
Ser Ser Asn Lys Phe Val Phe Gly Gln Asn Met Ser Glu Arg Val Leu	
317 322 327 332	
agc ccc cca aaa tta aac gag gtc agt tca gat gcc aac agg gaa aat	1117
Ser Pro Pro Lys Leu Asn Glu Val Ser Ser Asp Ala Asn Arg Glu Asn	
333 338 343 348	
gca gct gcc gag tca ggg tct gag tcc tcg tcc cag gag gcc acc cct	1165
Ala Ala Ala Glu Ser Gly Ser Glu Ser Ser Ser Gln Glu Ala Thr Pro	
349 354 359 364	
gag aaa gag tcc ctg gct gag tcg gca gcc gcc tac acc aag gca aca	1213
Glu Lys Glu Ser Leu Ala Glu Ser Ala Ala Ala Tyr Thr Lys Ala Thr	
365 370 375 380	
gcg cgg aag tgt ttg ttg gaa aaa gtg gaa gtc atc acc ggg gag gag	1261
Ala Arg Lys Cys Leu Leu Glu Lys Val Glu Val Ile Thr Gly Glu Glu	
381 386 391 396	
gcg gag agc aat gtg tta cag atg cag tgc aag ctg ttt gtc ttt gac	1309
Ala Glu Ser Asn Val Leu Gln Met Gln Cys Lys Leu Phe Val Phe Asp	
397 402 407 412	
aag acc tca cag tcc tgg gtg gag aga ggc cgg ggg ctg ctc aga ctc	1357
Lys Thr Ser Gln Ser Trp Val Glu Arg Gly Arg Gly Leu Leu Arg Leu	
413 418 423 428	
aat gac atg gcg tcc acc gat gac ggc aca cta cag tcc cga cta gtg	1405

ctgtccccc cctgtggttc tggcctctga ggttggggga ctacttgttt cccaccccag 2511
 gtctctccag gccaaagtcac ggggtgatga ggagttgggg cctgtgtctgt cctaggcctg 2571
 gagagtgcct gtctgggaaa aggtcaactgg acctggaagg gtccccaggg tcccctgact 2631
 cccgtctcca tctgtcacgt ggttcacacat catcaggcac caggcgcaaa ctgcttcccg 2691
 ctggttgcca tcccttcccc agccacaggt gtccctgccc ccaggacagt ccagggccag 2751
 gggcttctgt gagaggcaga gggggaccct caccaaactc tgggtggaaga gccacggggc 2811
 tgggtcccaga acaggcagtc tcacaagcac gcagcacact ggagtggacg cctgtgcccc 2871
 cccgagcctg gagcatggcc aagagccagc ttgcaccacc cacctgggag gccgaggagg 2931
 aggtccctctg ggcacagggc ctctttggga cttcagagga aatctcccag tcccactctc 2991
 ggaggggttaa gagaaggcct cctgcagctg tgccgtccac acctctaggt cgccagagcc 3051
 ctggccccc cccccagca agcctgagcc cggaagaac cagaggccct cccgagagac 3111
 ccagtcacac gtctctgctt taagccttag ccagctagtg acgagtacaa cgagataacg 3171
 cccatgtgtt ttggaacatt tatgtaagat tgcataatga aatgtatttg ggaactacat 3231
 taaactttta actaaaaaaaa aaaaaa 3256

<210> 393
 <211> 5714
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (272) .. (4312)

<400> 393
 ctgcacgacc ggtccggaat tcccgggtcg acgatttcgt gatcatagct gggggaggct 60
 gagcgtggga gcggtgctgc cagtcctgcc tgaaaacgcg aaatgagtct tgcttggttc 120
 tccctccact gggcgtgaga gccctgccc aggaggccca ggacaaatgg ccccatagtg 180
 gaaactggga agcttttagg catctgatca gagcgggagc cagccggggg accacagtgc 240
 tggacaggcc aaccaactca aacttgaaga c atg aaa tcc cca agg aga acc 292
 Met Lys Ser Pro Arg Arg Thr
 1 5
 act ttg tgc ctc atg ttt att gtg att tat tct tcc aaa gct gca ctg 340
 Thr Leu Cys Leu Met Phe Ile Val Ile Tyr Ser Ser Lys Ala Ala Leu
 8 13 18 23

aac tgg aat tac gag tct act att cat cct ttg agt ctt cat gaa cat	388
Asn Trp Asn Tyr Glu Ser Thr Ile His Pro Leu Ser Leu His Glu His	
24 29 34 39	
gaa cca gct ggt gaa gag gca ctg agg caa aaa cga gcc gtt gcc aca	436
Glu Pro Ala Gly Glu Glu Ala Leu Arg Gln Lys Arg Ala Val Ala Thr	
40 45 50 55	
aaa agt cct acg gct gaa gaa tac act gtt aat att gag atc agt ttt	484
Lys Ser Pro Thr Ala Glu Glu Tyr Thr Val Asn Ile Glu Ile Ser Phe	
56 61 66 71	
gaa aat gca tcc ttc ctg gat cct atc aaa gcc tac ttg aac agc ctc	532
Glu Asn Ala Ser Phe Leu Asp Pro Ile Lys Ala Tyr Leu Asn Ser Leu	
72 77 82 87	
agt ttt cca att cat ggg aat aac act gac caa att act gac att ttg	580
Ser Phe Pro Ile His Gly Asn Asn Thr Asp Gln Ile Thr Asp Ile Leu	
88 93 98 103	
agc ata aat gtg aca aca gtc tgc aga cct gct gga aat gaa atc tgg	628
Ser Ile Asn Val Thr Thr Val Cys Arg Pro Ala Gly Asn Glu Ile Trp	
104 109 114 119	
tgc tcc tgc gag aca ggt tat ggg tgg cct cgg gaa agg tgt ctt cac	676
Cys Ser Cys Glu Thr Gly Tyr Gly Trp Pro Arg Glu Arg Cys Leu His	
120 125 130 135	
aat ctc att tgt caa gag cgt gac gtc ttc ctc cca ggg cac cat tgc	724
Asn Leu Ile Cys Gln Glu Arg Asp Val Phe Leu Pro Gly His His Cys	
136 141 146 151	
agt tgc ctt aaa gaa ctg cct ccc aat gga cct ttt tgc ctg ctt cag	772
Ser Cys Leu Lys Glu Leu Pro Pro Asn Gly Pro Phe Cys Leu Leu Gln	
152 157 162 167	
gaa gat gtt acc ctg aac atg aga gtc aga cta aat gta ggc ttt caa	820
Glu Asp Val Thr Leu Asn Met Arg Val Arg Leu Asn Val Gly Phe Gln	
168 173 178 183	
gaa gac ctc atg aac act tcc tcc gcc ctc tat agg tcc tac aag acc	868
Glu Asp Leu Met Asn Thr Ser Ser Ala Leu Tyr Arg Ser Tyr Lys Thr	
184 189 194 199	
gac ttg gaa aca gcg ttc cgg aag ggt tac gga att tta cca ggc ttc	916
Asp Leu Glu Thr Ala Phe Arg Lys Gly Tyr Gly Ile Leu Pro Gly Phe	
200 205 210 215	
aag ggc gtg act gtg aca ggg ttc aag tct gga agt gtg gtt gtg aca	964
Lys Gly Val Thr Val Thr Gly Phe Lys Ser Gly Ser Val Val Val Thr	
216 221 226 231	
tat gaa gtc aag act aca cca cca tca ctt gag tta ata cat aaa gcc	1012
Tyr Glu Val Lys Thr Thr Pro Pro Ser Leu Glu Leu Ile His Lys Ala	
232 237 242 247	
aat gaa caa gtt gta cag agc ctc aat cag acc tac aaa atg gac tac	1060

Asn Glu Gln Val Val Gln Ser Leu Asn Gln Thr Tyr Lys Met Asp Tyr	
248 253 258 263	
aac tcc ttt caa gca gtt act atc aat gaa agc aat ttc ttt gtc aca	1108
Asn Ser Phe Gln Ala Val Thr Ile Asn Glu Ser Asn Phe Phe Val Thr	
264 269 274 279	
cca gaa atc atc ttt gaa ggg gac aca gtc agt ctg gtg tgt gaa aag	1156
Pro Glu Ile Ile Phe Glu Gly Asp Thr Val Ser Leu Val Cys Glu Lys	
280 285 290 295	
gaa gtt ttg tcc tcc aat gtg tct tgg cgc tat gaa gaa cag cag ttg	1204
Glu Val Leu Ser Ser Asn Val Ser Trp Arg Tyr Glu Glu Gln Gln Leu	
296 301 306 311	
gaa atc cag aac agc agc aga ttc tcg att tac acc gca ctt ttc aac	1252
Glu Ile Gln Asn Ser Ser Arg Phe Ser Ile Tyr Thr Ala Leu Phe Asn	
312 317 322 327	
aac atg act tcg gtg tcc aag ctc acc atc cac aac atc act cca ggt	1300
Asn Met Thr Ser Val Ser Lys Leu Thr Ile His Asn Ile Thr Pro Gly	
328 333 338 343	
gat gca ggt gaa tat gtt tgc aaa ctg ata tta gac att ttt gaa tat	1348
Asp Ala Gly Glu Tyr Val Cys Lys Leu Ile Leu Asp Ile Phe Glu Tyr	
344 349 354 359	
gag tgc aag aag aaa ata gat gtt atg ccc atc caa att ttg gca aat	1396
Glu Cys Lys Lys Lys Ile Asp Val Met Pro Ile Gln Ile Leu Ala Asn	
360 365 370 375	
gaa gaa atg aag gtg atg tgc gac aac aat cct gta tct ttg aac tgc	1444
Glu Glu Met Lys Val Met Cys Asp Asn Asn Pro Val Ser Leu Asn Cys	
376 381 386 391	
tgc agt cag ggt aat gtt aat tgg agc aaa gta gaa tgg aag cag gaa	1492
Cys Ser Gln Gly Asn Val Asn Trp Ser Lys Val Glu Trp Lys Gln Glu	
392 397 402 407	
gga aaa ata aat att cca gga acc cct gag aca gac ata gat tct agc	1540
Gly Lys Ile Asn Ile Pro Gly Thr Pro Glu Thr Asp Ile Asp Ser Ser	
408 413 418 423	
tgc agc aga tac acc ctc aag gct gat gga acc cag tgc cca agc ggg	1588
Cys Ser Arg Tyr Thr Leu Lys Ala Asp Gly Thr Gln Cys Pro Ser Gly	
424 429 434 439	
tcg tct gga aca aca gtc atc tac act tgt gag ttc atc agt gcc tat	1636
Ser Ser Gly Thr Thr Val Ile Tyr Thr Cys Glu Phe Ile Ser Ala Tyr	
440 445 450 455	
gga gcc aga ggc agt gca aac ata aaa gtg aca ttc atc tct gtg gcc	1684
Gly Ala Arg Gly Ser Ala Asn Ile Lys Val Thr Phe Ile Ser Val Ala	
456 461 466 471	
aat cta aca ata acc ccg gac cca att tct gtt tct gag gga caa aac	1732
Asn Leu Thr Ile Thr Pro Asp Pro Ile Ser Val Ser Glu Gly Gln Asn	

472	477	482	487	
ttt tct ata aaa tgc atc agt gat gtg agt aac tat gat gag gtt tat				1780
Phe Ser Ile Lys Cys Ile Ser Asp Val Ser Asn Tyr Asp Glu Val Tyr				
488	493	498	503	
tgg aac act tct gct gga att aaa ata tac caa aga ttt tat acc acg				1828
Trp Asn Thr Ser Ala Gly Ile Lys Ile Tyr Gln Arg Phe Tyr Thr Thr				
504	509	514	519	
agg agg tat ctt gat gga gca gaa tca gta ctg aca gtc aag acc tcg				1876
Arg Arg Tyr Leu Asp Gly Ala Glu Ser Val Leu Thr Val Lys Thr Ser				
520	525	530	535	
acc agg gag tgg aat gga acc tat cac tgc ata ttt aga tat aag aat				1924
Thr Arg Glu Trp Asn Gly Thr Tyr His Cys Ile Phe Arg Tyr Lys Asn				
536	541	546	551	
tca tac agt att gca acc aaa gac gtc att gtt cac ccg ctg cct cta				1972
Ser Tyr Ser Ile Ala Thr Lys Asp Val Ile Val His Pro Leu Pro Leu				
552	557	562	567	
aag ctg aac atc atg gtt gat cct ttg gaa gct act gtt tca tgc agt				2020
Lys Leu Asn Ile Met Val Asp Pro Leu Glu Ala Thr Val Ser Cys Ser				
568	573	578	583	
ggt tcc cat cac atc aag tgc tgc ata gag gag gat gga gac tac aaa				2068
Gly Ser His His Ile Lys Cys Cys Ile Glu Glu Asp Gly Asp Tyr Lys				
584	589	594	599	
gtt act ttc cat atg ggt tcc tca tcc ctt cct gct gca aaa gaa gtt				2116
Val Thr Phe His Met Gly Ser Ser Ser Leu Pro Ala Ala Lys Glu Val				
600	605	610	615	
aac aaa aaa caa gtg tgc tac aaa cac aat ttc aat gca agc tca gtt				2164
Asn Lys Lys Gln Val Cys Tyr Lys His Asn Phe Asn Ala Ser Ser Val				
616	621	626	631	
tcc tgg tgt tca aaa act gtt gat gtg tgt tgt cac ttt acc aat gct				2212
Ser Trp Cys Ser Lys Thr Val Asp Val Cys Cys His Phe Thr Asn Ala				
632	637	642	647	
gct aat aat tca gtt tgg agc cca tct atg aag ctg aat ctg gtt cct				2260
Ala Asn Asn Ser Val Trp Ser Pro Ser Met Lys Leu Asn Leu Val Pro				
648	653	658	663	
ggg gaa aac atc aca tgc cag gat ccc gta ata ggt gtc gga gag ccg				2308
Gly Glu Asn Ile Thr Cys Gln Asp Pro Val Ile Gly Val Gly Glu Pro				
664	669	674	679	
ggg aaa gtc atc cag aag cta tgc cgg ttc tca aac gtt ccc agc agc				2356
Gly Lys Val Ile Gln Lys Leu Cys Arg Phe Ser Asn Val Pro Ser Ser				
680	685	690	695	
cct gag agt ccc att ggc ggg acc atc act tac aaa tgt gta ggc tcc				2404
Pro Glu Ser Pro Ile Gly Gly Thr Ile Thr Tyr Lys Cys Val Gly Ser				
696	701	706	711	

cag tgg gag gag aag aga aat gac tgc atc tct gcc cca ata aac agt	2452
Gln Trp Glu Glu Lys Arg Asn Asp Cys Ile Ser Ala Pro Ile Asn Ser	
712 717 722 727	
ctg ctc cag atg gct aag gct ttg atc aag agc ccc tct cag gat gag	2500
Leu Leu Gln Met Ala Lys Ala Leu Ile Lys Ser Pro Ser Gln Asp Glu	
728 733 738 743	
atg ctc cct aca tac ctg aag gat ctt tct att agc ata gac aaa ggc	2548
Met Leu Pro Thr Tyr Leu Lys Asp Leu Ser Ile Ser Ile Asp Lys Ala	
744 749 754 759	
gaa cat gaa atc agc tct tct cct ggg agt ctg gga gcc att att aac	2596
Glu His Glu Ile Ser Ser Ser Pro Gly Ser Leu Gly Ala Ile Ile Asn	
760 765 770 775	
atc ctt gat ctg ctc tca aca gtt cca acc caa gta aat tca gaa atg	2644
Ile Leu Asp Leu Leu Ser Thr Val Pro Thr Gln Val Asn Ser Glu Met	
776 781 786 791	
atg acg cac gtg ctc tct acg gtt aat gtc atc ctt ggc aag ccc gtc	2692
Met Thr His Val Leu Ser Thr Val Asn Val Ile Leu Gly Lys Pro Val	
792 797 802 807	
ttg aac acc tgg aag gtt tta caa cag caa tgg acc aat cag agt tca	2740
Leu Asn Thr Trp Lys Val Leu Gln Gln Gln Trp Thr Asn Gln Ser Ser	
808 813 818 823	
cag cta cta cat tca gtg gaa aga ttt tcc caa gca tta cag tca gga	2788
Gln Leu Leu His Ser Val Glu Arg Phe Ser Gln Ala Leu Gln Ser Gly	
824 829 834 839	
gat agc cct cct ttg tcc ttc tcc caa act aat gtg cag atg agc agc	2836
Asp Ser Pro Pro Leu Ser Phe Ser Gln Thr Asn Val Gln Met Ser Ser	
840 845 850 855	
acg gta atc aag tcc agc cac cca gaa acc tat caa cag agg ttt gtt	2884
Thr Val Ile Lys Ser Ser His Pro Glu Thr Tyr Gln Gln Arg Phe Val	
856 861 866 871	
ttc cca tac ttt gac ctc tgg ggc aat gtg gtc att gac aag agc tac	2932
Phe Pro Tyr Phe Asp Leu Trp Gly Asn Val Val Ile Asp Lys Ser Tyr	
872 877 882 887	
cta gaa aac ttg cag tgc gat tgc tct att gtc acc atg gct ttc cca	2980
Leu Glu Asn Leu Gln Ser Asp Ser Ser Ile Val Thr Met Ala Phe Pro	
888 893 898 903	
act ctc caa gcc atc ctt gct cag gat atc cag gaa aat aac ttt gca	3028
Thr Leu Gln Ala Ile Leu Ala Gln Asp Ile Gln Glu Asn Asn Phe Ala	
904 909 914 919	
gag agc tta gtg atg aca acc act gtc agc cac aat acg act atg cca	3076
Glu Ser Leu Val Met Thr Thr Thr Val Ser His Asn Thr Thr Met Pro	
920 925 930 935	

ttc agg att tca atg act ttt aag aac aat agc cct tca ggc ggc gaa	3124
Phe Arg Ile Ser Met Thr Phe Lys Asn Asn Ser Pro Ser Gly Gly Glu	
936 941 946 951	
acg aag tgt gtc ttc tgg aac ttc agg ctt gcc aac aac aca ggg ggg	3172
Thr Lys Cys Val Phe Trp Asn Phe Arg Leu Ala Asn Asn Thr Gly Gly	
952 957 962 967	
tgg gac agc agt ggg tgc tat gtt gaa gaa ggt gat ggg gac aat gtc	3220
Trp Asp Ser Ser Gly Cys Tyr Val Glu Glu Gly Asp Gly Asp Asn Val	
968 973 978 983	
acc tgt atc tgt gac cac cta aca tca ttc tcc atc ctc atg tcc cct	3268
Thr Cys Ile Cys Asp His Leu Thr Ser Phe Ser Ile Leu Met Ser Pro	
984 989 994 999	
gac tcc cca gat cct agt tct ctc ctg gga ata ctc ctg gat att att	3316
Asp Ser Pro Asp Pro Ser Ser Leu Leu Gly Ile Leu Leu Asp Ile Ile	
1000 1005 1010 1015	
tct tat gtt ggg gtg ggc ttt tcc atc ttg agc ttg gca gcc tgt cta	3364
Ser Tyr Val Gly Val Gly Phe Ser Ile Leu Ser Leu Ala Ala Cys Leu	
1016 1021 1026 1031	
gtt gtg gaa gct gtg gtg tgg aaa tgg gtg acc aag aat cgg act tct	3412
Val Val Glu Ala Val Val Trp Lys Ser Val Thr Lys Asn Arg Thr Ser	
1032 1037 1042 1047	
tat atg cgc cac acc tgc ata gtg aat atc gct gcc tcc ctt ctg gtc	3460
Tyr Met Arg His Thr Cys Ile Val Asn Ile Ala Ala Ser Leu Leu Val	
1048 1053 1058 1063	
gcc aac acc tgg ttc att gtg gtc gct gcc atc cag gac aat cgc tac	3508
Ala Asn Thr Trp Phe Ile Val Val Ala Ala Ile Gln Asp Asn Arg Tyr	
1064 1069 1074 1079	
ata ctc tgc aag aca gcc tgt gtg gct gcc acc ttc ttc atc cac ttc	3556
Ile Leu Cys Lys Thr Ala Cys Val Ala Ala Thr Phe Phe Ile His Phe	
1080 1085 1090 1095	
ttc tac ctc agc gtc ttc ttc tgg atg ctg aca ctg ggc ctc atg ctg	3604
Phe Tyr Leu Ser Val Phe Phe Trp Met Leu Thr Leu Gly Leu Met Leu	
1096 1101 1106 1111	
ttc tat cgc ctg gtt ttc att ctg cat gaa aca agc agg tcc act cag	3652
Phe Tyr Arg Leu Val Phe Ile Leu His Glu Thr Ser Arg Ser Thr Gln	
1112 1117 1122 1127	
aaa gcc att gcc ttc tgt ctt ggc tat ggc tgc cca ctt gcc atc tgg	3700
Lys Ala Ile Ala Phe Cys Leu Gly Tyr Gly Cys Pro Leu Ala Ile Ser	
1128 1133 1138 1143	
gtc atc acg ctg gga gcc acc cag ccc cgg gaa gtc tat acg agg aag	3748
Val Ile Thr Leu Gly Ala Thr Gln Pro Arg Glu Val Tyr Thr Arg Lys	
1144 1149 1154 1159	
aat gtc tgt tgg ctc aac tgg gag gac acc aag gcc ctg ctg gct ttc	3796

Asn Val Cys Trp Leu Asn Trp Glu Asp Thr Lys Ala Leu Leu Ala Phe	
1160 1165 1170 1175	
gcc atc cca gca ctg atc att gtg gtg gtg aac ata acc atc act att	3844
Ala Ile Pro Ala Leu Ile Ile Val Val Val Asn Ile Thr Ile Thr Ile	
1176 1181 1186 1191	
gtg gtc atc acc aag atc ctg agg cct tcc att gga gac aag cca tgc	3892
Val Val Ile Thr Lys Ile Leu Arg Pro Ser Ile Gly Asp Lys Pro Cys	
1192 1197 1202 1207	
aag cag gag aag agc agc ctg ttt cag atc agc aag agc att ggg gtc	3940
Lys Gln Glu Lys Ser Ser Leu Phe Gln Ile Ser Lys Ser Ile Gly Val	
1208 1213 1218 1223	
ctc aca cca ctc ttg ggc ctc act tgg ggt ttt ggt ctc acc act gtg	3988
Leu Thr Pro Leu Leu Gly Leu Thr Trp Gly Phe Gly Leu Thr Thr Val	
1224 1229 1234 1239	
ttc cca ggg acc aac ctt gtg ttc cat atc ata ttt gcc atc ctc aat	4036
Phe Pro Gly Thr Asn Leu Val Phe His Ile Ile Phe Ala Ile Leu Asn	
1240 1245 1250 1255	
gtc ttc cag gga tta ttc att tta ctc ttt gga tgc ctc tgg gat ctg	4084
Val Phe Gln Gly Leu Phe Ile Leu Leu Phe Gly Cys Leu Trp Asp Leu	
1256 1261 1266 1271	
aag gta cag gaa gct ttg ctg aat aag ttt tca ttg tcg aga tgg tct	4132
Lys Val Gln Glu Ala Leu Leu Asn Lys Phe Ser Leu Ser Arg Trp Ser	
1272 1277 1282 1287	
tca cag cac tca aag tca aca tcc ctg ggt tca tcc aca cct gtg ttt	4180
Ser Gln His Ser Lys Ser Thr Ser Leu Gly Ser Ser Thr Pro Val Phe	
1288 1293 1298 1303	
tct atg agt tct cca ata tca agg aga ttt aac aat ttg ttt ggt aaa	4228
Ser Met Ser Ser Pro Ile Ser Arg Arg Phe Asn Asn Leu Phe Gly Lys	
1304 1309 1314 1319	
aca gga acg tat aat gtt tcc acc cca gaa gca acc agc tca tcc ctg	4276
Thr Gly Thr Tyr Asn Val Ser Thr Pro Glu Ala Thr Ser Ser Ser Leu	
1320 1325 1330 1335	
gaa aac tca tcc agt gct tct tcg ttg ctc aac taa gaac aggataatcc	4326
Glu Asn Ser Ser Ser Ala Ser Ser Leu Leu Asn *	
1336 1341 1346	
aacctacgtg acctcccggtg gacagtggct gtgcttttaa aaagagatgc ttgcaaagca	4386
atggggaacg tggtotcggg gcagggtttcc gggagcagat gccaaaaaga ctttttcata	4446
gagaagaggc tttcttttgt aaagacagaa taaaaataat tggtatgttt ctgtttgttc	4506
cctccccctc ccccttgtgt gataccacat gtgtatagta ttttaagtga actcaagccc	4566
tcaaggccca actttcttgt ctatattgta atatagaatt tcgaagagac attttcactt	4626

tttacacatt	gggcacaaag	ataagctttg	attaaagtag	taagtaaaag	gctacctagg	4686
aaatacttca	gtgaattcta	agaaggaagg	aaggaagaaa	ggaaggaaag	aagggagggg	4746
aacagggaga	aagggaaaaa	gaagaaaaag	agaaagatga	aaataggaac	aaataaagac	4806
aaacaacatt	aagggccata	ttgtaagatt	tccatgttaa	tgatctaata	taatcactca	4866
gtgcaacatt	gagaattttt	ttttaatggc	tcaaaaatgg	aaactgaaag	caagtcatgg	4926
ggaatgaata	ctttgggcag	tatcttcctc	atgtcttctt	agctaagagg	aggaaaaaaa	4986
ggctgaaaaa	atagggagga	aattccttca	tcagaacgac	ttcaagtggg	taacaatatt	5046
tataagaaat	gaatggaagg	aaatatgac	ctcctgagac	taactttgta	tggttaaggtt	5106
tgaactaagt	gaatgtatct	gcagaggaag	tattacaaag	atatgtcatt	agatccaagt	5166
gctgattaaa	tttttatagt	ttatcagaaa	agccttatat	tttagtttgt	tccacatttt	5226
gaaagcaaaa	aatatatatt	tgatataccc	ttcaattgcc	aaatttgata	tggtgcactg	5286
aagacagacc	ctgtcatata	tttaatggct	tcaagcaggt	acttctctgt	gcattataga	5346
atagatttta	ataatcttat	agcattgtat	attattattg	ctgttgtcac	tgttattatt	5406
attgtggata	ctggcccttg	gtgtgttgca	tagctcccta	tgtattctct	gtttccatct	5466
ttaagttccc	agaccaatat	acattaagag	ttttgcatgg	tctaaattgt	gtttattoca	5526
accacgtgga	aagctcctgg	aaagaaattt	tacattcggg	tggtctgtgc	tcctaatagac	5586
acttgacctt	gttgaacaaa	tggcagagcc	tttcccaagg	atttgattgt	ttgtgaatta	5646
tctgcatgtg	tgcttttttt	tgggtgtgtat	ttcattaaaa	aatataaata	tttatgaaaa	5706
aaaaaaaa						5714

<210> 394
 <211> 612
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (78) .. (521)

<400>	394	
cctggagctc	ggtgacctgca	ggtacccggc cgggaattccc gggctcgaccc acgcgtccgg 60
ctgggtccag	cagcgcg	atg gca gct cag cgg ctg ggc aag cgc gtg ctg 110
		Met Ala Ala Gln Arg Leu Gly Lys Arg Val Leu

1

5

agc aag ctg cag tct cca tgc cgg gcc cgc ggg cca ggg ggc agt ccc	158
Ser Lys Leu Gln Ser Pro Ser Arg Ala Arg Gly Pro Gly Gly Ser Pro	
12 17 22 27	
ggg ggg ctg cag aag cgg cac gcg cgc gtc acc gtc aag tat gac cgg	206
Gly Gly Leu Gln Lys Arg His Ala Arg Val Thr Val Lys Tyr Asp Arg	
28 33 38 43	
cgg gag ctg cag cgg cgg ctg gac gtg gag aag tgg atc gac ggg cgc	254
Arg Glu Leu Gln Arg Arg Leu Asp Val Glu Lys Trp Ile Asp Gly Arg	
44 49 54 59	
ctg gag gag ctg tac cgc ggc atg gag gca gac atg ccc gat gag atc	302
Leu Glu Glu Leu Tyr Arg Gly Met Glu Ala Asp Met Pro Asp Glu Ile	
60 65 70 75	
aac att gat gaa ttg ttg gag tta gag agt gaa gag gag aga agc cgg	350
Asn Ile Asp Glu Leu Leu Glu Leu Glu Ser Glu Glu Glu Arg Ser Arg	
76 81 86 91	
aaa atc cag gga ctc ctg aag tca tgt ggg aaa cct gtc gag gac ttc	398
Lys Ile Gln Gly Leu Leu Lys Ser Cys Gly Lys Pro Val Glu Asp Phe	
92 97 102 107	
atc cag gag ctg ctg gca aag ctt caa ggc ctc cac agg cag ccc ggc	446
Ile Gln Glu Leu Leu Ala Lys Leu Gln Gly Leu His Arg Gln Pro Gly	
108 113 118 123	
ctc cgc cag cca agc ccc tcc cac gac ggc agc ctc agc ccc ctc cag	494
Leu Arg Gln Pro Ser Pro Ser His Asp Gly Ser Leu Ser Pro Leu Gln	
124 129 134 139	
gac cgg gcc cgg act gct cac ccc tga ccctc ttgcactctc cctgcccccc	546
Asp Arg Ala Arg Thr Ala His Pro *	
140 145	
ggacgccgcc cagcttgctt gtgtataagt tgtatttaaat gggtctgttaa caataaaaaa	606
aaaaaa	612

<210> 395

<211> 1691

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153)..(1691)

<400> 395

taattcggca gagggcatca actccagtgt ccgttttctc tggttttgtg aagactgcac 60

aaaactotca tgatggagaa ccaaaggact tagttacctg ttccagtgtc atctaaagtc 120

aactgaaaag tgaagcaggc agtaatacag cc	atg gaa aga aat tca agt tta	173
	Met Glu Arg Asn Ser Ser Leu	
	1 5	
tgg aag aac cta ata gat gaa cac cca gtc tgc aca acc tgg aag caa	221	
Trp Lys Asn Leu Ile Asp Glu His Pro Val Cys Thr Thr Trp Lys Gln		
8 13 18 23		
gag gcc gaa gga gcc att tat cat ctt gcc agt att tta ttt gta gta	269	
Glu Ala Glu Gly Ala Ile Tyr His Leu Ala Ser Ile Leu Phe Val Val		
24 29 34 39		
ggt ttc atg ggt ggc agt gga ttc ttc ggg ctc ctt tat gtc ttc agt	317	
Gly Phe Met Gly Gly Ser Gly Phe Phe Gly Leu Leu Tyr Val Phe Ser		
40 45 50 55		
ttg ctg ggg ttg ggt ttt ctc tgt tct gct gtc tgg gct tgg gta gat	365	
Leu Leu Gly Leu Gly Phe Leu Cys Ser Ala Val Trp Ala Trp Val Asp		
56 61 66 71		
gtc tgt gca gct gac ata ttt tcc tgg aat ttt gta ctg ttt gtc atc	413	
Val Cys Ala Ala Asp Ile Phe Ser Trp Asn Phe Val Leu Phe Val Ile		
72 77 82 87		
tgc ttc atg caa ttt gtt cat att gca tat caa gtt cgc agc ata acc	461	
Cys Phe Met Gln Phe Val His Ile Ala Tyr Gln Val Arg Ser Ile Thr		
88 93 98 103		
ttt gcc cga gaa ttc caa gtg ttg tac agc tcc ctt ttc cag ccc ctg	509	
Phe Ala Arg Glu Phe Gln Val Leu Tyr Ser Ser Leu Phe Gln Pro Leu		
104 109 114 119		
ggg atc tct ttg cct gtc ttc aga acg att gct ttg agc tct gaa gtg	557	
Gly Ile Ser Leu Pro Val Phe Arg Thr Ile Ala Leu Ser Ser Glu Val		
120 125 130 135		
gtt act ttg gaa aag gaa cac tgt tat gcc atg cag ggg aaa act tcc	605	
Val Thr Leu Glu Lys Glu His Cys Tyr Ala Met Gln Gly Lys Thr Ser		
136 141 146 151		
att gat aaa ctc tcc ttg ctt gtt tca gga agg atc aga gtg aca gtt	653	
Ile Asp Lys Leu Ser Leu Leu Val Ser Gly Arg Ile Arg Val Thr Val		
152 157 162 167		
gat ggc gaa ttt ctg cat tac att ttc ccc ctt cag ttc ctg gat tct	701	
Asp Gly Glu Phe Leu His Tyr Ile Phe Pro Leu Gln Phe Leu Asp Ser		
168 173 178 183		
cct gag tgg gat tca ctg aga ccc aca gag gaa ggc att ttt cag gta	749	
Pro Glu Trp Asp Ser Leu Arg Pro Thr Glu Glu Gly Ile Phe Gln Val		
184 189 194 199		
acc ctc act gca gaa act gat tgt cga tat gtg tct tgg agg aga aag	797	
Thr Leu Thr Ala Glu Thr Asp Cys Arg Tyr Val Ser Trp Arg Arg Lys		
200 205 210 215		
aaa tta tat ctg ctc ttt gct cag cat cgc tac atc tcc cgc ctt ttt	845	

Lys	Leu	Tyr	Leu	Leu	Phe	Ala	Gln	His	Arg	Tyr	Ile	Ser	Arg	Leu	Phe		
216					221					226					231		
tca	gtg	cta	att	ggc	agt	gac	att	gca	gat	aaa	ctc	tat	gcc	ttg	aat	893	
Ser	Val	Leu	Ile	Gly	Ser	Asp	Ile	Ala	Asp	Lys	Leu	Tyr	Ala	Leu	Asn		
232					237					242					247		
gac	agg	tca	ggc	ccc	tct	tct	gca	gaa	atg	ctg	cag	ttt	gct	gga	ggg	941	
Asp	Arg	Ser	Gly	Pro	Ser	Ser	Ala	Glu	Met	Leu	Gln	Phe	Ala	Gly	Gly		
248					253					258					263		
cca	ctc	cag	acc	ctc	ttt	gcc	tgt	gtt	tgc	cca	gtg	gag	gat	gca	gga	989	
Pro	Leu	Gln	Thr	Leu	Phe	Ala	Cys	Val	Ser	Pro	Val	Glu	Asp	Ala	Gly		
264					269					274					279		
cag	gaa	aga	ttg	ttg	cct	gct	cct	tcc	tca	aga	agc	ttc	atc	caa	gag	1037	
Gln	Glu	Arg	Leu	Leu	Pro	Ala	Pro	Ser	Ser	Arg	Ser	Phe	Ile	Gln	Glu		
280					285					290					295		
ggg	cac	tgg	cct	gat	gcc	agc	cag	agg	tct	cct	ctg	caa	aaa	caa	aca	1085	
Gly	His	Trp	Pro	Asp	Ala	Ser	Gln	Arg	Ser	Pro	Leu	Gln	Lys	Gln	Thr		
296					301					306					311		
agc	aaa	caa	aaa	aca	ata	aaa	tac	tta	gga	ata	tac	cta	aca	aag	gag	1133	
Ser	Lys	Gln	Lys	Thr	Ile	Lys	Tyr	Leu	Gly	Ile	Tyr	Leu	Thr	Lys	Glu		
312					317					322					327		
ttg	aaa	gac	ctc	tgc	aag	gaa	aac	tac	aaa	aca	ctg	ctg	aaa	gaa	ata	1181	
Leu	Lys	Asp	Leu	Cys	Lys	Glu	Asn	Tyr	Lys	Thr	Leu	Leu	Lys	Glu	Ile		
328					333					338					343		
gat	gat	gca	aac	aaa	tgg	aaa	cac	atc	cca	tgc	tca	tgg	atg	ggg	aga	1229	
Asp	Asp	Ala	Asn	Lys	Trp	Lys	His	Ile	Pro	Cys	Ser	Trp	Met	Gly	Arg		
344					349					354					359		
atc	aat	gtg	aaa	atg	acc	atg	ctg	cca	aaa	gca	atc	tac	aaa	ttc	aat	1277	
Ile	Asn	Val	Lys	Met	Thr	Met	Leu	Pro	Lys	Ala	Ile	Tyr	Lys	Phe	Asn		
360					365					370					375		
gca	atc	ccc	atc	aaa	ata	cca	cca	tca	ttc	ttc	aca	gag	tta	gaa	aag	1325	
Ala	Ile	Pro	Ile	Lys	Ile	Pro	Pro	Ser	Phe	Phe	Thr	Glu	Leu	Glu	Lys		
376					381					386					391		
aca	att	cta	aaa	ttc	ata	tgg	aac	caa	aaa	aga	gcc	cac	att	gtc	aaa	1373	
Thr	Ile	Leu	Lys	Phe	Ile	Trp	Asn	Gln	Lys	Arg	Ala	His	Ile	Val	Lys		
392					397					402					407		
gca	aga	cta	agc	aaa	aag	aac	aaa	tct	gga	ggc	atc	aca	cta	cct	gat	1421	
Ala	Arg	Leu	Ser	Lys	Lys	Asn	Lys	Ser	Gly	Gly	Ile	Thr	Leu	Pro	Asp		
408					413					418					423		
ttc	aaa	cga	tac	tac	aag	gcc	aca	gtc	acc	aaa	aca	gca	tgg	tac	tgg	1469	
Phe	Lys	Arg	Tyr	Tyr	Lys	Ala	Thr	Val	Thr	Lys	Thr	Ala	Trp	Tyr	Trp		
424					429					434					439		
tat	aga	aat	agg	cgc	ata	gac	caa	tgg	aac	aga	ata	gag	aac	cca	gaa	1517	
Tyr	Arg	Asn	Arg	Arg	Ile	Asp	Gln	Trp	Asn	Arg	Ile	Glu	Asn	Pro	Glu		

440	445	450	455	
ata aac cca aat act tac agc caa ctg atc ttt gac aaa gca aac aaa				1565
Ile Asn Pro Asn Thr Tyr Ser Gln Leu Ile Phe Asp Lys Ala Asn Lys				
456	461	466	471	
aac ata aac cag gga agg gac acc ctt ttc aac aga tgg tgc tgg gat				1613
Asn Ile Asn Gln Gly Arg Asp Thr Leu Phe Asn Arg Trp Cys Trp Asp				
472	477	482	487	
aat tgg cta gcc aca tgt agg aga atg aaa ctg gat tct cat ctc tca				1661
Asn Trp Leu Ala Thr Cys Arg Arg Met Lys Leu Asp Ser His Leu Ser				
488	493	498	503	
cct tat ata aaa atc aac tcg atg gat taa				1691
Pro Tyr Ile Lys Ile Asn Ser Met Asp *				
504	509			

<210> 396
 <211> 1943
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (35)..(1657)

<400> 396		
atttgccct cgaggccaag aattcggcac gagg	atg gct cta gcg cgg ccg	52
	Met Ala Leu Ala Arg Pro	
	1	

gtg cgg ctc ttt tcc ctc gtg act cgg ttg ctc ctg gcg ccg cga cgg	100
Val Arg Leu Phe Ser Leu Val Thr Arg Leu Leu Leu Ala Pro Arg Arg	
7 12 17 22	

ggc ctc acg gtc cgc agt ccc gac gaa ccc ctg ccg gtg gtg cgc atc	148
Gly Leu Thr Val Arg Ser Pro Asp Glu Pro Leu Pro Val Val Arg Ile	
23 28 33 38	

cca gtg gct cta cag cgg cag ttg gaa cag cgg cag agc agg cgg cgg	196
Pro Val Ala Leu Gln Arg Gln Leu Glu Gln Arg Gln Ser Arg Arg Arg	
39 44 49 54	

aac ctc ccg agg ccg gtg ctg gtt cga ccc gga ccg ctg ctg gtt tgg	244
Asn Leu Pro Arg Pro Val Leu Val Arg Pro Gly Pro Leu Leu Val Ser	
55 60 65 70	

gcg cgg cgg ccg gag ttg aac cag ccg gcg cgc ctc aca ctg ggc cgt	292
Ala Arg Arg Pro Glu Leu Asn Gln Pro Ala Arg Leu Thr Leu Gly Arg	
71 76 81 86	

tgg gag cgc gcg ccg cta gcc tct caa ggc tgg aag agt cga cgc gcg	340
---	-----

Trp Glu Arg Ala Pro Leu Ala Ser Gln Gly Trp Lys Ser Arg Arg Ala
87 92 97 102

cgt cgg gac cac ttc tcc atc gag cgc gcg caa cag gag gcg cca gcg 388
Arg Arg Asp His Phe Ser Ile Glu Arg Ala Gln Gln Glu Ala Pro Ala
103 108 113 118

gtg cga aag ctc tcg tct aag ggc agc ttt gct gac ctg ggc ctg gag 436
Val Arg Lys Leu Ser Ser Lys Gly Ser Phe Ala Asp Leu Gly Leu Glu
119 124 129 134

ccc cgt gtg ctg cac gca cta cag gag gct gcg cct gaa gtc gtt cag 484
Pro Arg Val Leu His Ala Leu Gln Glu Ala Ala Pro Glu Val Val Gln
135 140 145 150

ccc aca acc gtg cag tct agc acc atc ccc tca cta ctt cgc ggc cgc 532
Pro Thr Thr Val Gln Ser Ser Thr Ile Pro Ser Leu Leu Arg Gly Arg
151 156 161 166

cat gtc gtt tgc gcc gca gaa acc ggc agt ggc aag act ctc agc tac 580
His Val Val Cys Ala Ala Glu Thr Gly Ser Gly Lys Thr Leu Ser Tyr
167 172 177 182

ctc ctg ccg ctg ctt caa cgg ctc ttg ggc cag cca agc ctg gac tcc 628
Leu Leu Pro Leu Leu Gln Arg Leu Leu Gly Gln Pro Ser Leu Asp Ser
183 188 193 198

ctt cct atc ccc gcg ccc cga ggc ctg gtc ctt gtt cct tcc cga gaa 676
Leu Pro Ile Pro Ala Pro Arg Gly Leu Val Leu Val Pro Ser Arg Glu
199 204 209 214

ttg gcc caa cag gtg cgg gct gtg gcc caa ccc ttg ggc cgc tcc ttg 724
Leu Ala Gln Gln Val Arg Ala Val Ala Gln Pro Leu Gly Arg Ser Leu
215 220 225 230

ggc ctg ctg gtg cgg gac ctg gag gga ggc cac ggc atg cgt agg atc 772
Gly Leu Leu Val Arg Asp Leu Glu Gly Gly His Gly Met Arg Arg Ile
231 236 241 246

agg ctg cag ctg tcc aga cag cct tca gca gat gtg ctt gtg gcc act 820
Arg Leu Gln Leu Ser Arg Gln Pro Ser Ala Asp Val Leu Val Ala Thr
247 252 257 262

cca ggg gct ctg tgg aag gcc ctg aaa agt cga ctg atc agt ctg gag 868
Pro Gly Ala Leu Trp Lys Ala Leu Lys Ser Arg Leu Ile Ser Leu Glu
263 268 273 278

caa ctc tcc ttc ttg gtg ttg gat gag gca gac aca ctg ctg gat gaa 916
Gln Leu Ser Phe Leu Val Leu Asp Glu Ala Asp Thr Leu Leu Asp Glu
279 284 289 294

agc ttc ctg gaa ctg gtg gac tac atc tta gag aag agc cac ata gca 964
Ser Phe Leu Glu Leu Val Asp Tyr Ile Leu Glu Lys Ser His Ile Ala
295 300 305 310

gaa ggc cca gct gac ttg gaa gac ccc ttc aat ccc aaa gct cag tta 1012
Glu Gly Pro Ala Asp Leu Glu Asp Pro Phe Asn Pro Lys Ala Gln Leu

311	316	321	326	
gtg ctg gta gga gcc aca ttt ccc gaa ggt gta ggc cag ttg ctg aat				1060
Val Leu Val Gly Ala Thr Phe Pro Glu Gly Val Gly Gln Leu Leu Asn				
327	332	337	342	
aaa gtc gcc agc cca gat gct gtc acc acc atc acc agc tcc aag ctc				1108
Lys Val Ala Ser Pro Asp Ala Val Thr Thr Ile Thr Ser Ser Lys Leu				
343	348	353	358	
cac tgt atc atg cct cat gtg aaa cag aca ttt ctg aga ctg aag gga				1156
His Cys Ile Met Pro His Val Lys Gln Thr Phe Leu Arg Leu Lys Gly				
359	364	369	374	
gca gat aag gtg gcc gag ctg gtg cac atc ctc aag cat cgt gac aga				1204
Ala Asp Lys Val Ala Glu Leu Val His Ile Leu Lys His Arg Asp Arg				
375	380	385	390	
gca gaa agg act ggt ccc tca gga act gtt ctg gtg ttc tgt aat agc				1252
Ala Glu Arg Thr Gly Pro Ser Gly Thr Val Leu Val Phe Cys Asn Ser				
391	396	401	406	
tcc agc act gtg aac tgg ctg gga tat att ctg gat gac cac aaa atc				1300
Ser Ser Thr Val Asn Trp Leu Gly Tyr Ile Leu Asp Asp His Lys Ile				
407	412	417	422	
caa cac cta agg ttg cag ggg caa atg cca gcc ttg atg agg gta gga				1348
Gln His Leu Arg Leu Gln Gly Gln Met Pro Ala Leu Met Arg Val Gly				
423	428	433	438	
atc ttc cag tcc ttc cag aag agc tcc cga gac ata ctt ctc tgc aca				1396
Ile Phe Gln Ser Phe Gln Lys Ser Ser Arg Asp Ile Leu Leu Cys Thr				
439	444	449	454	
gac ata gcc tct cgg ggc ctg gac agc act ggt gtg gag ctg gtt gtc				1444
Asp Ile Ala Ser Arg Gly Leu Asp Ser Thr Gly Val Glu Leu Val Val				
455	460	465	470	
aat tat gat ttc ccc cca acg ctg caa gat tac atc cac aga gca ggg				1492
Asn Tyr Asp Phe Pro Pro Thr Leu Gln Asp Tyr Ile His Arg Ala Gly				
471	476	481	486	
aga gtg ggc cgt gtg ggg agc gag gtg cca ggc acc gtc atc agt ttt				1540
Arg Val Gly Arg Val Gly Ser Glu Val Pro Gly Thr Val Ile Ser Phe				
487	492	497	502	
gtg acc cat ccc tgg gat gtg agc ctg gtt cag aag att gag ctg gcg				1588
Val Thr His Pro Trp Asp Val Ser Leu Val Gln Lys Ile Glu Leu Ala				
503	508	513	518	
gct cgc cga agg aga agt ctt cca gga cta gca tcc tcg gtg aaa gag				1636
Ala Arg Arg Arg Arg Ser Leu Pro Gly Leu Ala Ser Ser Val Lys Glu				
519	524	529	534	
cct ttg ccc caa gca acc tga tt ttgacaaatc tgattaaaat gtgatgctag				1689
Pro Leu Pro Gln Ala Thr *				
535	540			

aacagggatc tttccagta tcttgagtgg gtgaccacac ttgtcagtgg gaggctctgg 1749
 gctgccctgt cggctccttg agggcgggat gaactgcttt gtgacttggg aaggtacgct 1809
 gctggccagc attggagaag aagctgctga gcatggcttt ctgtagtctt tagcaagaca 1869
 caagtggatt ttgactttgt atcatgtcat gatttctaac aataaatgat gtttttatgt 1929
 gcaaaaaaaaa aaaa 1943

<210> 397
 <211> 1895
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (71)..(808)

<400> 397
 ttggactgag tgcaatcgga cgcgccgacc gggctoggaat taccgggccc acccacgcgt 60
 ccgccggaag atg gaa agg act gag atg atg ccc aca att aac tcc cag 109
 Met Glu Arg Thr Glu Met Met Pro Thr Ile Asn Ser Gln
 1 5 10
 ctg gaa ttt aaa agt aag cct ttt cct tta gtc tcc tct tcc cgg tgg 157
 Leu Glu Phe Lys Ser Lys Pro Phe Pro Leu Val Ser Ser Ser Arg Trp
 14 19 24 29
 ttg gta aaa aga ggt gaa ttg aca gcc tat gtt gaa gac act gtg ctt 205
 Leu Val Lys Arg Gly Glu Leu Thr Ala Tyr Val Glu Asp Thr Val Leu
 30 35 40 45
 ttc tca aga agg aca tcc aaa cag caa gtc tac ttc ttt ctc ttt aac 253
 Phe Ser Arg Arg Thr Ser Lys Gln Gln Val Tyr Phe Phe Leu Phe Asn
 46 51 56 61
 gat gtg ctc att atc acc aag aag aag agt gaa gaa agt tac aac gtc 301
 Asp Val Leu Ile Ile Thr Lys Lys Lys Ser Glu Glu Ser Tyr Asn Val
 62 67 72 77
 aat gat tat tcc tta aga gat cag cta ttg gtg gaa tct tgt gac aat 349
 Asn Asp Tyr Ser Leu Arg Asp Gln Leu Leu Val Glu Ser Cys Asp Asn
 78 83 88 93
 gaa gag ctt aat tct tct cca ggg aag aac agc tcc aca atg ctc tat 397
 Glu Glu Leu Asn Ser Ser Pro Gly Lys Asn Ser Ser Thr Met Leu Tyr
 94 99 104 109
 tca aga cag agc tct gcc agt cac ctc ttt act ctg aca gtc ctt agt 445
 Ser Arg Gln Ser Ser Ala Ser His Leu Phe Thr Leu Thr Val Leu Ser
 110 115 120 125

aac cac gcg aat gag aaa gtg gag atg cta cta gga gct gag acg cag	493
Asn His Ala Asn Glu Lys Val Glu Met Leu Leu Gly Ala Glu Thr Gln	
126 131 136 141	
agc gag cga gcc cgc tgg ata act gcc ctg gga cac agc agc ggg aag	541
Ser Glu Arg Ala Arg Trp Ile Thr Ala Leu Gly His Ser Ser Gly Lys	
142 147 152 157	
ccg cct gca gac cga acc tca ctg acc cag gtg gaa atc gtt agg tca	589
Pro Pro Ala Asp Arg Thr Ser Leu Thr Gln Val Glu Ile Val Arg Ser	
158 163 168 173	
ttt act gct aag cag cca gat gaa ctc tcc ctg cag gtg gct gac gtc	637
Phe Thr Ala Lys Gln Pro Asp Glu Leu Ser Leu Gln Val Ala Asp Val	
174 179 184 189	
gtc ctc atc tat caa cgt gtc agc gat ggc tgg tat gag ggg gaa cga	685
Val Leu Ile Tyr Gln Arg Val Ser Asp Gly Trp Tyr Glu Gly Glu Arg	
190 195 200 205	
cta cga gat gga gaa aga ggc tgg ttt cct atg gaa tgt gcc aag gag	733
Leu Arg Asp Gly Glu Arg Gly Trp Phe Pro Met Glu Cys Ala Lys Glu	
206 211 216 221	
ata aca tgt caa gct aca att gat aag aat gtg gag aga atg gga cgc	781
Ile Thr Cys Gln Ala Thr Ile Asp Lys Asn Val Glu Arg Met Gly Arg	
222 227 232 237	
ttg cta gga ctg gag acc aac gtg tag tctct cagatggtct tttgttactg	833
Leu Leu Gly Leu Glu Thr Asn Val *	
238 243	
caagatttgc acgacactta ccgggctggt tgggtctggg ctagttttat tgttaatttt	893
gtcacagcct atttaattaa aagaacgaaa acacttgcct ttaagcttgc caggttggtc	953
cgctctctca tgagaagagc ttggatacag tgagtttgca cagctcagtt tttacctaac	1013
cacacacttg cagacctcct gaggtacaca gaatagctga gcagttcact tcagggatca	1073
ggtcactctct gctcctccta gtttcaocat gttctggcaa taaaaaacac atatttatatc	1133
ctggttttct ctatccttgc attactaagg tgactgtctc tctttataca tccttgatatg	1193
gttctcccag tattagcaag attgtatatc tgtaaagaat gtccagtttt gtaaataattt	1253
ccctgccttt ttttttcttt ttttacctct gattttaatg cttcgttaac ttcaaaagga	1313
actggtagag ttcagaaggt gagctgttgt ttttctaaac ctcttcccag gaaggggaca	1373
ttgacacttg aatttttgtc acctttttcc tcattagaag gaaagtagaa agccttactg	1433
taggattttt aaaaaaaaaat ccatctcacc/ccatattggt cttaaataag tatagactaa	1493
ttaacctaag ctacctttta caacgtagaa tttagatggg ttcatatatg tgagaaaaac	1553

ctgaatatag gacaggggtc ctactttttt cccacctct gtcgccagg ctagagtata 1613
gtggtgtgat cttggccac tgcaacctct gcttcctagg ttcaagtgat tctcctgcct 1673
cagcctccca agtagctggg attgtaagag tatgccacca cgcacagcta ctttttgtat 1733
ttttagtaga gacaggggtt catcatgttg gccaggatgg tctcttaact cctgccctca 1793
agtgatccac cagagaggag atcctcggcc tccccaaagt ctgggattat aggcatgagc 1853
cacctgccc agcctacttt ctaattaatt aaaaaaaaaa aa 1895

<210> 398
<211> 1878
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (550)..(1185)

<400> 398
ccgtgccagc ttggcacgag gggctcgtgg gggggttggc tggggagccc acgctgcctg 60
gcgactcggg ccaccgaatg tgagaccgag tccctttatg tccactagcg acacgctgat 120
ttgaaccctg cttcgacgtg tgtgtcatgg cttaaaaata gctgctaata tgtcaacctg 180
tcttgggcag aaacagcggc ggcgacagca gcaggagcgt catggccgtg gcgctgtctg 240
cgccggcgat ccgcctttcg gactgaggcc cagcgcagcg cttgcaaaga gagccaaaga 300
gctgagcaaaa aggagctgct gcagcttgaa gaaaaagcca cccctgaagg ctctgccag 360
agccaggctt accttctctc cctcgagaat cttctccga aggaccagcc caggggaagg 420
aagcagctgc tctggactca ctcaagtgtg tctcacatcc tttcctcttc cagcagcagc 480
tacctggcaa ctgaacccat catcaccaca gccactcctg cagctgccac ggtttctgcc 540
acctctaag atg tgc cct ggt aac tgg ctt tgg gct tct atg act ttt 588
Met Cys Pro Gly Asn Trp Leu Trp Ala Ser Met Thr Phe
1 5 10
atg gcc cgc ttc tcc cgg agt agc tca agg tct cct gtt cga act cga 636
Met Ala Arg Phe Ser Arg Ser Ser Ser Arg Ser Pro Val Arg Thr Arg
14 19 24 29
ggg acc ctg gag gag atg cca acc gtt caa cat cct ttc ctc aat gtc 684
Gly Thr Leu Glu Glu Met Pro Thr Val Gln His Pro Phe Leu Asn Val
30 35 40 45
ttc gag ttg gag cgg ctc ctc tac aca ggc aag aca gcc tgt aac cat 732
Phe Glu Leu Glu Arg Leu Leu Tyr Thr Gly Lys Thr Ala Cys Asn His

46	51	56	61	
gcc gac gag gtc tgg cca ggc ctc tat ctc gga gac cag gac atg gct				780
Ala Asp Glu Val Trp Pro Gly Leu Tyr Leu Gly Asp Gln Asp Met Ala				
62	67	72	77	
aac aac cgc cgg gag ctt cgc cgc ctg ggc atc acg cac gtc ctc aat				828
Asn Asn Arg Arg Glu Leu Arg Arg Leu Gly Ile Thr His Val Leu Asn				
78	83	88	93	
gcc tca cac agc cgg tgg cga ggc acg ccc gag gcc tat gag ggg ctg				876
Ala Ser His Ser Arg Trp Arg Gly Thr Pro Glu Ala Tyr Glu Gly Leu				
94	99	104	109	
ggc atc cgc tac ctg ggt gtt gag gcc cac gac tcg cca gcc ttt gac				924
Gly Ile Arg Tyr Leu Gly Val Glu Ala His Asp Ser Pro Ala Phe Asp				
110	115	120	125	
atg agc atc cac ttc cag acg gct gcc gac ttc atc cac cgg gcg ctg				972
Met Ser Ile His Phe Gln Thr Ala Ala Asp Phe Ile His Arg Ala Leu				
126	131	136	141	
agc cag cca gga ggg aag atc ctg gtg cat tgt gct gtg ggc gtg agc				1020
Ser Gln Pro Gly Gly Lys Ile Leu Val His Cys Ala Val Gly Val Ser				
142	147	152	157	
cga tcc gcc acc ctg gta ctg gcc tac ctc atg ctg tac cac cac ctt				1068
Arg Ser Ala Thr Leu Val Leu Ala Tyr Leu Met Leu Tyr His His Leu				
158	163	168	173	
acc ctc gtg gag gcc atc aag aaa gtc aaa gac cac cga ggc atc atc				1116
Thr Leu Val Glu Ala Ile Lys Lys Val Lys Asp His Arg Gly Ile Ile				
174	179	184	189	
ccc aac cgg ggc ttc ctg agg cag ctc ctg gcc ctg gac cgc agg ctg				1164
Pro Asn Arg Gly Phe Leu Arg Gln Leu Leu Ala Leu Asp Arg Arg Leu				
190	195	200	205	
cgg cag ggt ctg gaa gca tga gg ggagggggag agaggtcagg ccaggcccgt				1217
Arg Gln Gly Leu Glu Ala *				
206	211			
gggtaggtcc ctggctccca gctggagata ggaggcccag gtggcaggta gcaggaggcc				1277
cagatcacc atcctcccct ggggtcagga gaggccgagc ccaggccac tgtcactctt				1337
tgtgggaggg gacggggagt gaggttgggc agtgtggtgg atgggcaccc aggaagggtt				1397
gaccagggaa ggaggcagct aggotgtaga tggaagatgg tcctgggatt cgaacaccgc				1457
tgggatctgg ccagggtgct coctgggatt cacagtccct tcccctcttt gtgcccaggt				1517
gtttccctct ctcctcacc aaaacaaaag ggccatctct gccctgcact tgtgcagaaa				1577
gtcagggata cggcaagcat gaatgcaatg gtgtagagtt gtgtgaaacc cctagcatag				1637
agacagacag cgaagagatg gtgtgaaaag cttgcagaac cagacagaga accccacaga				1697

ctttccactc caagcacagg aggaggtagc tagcgtgtga gggttggcac taggcccacg 1757
gctgctgctt gggccaaaaa catacagagg tgcattggctg gcagtcttga aattgtcact 1817
cgcttactgg atccaagcgt ctcgaggata aataaagatc atgaaaaaga aaaaaaaaaa 1877
a 1878

<210> 399
<211> 1573
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (163) .. (1092)

<400> 399
accggaccgg aattcccggg tcgacgattt catggccagc caggggttaga tggtctgagg 60
aggcggggagc aaccgagaga gcacgtgagc atctgtcctt tctaccggtt catctttatc 120
tttagtggtc agtagcagcg gggatagccc gggggccggg gt atg gcc acg gag 174
Met Ala Thr Glu
1
tta cag tgt ccg gac tcc atg ccc tgt cac aac cag caa gta aac tct 222
Leu Gln Cys Pro Asp Ser Met Pro Cys His Asn Gln Gln Val Asn Ser
5 10 15 20
gcc tca acc cca agt ccc gag cag ctg cga cct ggc gat ctg atc ctg 270
Ala Ser Thr Pro Ser Pro Glu Gln Leu Arg Pro Gly Asp Leu Ile Leu
21 26 31 36
gac cac gca ggg gga aac aga gcc tcc agg gcc aag gtg att ctc ctc 318
Asp His Ala Gly Gly Asn Arg Ala Ser Arg Ala Lys Val Ile Leu Leu
37 42 47 52
acg ggg tac gcc cat tct agc ctg ccg gcc gag ctg gac tct ggg gcc 366
Thr Gly Tyr Ala His Ser Ser Leu Pro Ala Glu Leu Asp Ser Gly Ala
53 58 63 68
tgc ggc ggc tcc agc ctc aac tca gag ggc aac agt ggt agt ggt gac 414
Cys Gly Gly Ser Ser Leu Asn Ser Glu Gly Asn Ser Gly Ser Gly Asp
69 74 79 84
agt agc agc tat gac gca cca gct ggc aac tcc ttc cta gag gac tgc 462
Ser Ser Ser Tyr Asp Ala Pro Ala Gly Asn Ser Phe Leu Glu Asp Cys
85 90 95 100
gaa ctc tcc cgg cag atc ggg gcg cag ctt aag ctg ctg cct atg aat 510
Glu Leu Ser Arg Gln Ile Gly Ala Gln Leu Lys Leu Leu Pro Met Asn
101 106 111 116

gat cag ata cgg gag cta cag acc atc atc cgg gac aag aca gcc agt	558
Asp Gln Ile Arg Glu Leu Gln Thr Ile Ile Arg Asp Lys Thr Ala Ser	
117 122 127 132	
aga ggt gac ttc atg ttt tct gcg gat cgt ttg atc aga ctt gtt gtg	606
Arg Gly Asp Phe Met Phe Ser Ala Asp Arg Leu Ile Arg Leu Val Val	
133 138 143 148	
gaa gag gga ttg aat cag ctg cca tat aaa gaa tgc atg gtg acc act	654
Glu Glu Gly Leu Asn Gln Leu Pro Tyr Lys Glu Cys Met Val Thr Thr	
149 154 159 164	
cca aca ggg tac aag tat gaa gga gtg aaa ttt gag aag gga aat tgt	702
Pro Thr Gly Tyr Lys Tyr Glu Gly Val Lys Phe Glu Lys Gly Asn Cys	
165 170 175 180	
ggg gtc agc ata atg aga agc ggt gag gca atg gaa caa ggt tta cga	750
Gly Val Ser Ile Met Arg Ser Gly Glu Ala Met Glu Gln Gly Leu Arg	
181 186 191 196	
gac tgc tgt cga tcc ata cga att gga aag atc ctg att cag agt gat	798
Asp Cys Cys Arg Ser Ile Arg Ile Gly Lys Ile Leu Ile Gln Ser Asp	
197 202 207 212	
gag gag aca caa aga gcc aaa gta tat tat gcc aaa ttc ccc cca gac	846
Glu Glu Thr Gln Arg Ala Lys Val Tyr Tyr Ala Lys Phe Pro Pro Asp	
213 218 223 228	
att tac cgg aga aaa gtc ctt ctg atg tat cca att ctc agc act gga	894
Ile Tyr Arg Arg Lys Val Leu Leu Met Tyr Pro Ile Leu Ser Thr Gly	
229 234 239 244	
aat act gta att gaa gct gta aag gtt ctt ata gaa cat gga gtt caa	942
Asn Thr Val Ile Glu Ala Val Lys Val Leu Ile Glu His Gly Val Gln	
245 250 255 260	
ccc agt gtt atc atc cta ctc agt ctg ttc tcc act cct cat ggt gcc	990
Pro Ser Val Ile Ile Leu Leu Ser Leu Phe Ser Thr Pro His Gly Ala	
261 266 271 276	
aaa tca atc att cag gag ttt cca gag atc aca att tta act act gaa	1038
Lys Ser Ile Ile Gln Glu Phe Pro Glu Ile Thr Ile Leu Thr Thr Glu	
277 282 287 292	
gtt cat cct gtt gca cct aca cat ttt gga cag aaa tac ttt gga aca	1086
Val His Pro Val Ala Pro Thr His Phe Gly Gln Lys Tyr Phe Gly Thr	
293 298 303 308	
gac taa gttatttaag taaaataatt gtcttatgta atattacaat catgttttga	1142
Asp *	
309	
ttttctatatt gttttactga ttcacttgag ggtggcagag aaaaatgtgt taaaatgctt	1202
tttagttttg gaagtgggta tatttgaggt tatatctcat ttagttattt gtttactgtt	1262

ggcaccgaat tcaacaatga agtatatgca actottacaa aacataaatt ttaataatat 1322
tctaatagcaa attactgaac cctcagtgca ttaaaattat ttcttaattt atgagcctct 1382
tagtttggag gttgcttgaa gccacaaata aaactcaaat gagagtcagt tctttgtccc 1442
actgtagttt gcattttgtt tagtttggtt ttagctctac taaggtttca catatgtggc 1502
tattgccaca ttctataact gttttctttc tgatactgga caatgtattg cggcgcctct 1562
agaggatcca t 1573

<210> 400
<211> 3889
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (8)..(2908)

<400> 400
ttcacag atg cac tgc tca ggc ctg gcc tgg cat cct gac ata gcc acc 49
Met His Cys Ser Gly Leu Ala Trp His Pro Asp Ile Ala Thr
1 5 10
cag tta gtg ctg tgc tca gag gat gat cga ctt ccc gtg att cag ctg 97
Gln Leu Val Leu Cys Ser Glu Asp Asp Arg Leu Pro Val Ile Gln Leu
15 20 25 30
tgg gac ttg cgc ttt gcc tcc tcg ccc ttg aag gtg ctg gag agc cac 145
Trp Asp Leu Arg Phe Ala Ser Ser Pro Leu Lys Val Leu Glu Ser His
31 36 41 46
agc agg ggg atc ttg tca gtg tca tgg agc cag gct gat gct gag ctg 193
Ser Arg Gly Ile Leu Ser Val Ser Trp Ser Gln Ala Asp Ala Glu Leu
47 52 57 62
ctg ctc act agt gct aag gac agc cag atc ttg tgc cgg aac ctg ggg 241
Leu Leu Thr Ser Ala Lys Asp Ser Gln Ile Leu Cys Arg Asn Leu Gly
63 68 73 78
agc agt gag gtg gta tat aag cta cca aca cag agc agc tgg tgc ttt 289
Ser Ser Glu Val Val Tyr Lys Leu Pro Thr Gln Ser Ser Trp Cys Phe
79 84 89 94
gat gtg cag tgg tgc cct cgg gac cct tca gtg ttc tct gct gcc tcc 337
Asp Val Gln Trp Cys Pro Arg Asp Pro Ser Val Phe Ser Ala Ala Ser
95 100 105 110
ttc aac ggc tgg atc agt ttg tac tct gtg atg ggt agg agc tgg gaa 385
Phe Asn Gly Trp Ile Ser Leu Tyr Ser Val Met Gly Arg Ser Trp Glu
111 116 121 126

gtc cag cat atg aga cag gct gac aag atc tcc tct tcc ttc agc aaa	433
Val Gln His Met Arg Gln Ala Asp Lys Ile Ser Ser Ser Phe Ser Lys	
127 132 137 142	
ggc cag cct ctc cca cca ctg cag gtg cca gag caa gtg gca caa gca	481
Gly Gln Pro Leu Pro Pro Leu Gln Val Pro Glu Gln Val Ala Gln Ala	
143 148 153 158	
cca ctg ata cct ccc ctg aaa aaa ccc ccc aaa tgg att aga aga cca	529
Pro Leu Ile Pro Pro Leu Lys Lys Pro Pro Lys Trp Ile Arg Arg Pro	
159 164 169 174	
aca ggt gtt tca ttt gct ttt gga ggg aag ctg gtt act ttt ggc ctc	577
Thr Gly Val Ser Phe Ala Phe Gly Gly Lys Leu Val Thr Phe Gly Leu	
175 180 185 190	
ccc agc acc cct gcc cat ctg gtg cca cag cct tgc ccc cgc cta gtc	625
Pro Ser Thr Pro Ala His Leu Val Pro Gln Pro Cys Pro Arg Leu Val	
191 196 201 206	
ttc atc agt caa gtc acc aca gaa tct gaa ttc ctg atg cga tca gct	673
Phe Ile Ser Gln Val Thr Thr Glu Ser Glu Phe Leu Met Arg Ser Ala	
207 212 217 222	
gag ctg cag gag gcc ttg gga tca gga aat cta ctg aat tac tgt cag	721
Glu Leu Gln Glu Ala Leu Gly Ser Gly Asn Leu Leu Asn Tyr Cys Gln	
223 228 233 238	
aac aag agc cag caa gct tta ctg caa agt gaa aag atg ctg tgg cag	769
Asn Lys Ser Gln Gln Ala Leu Leu Gln Ser Glu Lys Met Leu Trp Gln	
239 244 249 254	
ttc ctg aag gtg acc tta gag caa gac tcc aga atg aaa ttc cta aag	817
Phe Leu Lys Val Thr Leu Glu Gln Asp Ser Arg Met Lys Phe Leu Lys	
255 260 265 270	
ctt tta gga tac agt aaa gat gag ctt cag aag aag gtg gcc aca tgg	865
Leu Leu Gly Tyr Ser Lys Asp Glu Leu Gln Lys Lys Val Ala Thr Trp	
271 276 281 286	
ttg aag agt gac gtg ggg cta ggt gag agt cct cag ccc aag gga aat	913
Leu Lys Ser Asp Val Gly Leu Gly Glu Ser Pro Gln Pro Lys Gly Asn	
287 292 297 302	
gac ctc aac agt gac aga caa cag gcc ttc tgc agc cag gcc tcc aaa	961
Asp Leu Asn Ser Asp Arg Gln Gln Ala Phe Cys Ser Gln Ala Ser Lys	
303 308 313 318	
cac acc aca aag gaa gcc tct gct tcc tca gcc ttc ttt gat gag ctg	1009
His Thr Thr Lys Glu Ala Ser Ala Ser Ser Ala Phe Phe Asp Glu Leu	
319 324 329 334	
gtc cct cag aac atg act cct tgg gag atc ccc atc aca aaa gat att	1057
Val Pro Gln Asn Met Thr Pro Trp Glu Ile Pro Ile Thr Lys Asp Ile	
335 340 345 350	
gat gga ctc cta agc cag gct ctc ctg ctt ggg gaa ctg ggt ccg gcc	1105

Asp Gly Leu Leu Ser Gln Ala Leu Leu Leu Gly Glu Leu Gly Pro Ala	
351 356 361 366	
gtg gag ctg tgt ctg aag gag gag cgc ttt gct gat gcc att atc ctg	1153
Val Glu Leu Cys Leu Lys Glu Glu Arg Phe Ala Asp Ala Ile Ile Leu	
367 372 377 382	
gcc cag gct ggg ggt aca gat ctg ctg aag caa aca cag gag cgc tac	1201
Ala Gln Ala Gly Gly Thr Asp Leu Leu Lys Gln Thr Gln Glu Arg Tyr	
383 388 393 398	
ttg gcc aag aag aaa acc aaa atc tcc tgc ctt cta gcc tgt gtt gtg	1249
Leu Ala Lys Lys Lys Thr Lys Ile Ser Ser Leu Leu Ala Cys Val Val	
399 404 409 414	
caa aag aat tgg aag gat gtg gtg tgt acc tgt agc ctg aag aac tgg	1297
Gln Lys Asn Trp Lys Asp Val Val Cys Thr Cys Ser Leu Lys Asn Trp	
415 420 425 430	
aga gag gca ctg gct ttg cta ctg aca tac tca ggc aca gag aaa ttt	1345
Arg Glu Ala Leu Ala Leu Leu Leu Thr Tyr Ser Gly Thr Glu Lys Phe	
431 436 441 446	
ccc gag ctc tgt gac atg ctg gga act cgc atg gaa cag gag ggc agg	1393
Pro Glu Leu Cys Asp Met Leu Gly Thr Arg Met Glu Gln Glu Gly Arg	
447 452 457 462	
agg gta cta acc tcc gaa gcc aga ctc tgt tat gtg tgc tca ggg agt	1441
Arg Val Leu Thr Ser Glu Ala Arg Leu Cys Tyr Val Cys Ser Gly Ser	
463 468 473 478	
gtg gag cgg ctg gtg gag tgc tgg gca aaa tgc cac cag gct ttg tcc	1489
Val Glu Arg Leu Val Glu Cys Trp Ala Lys Cys His Gln Ala Leu Ser	
479 484 489 494	
ccc atg gct ctg cag gac ctg atg gag aag gtg atg gtt ctt aac agg	1537
Pro Met Ala Leu Gln Asp Leu Met Glu Lys Val Met Val Leu Asn Arg	
495 500 505 510	
agc ttg gag caa ctg cgg ggt cct cat ggg gtg agc cca ggc cct gcc	1585
Ser Leu Glu Gln Leu Arg Gly Pro His Gly Val Ser Pro Gly Pro Ala	
511 516 521 526	
aca acc tac agg gtc act cag tat gcc aac ctc ctg gca gcc cag ggc	1633
Thr Thr Tyr Arg Val Thr Gln Tyr Ala Asn Leu Leu Ala Ala Gln Gly	
527 532 537 542	
agc ctg gcc act gcc atg agc ttt cta ccc agg gac tgt gct cag cca	1681
Ser Leu Ala Thr Ala Met Ser Phe Leu Pro Arg Asp Cys Ala Gln Pro	
543 548 553 558	
cca gtt cag cag cta aga gat cgg ctt ttt cat gct caa ggt tct gct	1729
Pro Val Gln Gln Leu Arg Asp Arg Leu Phe His Ala Gln Gly Ser Ala	
559 564 569 574	
gtc ttg ggc caa cag tct ccc cct ttc ccc ttc ccc cgg att gtt gtg	1777
Val Leu Gly Gln Gln Ser Pro Pro Phe Pro Phe Pro Arg Ile Val Val	

575	580	585	590	
gga gct acc ctc cac tct aaa gag aca tca tct tac aga ttg gga tcc				1825
Gly Ala Thr Leu His Ser Lys Glu Thr Ser Ser Tyr Arg Leu Gly Ser				
591	596	601	606	
cag cct tct cac cag gtc cca act cca tct cca agg cca agg gtt ttc				1873
Gln Pro Ser His Gln Val Pro Thr Pro Ser Pro Arg Pro Arg Val Phe				
607	612	617	622	
acc cct cag tca tca cca gcg atg ccc ttg gca cct tcc cat cct agc				1921
Thr Pro Gln Ser Ser Pro Ala Met Pro Leu Ala Pro Ser His Pro Ser				
623	628	633	638	
cct tat cag ggt ccc agg aca cag aat ata agt gac tac agg gca cct				1969
Pro Tyr Gln Gly Pro Arg Thr Gln Asn Ile Ser Asp Tyr Arg Ala Pro				
639	644	649	654	
ggg ccc cag gcc atc cag cct ttg cct ttg agc cct ggg gta agg cct				2017
Gly Pro Gln Ala Ile Gln Pro Leu Pro Leu Ser Pro Gly Val Arg Pro				
655	660	665	670	
gct tca tct cag cca cag cta tta gga ggg caa agg gtg caa gtt cct				2065
Ala Ser Ser Gln Pro Gln Leu Leu Gly Gly Gln Arg Val Gln Val Pro				
671	676	681	686	
aac ccg gtg gga ttc cct ggg aca tgg cct ctt cct ggt tcc cct cta				2113
Asn Pro Val Gly Phe Pro Gly Thr Trp Pro Leu Pro Gly Ser Pro Leu				
687	692	697	702	
ccc atg gca tgc cca ggc atc atg cga cct ggc tct acc tcc ctg cct				2161
Pro Met Ala Cys Pro Gly Ile Met Arg Pro Gly Ser Thr Ser Leu Pro				
703	708	713	718	
gag act cct aga ctg ttc cct ctg ctt cct ctg aga cca cta ggc ccc				2209
Glu Thr Pro Arg Leu Phe Pro Leu Leu Pro Leu Arg Pro Leu Gly Pro				
719	724	729	734	
ggc cgc atg gtc tcc cac acc cca gcc cct cct gca agc ttc cct gtg				2257
Gly Arg Met Val Ser His Thr Pro Ala Pro Pro Ala Ser Phe Pro Val				
735	740	745	750	
cca tac ctt cca ggg gac cca ggt gcc cca tgc tct agt gtc ctc cca				2305
Pro Tyr Leu Pro Gly Asp Pro Gly Ala Pro Cys Ser Ser Val Leu Pro				
751	756	761	766	
acc act ggc atc ttg act cct cac cca gga cct caa gat tcc tgg aaa				2353
Thr Thr Gly Ile Leu Thr Pro His Pro Gly Pro Gln Asp Ser Trp Lys				
767	772	777	782	
gaa gcc cca gcc ccc agg gga aac ctc cag agg aac aag ctg cca gag				2401
Glu Ala Pro Ala Pro Arg Gly Asn Leu Gln Arg Asn Lys Leu Pro Glu				
783	788	793	798	
aca ttt atg ccc cca gca cca att act gct cca gtt atg agc ctc acc				2449
Thr Phe Met Pro Pro Ala Pro Ile Thr Ala Pro Val Met Ser Leu Thr				
799	804	809	814	

cct gag cta caa ggg att ctt ccc tca cag ccc cct gtc tcc agt gtg	2497
Pro Glu Leu Gln Gly Ile Leu Pro Ser Gln Pro Pro Val Ser Ser Val	
815 820 825 830	
agt cat gct ccc cca gga gtt cca gga gaa ctc agc ctg cag ctt cag	2545
Ser His Ala Pro Pro Gly Val Pro Gly Glu Leu Ser Leu Gln Leu Gln	
831 836 841 846	
cac ctg cca cct gag aag atg gaa agg aag gag ctg ccc cca gag cat	2593
His Leu Pro Pro Glu Lys Met Glu Arg Lys Glu Leu Pro Pro Glu His	
847 852 857 862	
cag tcc ttg aag agc agc ttt gag gcg ctt ctc caa cgc tgc tcc ctg	2641
Gln Ser Leu Lys Ser Ser Phe Glu Ala Leu Leu Gln Arg Cys Ser Leu	
863 868 873 878	
tct gca act gac tta aag aca aaa agg aag ctg gaa gag gca gcc cag	2689
Ser Ala Thr Asp Leu Lys Thr Lys Arg Lys Leu Glu Glu Ala Ala Gln	
879 884 889 894	
cgt ctg gag tat cta tat gag aag ctc tgt gag ggg aca ctc tca cct	2737
Arg Leu Glu Tyr Leu Tyr Glu Lys Leu Cys Glu Gly Thr Leu Ser Pro	
895 900 905 910	
cat gtc gtg gct ggg ctc cat gag gtt gcc cga tgt gtg gat gca gga	2785
His Val Val Ala Gly Leu His Glu Val Ala Arg Cys Val Asp Ala Gly	
911 916 921 926	
agc ttt gag cag ggc ctt gca gtg cat gcc cag gtg gcg ggc tgt agc	2833
Ser Phe Glu Gln Gly Leu Ala Val His Ala Gln Val Ala Gly Cys Ser	
927 932 937 942	
agc ttc agc gag gtg tcc agc ttc atg cct atc ctg aag gct gtc ctc	2881
Ser Phe Ser Glu Val Ser Ser Phe Met Pro Ile Leu Lys Ala Val Leu	
943 948 953 958	
atc atc gct cat aag ctg ctg gtc taa accag gcagcctctc ttgctaggag	2933
Ile Ile Ala His Lys Leu Leu Val *	
959 964	
gccacttctg ctgttacata actcctccct gcagaagagg ggacttctgc aacagattct	2993
gtttcttttt cccgactctt ttccttgctg ccaggatatgt gatgctgtag gcttggetcc	3053
aaaccagctg agtgccctgct ttttactcct ttatgtctgg cttcttagga tctgtccaag	3113
acactctcag gcctggaggc agggcataga atcagttctt cactctccct aatactacac	3173
tctgtaagga cctggggcag gatattctt ccccaggga tcttctatct aagtggcttc	3233
tgagaggggtg aacaggattg ttacttttaa gcctacctct gctgtgaccc atcatgtggg	3293
tcttttgttt ctcccttctg tggtttatga gcctgccctt accttttccc tgccctctgac	3353
ttgggtatttc cagggtccgta tttctctgta gccagggtc tggggtagag ctgactgctg	3413

ttcaccccttt gaacaactca tggacgtgag ggatgggtgc tgagcagaac caagagagga 3473
aactttggcg ctgttaaaat ggaatttctc atctgccggc attattaagg gtgggctagg 3533
ttggatggaa ggtgaaagg atgaactgcc ttttgctgga agctgtctta ggctgtgaga 3593
caggagcagg ggaaccacag cctatgggga actgcccttg actccaccta tgttggagcc 3653
ttagcccaag gccattcctt ctgtgatgat aaagcccagt tctggaattg gagccatatt 3713
aaggaatgat tctcttcag cgtgtctcct caagggttgg gggtccttct ccctcgcagc 3773
caccacatgt ctcagggcta ccttctccga ttggatttgc atttgtggca ctgtctttga 3833
tgcagtgatg tacttaatgg tgcaataaag ctgcttcgat ttggaaaaaa aaaaaa 3889

<210> 401
<211> 2697
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (135)..(1136)

<400> 401
gaggtgcgcc cctgccgtac cgggtccgga ttcccgggtc gacgatttcg tgcgccatgt 60
gaggggggctc gggggccgcg gggggccggg cgctccccgc cggagatgag gaaactgagg 120
ctcagagagg tcac atg gct tgc tgc agg ccc ccc agc cag tgt gaa ccc 170
Met Ala Cys Ser Arg Pro Pro Ser Gln Cys Glu Pro
1 5 10
aca tcc ctg ccc cca ggg cca cct gca gga cgc cga cac cta ccc ctc 218
Thr Ser Leu Pro Pro Gly Pro Pro Ala Gly Arg Arg His Leu Pro Leu
13 18 23 28
agc aga cgc cgg aga gaa atg agt agc aac aaa gag cag cgg tca gca 266
Ser Arg Arg Arg Arg Glu Met Ser Ser Asn Lys Glu Gln Arg Ser Ala
29 34 39 44
gtg ttc gtg atc ctc ttt gcc ctc atc acc atc ctc atc ctc tac agc 314
Val Phe Val Ile Leu Phe Ala Leu Ile Thr Ile Leu Ile Leu Tyr Ser
45 50 55 60
tcc aac agt gcc aat gag gtc ttc cat tac ggc tcc ctg cgg ggc cgt 362
Ser Asn Ser Ala Asn Glu Val Phe His Tyr Gly Ser Leu Arg Gly Arg
61 66 71 76
agc cgc cga cct gtc aac ctc aag aag tgg agc atc act gac ggc tat 410
Ser Arg Arg Pro Val Asn Leu Lys Lys Trp Ser Ile Thr Asp Gly Tyr
77 82 87 92

gtc ccc att ctc ggc aac aag aca ctg ccc tct cgg tgc cac cag tgt	458
Val Pro Ile Leu Gly Asn Lys Thr Leu Pro Ser Arg Cys His Gln Cys	
93 98 103 108	
gtg att gtc agc agc tcc agc cac ctg ctg ggc acc aag ctg ggc cct	506
Val Ile Val Ser Ser Ser Ser His Leu Leu Gly Thr Lys Leu Gly Pro	
109 114 119 124	
gag atc gag cgg gct gag tgt aca atc cgc atg aat gat gca ccc acc	554
Glu Ile Glu Arg Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro Thr	
125 130 135 140	
act ggc tac tca gct gat gtg ggc aac aag acc acc tac cgc gtc gtg	602
Thr Gly Tyr Ser Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg Val Val	
141 146 151 156	
gcc cat tcc agt gtg ttc cgc gtg ctg agg agg ccc cag gag ttt gtc	650
Ala His Ser Ser Val Phe Arg Val Leu Arg Arg Pro Gln Glu Phe Val	
157 162 167 172	
aac cgg acc cct gaa acc gtg ttc atc ttc tgg ggg ccc ccg agc aag	698
Asn Arg Thr Pro Glu Thr Val Phe Ile Phe Trp Gly Pro Pro Ser Lys	
173 178 183 188	
atg cag aag ccc cag ggc agc ctc gtg cgt gtg atc cag cga gcg ggc	746
Met Gln Lys Pro Gln Gly Ser Leu Val Arg Val Ile Gln Arg Ala Gly	
189 194 199 204	
ctg gtg ttc ccc aac atg gaa gca tat gcc gtc tct ccc ggc cgc atg	794
Leu Val Phe Pro Asn Met Glu Ala Tyr Ala Val Ser Pro Gly Arg Met	
205 210 215 220	
cgg caa ttt gac gac ctc ttc cgg ggt gag acg ggc aag gac agg gag	842
Arg Gln Phe Asp Asp Leu Phe Arg Gly Glu Thr Gly Lys Asp Arg Glu	
221 226 231 236	
aag tct cat tcg tgg ttg agc aca ggc tgg ttt acc atg gtg atc gcg	890
Lys Ser His Ser Trp Leu Ser Thr Gly Trp Phe Thr Met Val Ile Ala	
237 242 247 252	
gtg gag ttg tgt gac cac gtg cat gtc tat ggc atg gtc ccc ccc aac	938
Val Glu Leu Cys Asp His Val His Val Tyr Gly Met Val Pro Pro Asn	
253 258 263 268	
tac tgc agc cag cgg ccc cgc ctc cag cgc atg ccc tac cac tac tac	986
Tyr Cys Ser Gln Arg Pro Arg Leu Gln Arg Met Pro Tyr His Tyr Tyr	
269 274 279 284	
gag ccc aag ggg ccg gac gaa tgt gtc acc tac atc cag aat gag cac	1034
Glu Pro Lys Gly Pro Asp Glu Cys Val Thr Tyr Ile Gln Asn Glu His	
285 290 295 300	
agt cgc aag ggc aac cac cac cgc ttc atc acc gag aaa agg gtc ttc	1082
Ser Arg Lys Gly Asn His His Arg Phe Ile Thr Glu Lys Arg Val Phe	
301 306 311 316	
tca tcg tgg gcc cag ctg tat ggc atc acc ttc tcc cac ccc tcc tgg	1130

Ser Ser Trp Ala Gln Leu Tyr Gly Ile Thr Phe Ser His Pro Ser Trp
 317 322 327 332

acc tag gccacccagc ctgtgggacc tcaggagggt cagaggagaa gcagcctccg 1186
 Thr *
 333

cccagccgct aggccagga ccatcttctg gccaatcaag gcttgctgga gtgtctccca 1246

gccaatcagg gccttgagga ggatgtatcc tccagccaat cagggcctgg ggaatctgtt 1306

ggogaatcag ggatttggga gtctatgtgg ttaatcaggg gtgtctttct tgtgcagtca 1366

gggtctgccc acagtcaatc agggtagagg gggatattct gagtcaatct gaggctaagg 1426

acatgtcctt tcccatgagg ccttggttca gagccccagg aatggacccc ccaatcactc 1486

cccactctgc tgggataatg gggtcctgtc ccaaggagct gggaacttgg tgttgcccc 1546

tcaatttcca gcaccagaaa gagagattgt gtgggggtag aagctgtctg gaggcccgcc 1606

cagagaattt gtgggggtgt ggaggttgtg ggggcggtgg ggaggtccca gaggtgggag 1666

gctggcatcc aggtcttggc tctgccctga gaccttggac aaacccttcc ccctctctgg 1726

gcacccttct gccacacca gtttccagtg cggagtctga gacccttcc acctccccta 1786

caagtgcctt cgggtctgtc ctccccgtct ggaccctccc agccactatc ccttgctgga 1846

aggctcagct ctttgggggg tctgggggtga cctccccacc tcttgaaaaa ctttagggta 1906

tttttgcgca aactccttca ggggttggggg actctgaagg aaacgggaca aaaccttaag 1966

ctgttttctt agccctcag ccagctgcca ttagcttggc tcttaaaggg ccaggcctcc 2026

ttttctgccc tctagcaggg aggttttcca actgttggag gcgcctttgg ggctgcccc 2086

ttgtctggag tcaactggggg cttccgaggg tctccctcga ccctctgtcg tcttgggatg 2146

gctgtcggga gctgtatcac ctgggttctg tcccctggct ctgtatcagg caactttatta 2206

aagctgggcc tcagtggggt gtgtttgtct cctgctcttc tggagcctgg aaggaaaggg 2266

cttcaggagg aggctgtgag gctggaggga ccagatggag gaggccagca gctagccatt 2326

gcacactggg gtgatgggtg ggggcggtga ctgcccaga cttgggtttg taatgatttg 2386

tacaggaata aacacaccta cgctccggct tcgtgtcctg tgctgcctgg gtgcagcaca 2446

gccttctggt ccagcgctgc atgcggcctc aggaaccagc cttccggttg ggggctccca 2506

gtaaagcgat cctcagcttc ttcagcagcc agtggccagt gagagcactg acacggctcc 2566

cgggacctcg gcaggatgga agagaagctg aagaaaacca agatcatctt tgtgggtgggt 2626

gggcctggct caaggaaggg caccagtggt gagaagatcg tgcagaagta tggctacacc 2686

2697

```
<220>
<221> CDS
<222> (156)..(1742)
```

tggcgcgctcg cccccccatc gaaggacgat gatatatcta tctattcgat gatgaagata 60

ccctacaga agccccaga ggcagcacc tcacc atg gac tgc acc tgg agg 173
Met Asp Cys Thr Trp Arg

7

ctg gta cag tct ggg gct gag gtg aag aag cct ggg gcc tca gtg aag 269
Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys
23 28 33 38

tgg gtg cga cag gct cct gga aaa ggg ctt gag tgg atg gga gct ttt 365
 Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met Gly Ala Phe
 55 60 65 70

gtc acc atg acc gag gac aca tct aca gac aca gcc tac atg gag ctg 461
Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr Met Glu Leu
87 92 97 102

gtt gga agg tgt agt agt acc agc tgc tat cac ccc ctt gga tac tgg 557
Val Gly Arg Cys Ser Ser Thr Ser Cys Tyr His Pro Leu Gly Tyr Trp
119 124 129 134

ggc cag gga acc ctg gtc acc gtc tcc tca gca ccc acc aag gct ccg 605
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Pro Thr Lys Ala Pro

135	140	145	150	
gat gtg ttc ccc atc	ata tca ggg tgc aga	cac cca aag gat aac agc		653
Asp Val Phe Pro Ile	Ile Ser Gly Cys Arg	His Pro Lys Asp Asn Ser		
151	156	161	166	
cct gtg gtc ctg gca	tgc ttg ata act ggg	tac cac cca acg tcc gtg		701
Pro Val Val Leu Ala	Cys Leu Ile Thr Gly	Tyr His Pro Thr Ser Val		
167	172	177	182	
act gtc acc tgg tac	atg ggg aca cag agc	cag ccc cag aga acc ttc		749
Thr Val Thr Trp Tyr	Met Gly Thr Gln Ser	Gln Pro Gln Arg Thr Phe		
183	188	193	198	
cct gag ata caa aga	cgg gac agc tac tac	atg aca agc agc cag ctc		797
Pro Glu Ile Gln Arg	Arg Asp Ser Tyr Tyr	Met Thr Ser Ser Gln Leu		
199	204	209	214	
tcc acc ccc ctc cag	cag tgg cgc caa ggc	gag tac aaa tgc gtg gtc		845
Ser Thr Pro Leu Gln	Gln Trp Arg Gln Gly	Glu Tyr Lys Cys Val Val		
215	220	225	230	
cag cac acc gcc agc	aag agt aag aag gag	atc ttc cgc tgg cca gag		893
Gln His Thr Ala Ser	Lys Ser Lys Lys Glu	Ile Phe Arg Trp Pro Glu		
231	236	241	246	
tct cca aag gca cag	gcc tcc tca gtg ccc	act gca caa ccc caa gca		941
Ser Pro Lys Ala Gln	Ala Ser Ser Val Pro	Thr Ala Gln Pro Gln Ala		
247	252	257	262	
gag ggc agc ctc gcc	aag gca acc aca gcc	cca gcc acc acc cgt aac		989
Glu Gly Ser Leu Ala	Lys Ala Thr Thr Ala	Pro Ala Thr Thr Arg Asn		
263	268	273	278	
aca gga aga gga gga	gaa gag aag aag aag	gag aag gag aaa gag gaa		1037
Thr Gly Arg Gly Gly	Glu Glu Lys Lys Lys	Glu Lys Glu Lys Glu Glu		
279	284	289	294	
caa gaa gag aga gag	aca aag aca cca gag	tgt ccg agc cac acc cag		1085
Gln Glu Glu Arg Glu	Thr Lys Thr Pro Glu	Cys Pro Ser His Thr Gln		
295	300	305	310	
cct ctt ggc gtc tac	ctg cta acc cct gca	gtg cag gac ctg tgg ctc		1133
Pro Leu Gly Val Tyr	Leu Leu Thr Pro Ala	Val Gln Asp Leu Trp Leu		
311	316	321	326	
cgg gac aaa gcc acc	ttc acc tgc ttc gtg	gtg ggc agt gac ctg aag		1181
Arg Asp Lys Ala Thr	Phe Thr Cys Phe Val	Val Gly Ser Asp Leu Lys		
327	332	337	342	
gat gct cac ctg acc	tgg gag gtg gct ggg	aag gtc ccc aca ggg ggc		1229
Asp Ala His Leu Thr	Trp Glu Val Ala Gly	Lys Val Pro Thr Gly Gly		
343	348	353	358	
gtg gag gaa ggg ctg	ctg gag cgg cac agc	aac ggc tcc cag agc cag		1277
Val Glu Glu Gly Leu	Leu Glu Arg His Ser	Asn Gly Ser Gln Ser Gln		
359	364	369	374	

cac agc cgt ctg acc ctg ccc agg tcc ttg tgg aac gcg ggg acc tcc	1325
His Ser Arg Leu Thr Leu Pro Arg Ser Leu Trp Asn Ala Gly Thr Ser	
375 380 385 390	
gtc acc tgc aca ctg aac cat ccc agc ctc cca ccc cag agg ttg atg	1373
Val Thr Cys Thr Leu Asn His Pro Ser Leu Pro Pro Gln Arg Leu Met	
391 396 401 406	
gcg ctg aga gaa ccc gct gcg cag gca ccc gtc aag ctt tcc ctg aac	1421
Ala Leu Arg Glu Pro Ala Ala Gln Ala Pro Val Lys Leu Ser Leu Asn	
407 412 417 422	
ctg ctg gcc tcg tct gac cct ccc gag gcg gcc tcg tgg ctc ctg tgt	1469
Leu Leu Ala Ser Ser Asp Pro Pro Glu Ala Ala Ser Trp Leu Leu Cys	
423 428 433 438	
gag gtg tct ggc ttc tcg ccc ccc aac atc ctc ctg atg tgg ctg gag	1517
Glu Val Ser Gly Phe Ser Pro Pro Asn Ile Leu Leu Met Trp Leu Glu	
439 444 449 454	
gac cag cgt gag gtg aac act tct ggg ttt gcc ccc gca cgc ccc cct	1565
Asp Gln Arg Glu Val Asn Thr Ser Gly Phe Ala Pro Ala Arg Pro Pro	
455 460 465 470	
cca cag ccc agg agc acc acg ttc tgg gcc tgg agt gtg ctg cgt gtc	1613
Pro Gln Pro Arg Ser Thr Thr Phe Trp Ala Trp Ser Val Leu Arg Val	
471 476 481 486	
cca gcc ccg ccc agc cct cag cca gcc acc tac acg tgt gtg gtc agc	1661
Pro Ala Pro Pro Ser Pro Gln Pro Ala Thr Tyr Thr Cys Val Val Ser	
487 492 497 502	
cac gag gac tcc cgg act ctg ctc aac gcc agc cgg agc cta gaa gtc	1709
His Glu Asp Ser Arg Thr Leu Leu Asn Ala Ser Arg Ser Leu Glu Val	
503 508 513 518	
agc tat gta aca gac cat ggc ccc atg aaa tga tcccgac cagatccgtc	1760
Ser Tyr Val Thr Asp His Gly Pro Met Lys *	
519 524 529	
cacacccgcc actcagcagc tctggccgag ctcacagtac aaccacaata aactottgtt	1820
gaatgaactc taaaaaaaaa aaa	1843

<210> 403
 <211> 3727
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (152)..(2548)

<400> 403

ttataactct ctattcgatg atgaagatac cccaccaaac ccaaaaaaag agatctctcg	60
aggatccgaa ttcgcggccg cgtttaacgcg ggagtcgcgg aacagcaggc ccgagcccac	120
cgcgccggggc cccggacgcc gcgcggaaaa g atg aat tta caa cca att ttc	172
Met Asn Leu Gln Pro Ile Phe	
1 5	
tgg att gga ctg atc agt tca gtt tgc tgt gtg ttt gct caa aca gat	220
Trp Ile Gly Leu Ile Ser Ser Val Cys Cys Val Phe Ala Gln Thr Asp	
8 13 18 23	
gaa aat aga tgt tta aaa gca aat gcc aaa tca tgt gga gaa tgt ata	268
Glu Asn Arg Cys Leu Lys Ala Asn Ala Lys Ser Cys Gly Glu Cys Ile	
24 29 34 39	
caa gca ggg cca aat tgt ggg tgg tgc aca aat tca aca ttt tta cag	316
Gln Ala Gly Pro Asn Cys Gly Trp Cys Thr Asn Ser Thr Phe Leu Gln	
40 45 50 55	
gaa gga atg cct act tct gca cga tgt gat gat tta gaa gcc tta aaa	364
Glu Gly Met Pro Thr Ser Ala Arg Cys Asp Asp Leu Glu Ala Leu Lys	
56 61 66 71	
aag aag ggt tgc cct cca gat gac ata gaa aat ccc aga ggc tcc aaa	412
Lys Lys Gly Cys Pro Pro Asp Asp Ile Glu Asn Pro Arg Gly Ser Lys	
72 77 82 87	
gat ata aag aaa aat aaa aat gta acc aac cgt agc aaa gga aca gca	460
Asp Ile Lys Lys Asn Lys Asn Val Thr Asn Arg Ser Lys Gly Thr Ala	
88 93 98 103	
gag aag ctc aag cca gag gat att act cag atc caa cca cag cag ttg	508
Glu Lys Leu Lys Pro Glu Asp Ile Thr Gln Ile Gln Pro Gln Gln Leu	
104 109 114 119	
gtt ttg cga tta aga tca ggg gag cca cag aca ttt aca tta aaa ttc	556
Val Leu Arg Leu Arg Ser Gly Glu Pro Gln Thr Phe Thr Leu Lys Phe	
120 125 130 135	
aag aga gct gaa gac tat ccc att gac ctc tac tac ctt atg gac ctg	604
Lys Arg Ala Glu Asp Tyr Pro Ile Asp Leu Tyr Tyr Leu Met Asp Leu	
136 141 146 151	
tct tac tca atg aaa gac gat ttg gag aat gta aaa agt ctt gga aca	652
Ser Tyr Ser Met Lys Asp Asp Leu Glu Asn Val Lys Ser Leu Gly Thr	
152 157 162 167	
gat ctg atg aat gaa atg agg agg att act tcg gac ttc aga att gga	700
Asp Leu Met Asn Glu Met Arg Arg Ile Thr Ser Asp Phe Arg Ile Gly	
168 173 178 183	
ttt ggc tca ttt gtg gaa aag act gtg atg cct tac att agc aca aca	748
Phe Gly Ser Phe Val Glu Lys Thr Val Met Pro Tyr Ile Ser Thr Thr	
184 189 194 199	

cca gct aag ctc agg aac cct tgc aca agt gaa cag aac tgc acc agc	796
Pro Ala Lys Leu Arg Asn Pro Cys Thr Ser Glu Gln Asn Cys Thr Ser	
200 205 210 215	
cca ttt agc tac aaa aat gtg ctc agt ctt act aat aaa gga gaa gta	844
Pro Phe Ser Tyr Lys Asn Val Leu Ser Leu Thr Asn Lys Gly Glu Val	
216 221 226 231	
ttt aat gaa ctt gtt gga aaa cag cgc ata tct gga aat ttg gat tct	892
Phe Asn Glu Leu Val Gly Lys Gln Arg Ile Ser Gly Asn Leu Asp Ser	
232 237 242 247	
cca gaa ggt ggt ttc gat gcc atc atg caa gtt gca gtt tgt gga tca	940
Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Val Ala Val Cys Gly Ser	
248 253 258 263	
ctg att ggc tgg agg aat gtt aca cgg ctg ctg gtg ttt tcc aca gat	988
Leu Ile Gly Trp Arg Asn Val Thr Arg Leu Leu Val Phe Ser Thr Asp	
264 269 274 279	
gcc ggg ttt cac ttt gct gga gat ggg aaa ctt ggt ggc att gtt tta	1036
Ala Gly Phe His Phe Ala Gly Asp Gly Lys Leu Gly Gly Ile Val Leu	
280 285 290 295	
cca aat gat gga caa tgt cac ctg gaa aat aat atg tac aca atg agc	1084
Pro Asn Asp Gly Gln Cys His Leu Glu Asn Asn Met Tyr Thr Met Ser	
296 301 306 311	
cat tat tat gat tat cct tct att gct cac ctt gtc cag aaa ctg agt	1132
His Tyr Tyr Asp Tyr Pro Ser Ile Ala His Leu Val Gln Lys Leu Ser	
312 317 322 327	
gaa aat aat att cag aca att ttt gca gtt act gaa gaa ttt cag cct	1180
Glu Asn Asn Ile Gln Thr Ile Phe Ala Val Thr Glu Glu Phe Gln Pro	
328 333 338 343	
gtt tac aag gag ctg aaa aac ttg atc cct aag tca gca gta gga aca	1228
Val Tyr Lys Glu Leu Lys Asn Leu Ile Pro Lys Ser Ala Val Gly Thr	
344 349 354 359	
tta tct gca aat tct agc aat gta att cag ttg atc att gat gca tac	1276
Leu Ser Ala Asn Ser Ser Asn Val Ile Gln Leu Ile Ile Asp Ala Tyr	
360 365 370 375	
aat tcc ctt tcc tca gaa gtc att ttg gaa aac ggc aaa ttg tca gaa	1324
Asn Ser Leu Ser Ser Glu Val Ile Leu Glu Asn Gly Lys Leu Ser Glu	
376 381 386 391	
gga gta aca ata agt tac aaa tct tac tgc aag aac ggg gtg aat gga	1372
Gly Val Thr Ile Ser Tyr Lys Ser Tyr Cys Lys Asn Gly Val Asn Gly	
392 397 402 407	
aca ggg gaa aat gga aga aaa tgt tcc aat att tcc att gga gat gag	1420
Thr Gly Glu Asn Gly Arg Lys Cys Ser Asn Ile Ser Ile Gly Asp Glu	
408 413 418 423	
gtt caa ttt gaa att agc ata act tca aat aag tgt cca aaa aag gat	1468

Val Gln Phe Glu Ile Ser Ile Thr Ser Asn Lys Cys Pro Lys Lys Asp	
424 429 434 439	
tct gac agc ttt aaa att agg cct ctg ggc ttt acg gag gaa gta gag	1516
Ser Asp Ser Phe Lys Ile Arg Pro Leu Gly Phe Thr Glu Glu Val Glu	
440 445 450 455	
ggt att ctt cag tac atc tgt gaa tgt gaa tgc caa agc gaa ggc atc	1564
Val Ile Leu Gln Tyr Ile Cys Glu Cys Glu Cys Gln Ser Glu Gly Ile	
456 461 466 471	
cct gaa agt ccc aag tgt cat gaa gga aat ggg aca ttt gag tgt ggc	1612
Pro Glu Ser Pro Lys Cys His Glu Gly Asn Gly Thr Phe Glu Cys Gly	
472 477 482 487	
gcg tgc agg tgc aat gaa ggg cgt gtt ggt aga cat tgt gaa tgc agc	1660
Ala Cys Arg Cys Asn Glu Gly Arg Val Gly Arg His Cys Glu Cys Ser	
488 493 498 503	
aca gat gaa gtt aac agt gaa gac atg gat gct tac tgc agg aaa gaa	1708
Thr Asp Glu Val Asn Ser Glu Asp Met Asp Ala Tyr Cys Arg Lys Glu	
504 509 514 519	
aac agt tca gaa atc tgc agt aac aat gga gag tgc gtc tgc gga cag	1756
Asn Ser Ser Glu Ile Cys Ser Asn Asn Gly Glu Cys Val Cys Gly Gln	
520 525 530 535	
tgt gtt tgt agg aag agg gat aat aca aat gaa att tat tct ggc aaa	1804
Cys Val Cys Arg Lys Arg Asp Asn Thr Asn Glu Ile Tyr Ser Gly Lys	
536 541 546 551	
ttc tgc gag tgt gat aat ttc aac tgt gat aga tcc aat ggc tta att	1852
Phe Cys Glu Cys Asp Asn Phe Asn Cys Asp Arg Ser Asn Gly Leu Ile	
552 557 562 567	
tgt gga gga aat ggt gtt tgc aag tgt cgt gtg tgt gag tgc aac ccc	1900
Cys Gly Gly Asn Gly Val Cys Lys Cys Arg Val Cys Glu Cys Asn Pro	
568 573 578 583	
aac tac act ggc agt gca tgt gac tgt tct ttg gat act agt act tgt	1948
Asn Tyr Thr Gly Ser Ala Cys Asp Cys Ser Leu Asp Thr Ser Thr Cys	
584 589 594 599	
gaa gcc agc aac gga cag atc tgc aat ggc cgg ggc atc tgc gag tgt	1996
Glu Ala Ser Asn Gly Gln Ile Cys Asn Gly Arg Gly Ile Cys Glu Cys	
600 605 610 615	
ggt gtc tgt aag tgt aca gat ccg aag ttt caa ggg caa acg tgt gag	2044
Gly Val Cys Lys Cys Thr Asp Pro Lys Phe Gln Gly Gln Thr Cys Glu	
616 621 626 631	
atg tgt cag acc tgc ctt ggt gtc tgt gct gag cat aaa gaa tgt gtt	2092
Met Cys Gln Thr Cys Leu Gly Val Cys Ala Glu His Lys Glu Cys Val	
632 637 642 647	
cag tgc aga gcc ttc aat aaa gga gaa aag aaa gac aca tgc aca cag	2140
Gln Cys Arg Ala Phe Asn Lys Gly Glu Lys Lys Asp Thr Cys Thr Gln	

648	653	658	663	
gaa tgt tcc tat ttt aac att acc aag gta gaa agt cgg gac aaa tta				2188
Glu Cys Ser Tyr Phe Asn Ile Thr Lys Val Glu Ser Arg Asp Lys Leu				
664	669	674	679	
ccc cag ccg gtc caa cct gat cct gtg tcc cat tgt aag gag aag gat				2236
Pro Gln Pro Val Gln Pro Asp Pro Val Ser His Cys Lys Glu Lys Asp				
680	685	690	695	
gtt gac gac tgt tgg ttc tat ttt acg tat tca gtg aat ggg aac aac				2284
Val Asp Asp Cys Trp Phe Tyr Phe Thr Tyr Ser Val Asn Gly Asn Asn				
696	701	706	711	
gag gtc atg gtt cat gtt gtg gag aat cca gag tgt ccc act ggt cca				2332
Glu Val Met Val His Val Val Glu Asn Pro Glu Cys Pro Thr Gly Pro				
712	717	722	727	
gac atc att cca att gta gct ggt gtg gtt gct gga att gtt ctt att				2380
Asp Ile Ile Pro Ile Val Ala Gly Val Val Ala Gly Ile Val Leu Ile				
728	733	738	743	
ggc ctt gca tta ctg ctg ata tgg aag ctt tta atg ata att cat gac				2428
Gly Leu Ala Leu Leu Leu Ile Trp Lys Leu Leu Met Ile Ile His Asp				
744	749	754	759	
aga agg gag ttt gct aaa ttt gaa aag gag aaa atg aat gcc aaa tgg				2476
Arg Arg Glu Phe Ala Lys Phe Glu Lys Glu Lys Met Asn Ala Lys Trp				
760	765	770	775	
gac acg ggt gaa aat cct att tat aag agt gcc gta aca act gtg gtc				2524
Asp Thr Gly Glu Asn Pro Ile Tyr Lys Ser Ala Val Thr Thr Val Val				
776	781	786	791	
aat ccg aag tat gag gga aaa tga gtactgcccg tgcaaatccc acaacactga				2578
Asn Pro Lys Tyr Glu Gly Lys *				
792	797			
atgcaaagta gcaattttcca tagtcacagt taggtagctt tagggcaata ttgccatggt				2638
tttactcatg tgcagggtttt gaaaatgtac aatatgtata atttttaaaa tgttttatta				2698
ttttgaaaat aatgttgttaa ttcattgccag ggactgacaa aagacttgag acaggatggt				2758
tattcttgtc agctaaggctc acattgtgcc tttttgacct tttcttctcg gactattgaa				2818
atcaagctta ttggattaag tgatatattct atagcgattg aaagggcaat agttaagta				2878
atgagcatga tgagagtttc tgtaaatcat gtattaaaac tgatttttag ctttaciaat				2938
atgtcagttt gcagttatgc agaattccaaa gtaaattgtcc tgctagctag ttaaggattg				2998
ttttaaatct gttattttgc tatttgctg ttagacatga ctgatgacat atctgaaaga				3058
caagtatggt gagagttgct ggtgtaaaat acgtttgaaa tagttgatct acaaaggcca				3118
tgggaaaaat tcagagagtt aggaaggaaa aaccaatagc tttaaaacct gtgtgccatt				3178

```

ttaagagtta cttaatgttt ggtaactttt atgccttcac tttacaaatt caagccttag 3238
ataaaagaac cgagcaattt tctgctaaaa agtccttgat ttagcactat ttacatacag 3298
gccatacttt acaaagtatt tgctgaatgg ggaccttttg agttgaattt attttattat 3358
ttttattttg tttaatgtct ggtgctttct atcacctctt ctaatctttt aatgtatttg 3418
tttgcaattt tggggtaaga cttttttatg agtacttttt ctttgaagtt ttagcgggtca 3478
atttgccttt ttaatgaaca tgtgaagtta tactgtggct atgcaacagc tctcacctac 3538
gcgagtctta ctttgagtta gtgccataac agaccactgt atgtttactt ctcaccattt 3598
gagttgcca tcttgtttca cactagtcac attcttgttt taagtgcctt tagttttaac 3658
agttcacttt ttacagtgct atttactgaa gttatttatt aaatatgcct aaaatactta 3718
aaaaaaaaa 3727

```

```

<210> 404
<211> 1801
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (217)..(1440)

```

```

<220>
<221> misc_feature
<222> (1)..(1801)
<223> n = a,t,c or g

```

```

<400> 404
taagcttgcg gccgcttttt tttttttttt ttttggggct gtgcttggcg cgtaccgtgc 60
ggtccctgta gttggaggac gggcggtcgc gcggcctttc ccactagccg gagtagcctc 120
tagttcgta gtcaaaacgt gaaaaaaaag acctgctttg cctggggaaa tagtaaccct 180
gccaaataca tcagcttgta ggagacagag gatgtg atg gag ctg ctt gaa gaa 234
Met Glu Leu Leu Glu Glu
1
gat ctc aca tgc cct att tgt tgt agt ctg ttt gat gat cca cgg gtt 282
Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu Phe Asp Asp Pro Arg Val
7 12 17 22
ttg cct tgc tcc cac aac ttc tgc aaa aaa tgc tta gaa ggt atc tta 330
Leu Pro Cys Ser His Asn Phe Cys Lys Lys Cys Leu Glu Gly Ile Leu
23 28 33 38

```

gaa ggg agt gtg cgg aat tcc ttg tgg aga cca gct cca ttc aag tgt	378
Glu Gly Ser Val Arg Asn Ser Leu Trp Arg Pro Ala Pro Phe Lys Cys	
39 44 49 54	
cct aca tgc cgt aag gaa act tca gct act gga att aat agc ctg cag	426
Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr Gly Ile Asn Ser Leu Gln	
55 60 65 70	
gtt aat tac tcc ctg aag ggt att gtg gaa aag tat aac aag atc aag	474
Val Asn Tyr Ser Leu Lys Gly Ile Val Glu Lys Tyr Asn Lys Ile Lys	
71 76 81 86	
atc tct ccc aaa atg cca gta tgc aaa gga cac ttg ggg cag cct ctc	522
Ile Ser Pro Lys Met Pro Val Cys Lys Gly His Leu Gly Gln Pro Leu	
87 92 97 102	
aac att ttc tgc ctg act gat atg cag ctg att tgt ggg atc tgt gct	570
Asn Ile Phe Cys Leu Thr Asp Met Gln Leu Ile Cys Gly Ile Cys Ala	
103 108 113 118	
act cgt ggg gag cac acc aaa cat gtc ttc tgt tct att gaa gat gcc	618
Thr Arg Gly Glu His Thr Lys His Val Phe Cys Ser Ile Glu Asp Ala	
119 124 129 134	
tat gct cag gaa agg gat gcc ttt gag tcc ctc ttc cag agc ttt gag	666
Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser Leu Phe Gln Ser Phe Glu	
135 140 145 150	
acc tgg cgt cgg gga gat gct ctt tct cgc ttg gat acc ttg gaa act	714
Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg Leu Asp Thr Leu Glu Thr	
151 156 161 166	
agt aag agg aaa tcc cta cag tta ctg act aaa gat tca gat aaa gtg	762
Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr Lys Asp Ser Asp Lys Val	
167 172 177 182	
aag gaa ttt ttt gag aag tta caa cac aca ctg gat caa aag aag aat	810
Lys Glu Phe Phe Glu Lys Leu Gln His Thr Leu Asp Gln Lys Lys Asn	
183 188 193 198	
gaa att ctg tct gac ttt gag acc atg aaa ctt gct gtt atg caa gca	858
Glu Ile Leu Ser Asp Phe Glu Thr Met Lys Leu Ala Val Met Gln Ala	
199 204 209 214	
tat gac cca gag atc aac aaa ctc aac acc atc ttg cag gag caa cgg	906
Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr Ile Leu Gln Glu Gln Arg	
215 220 225 230	
atg gcc ttt aac att gct gag gct ttc aaa gat gtg tca gaa ccc att	954
Met Ala Phe Asn Ile Ala Glu Ala Phe Lys Asp Val Ser Glu Pro Ile	
231 236 241 246	
gta ttt ctg caa cag atg cag gag ttt aga gag aaa atc aaa gta atc	1002
Val Phe Leu Gln Gln Met Gln Glu Phe Arg Glu Lys Ile Lys Val Ile	
247 252 257 262	
aag gaa act cct tta cct ccc tct aat ttg cct gca agc cct tta atg	1050

Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu Pro Ala Ser Pro Leu Met	
263 268 273 278	
aag aac ttt gat acc agt cag tgg gaa gac ata aaa cta gtc gat gtg	1098
Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp Ile Lys Leu Val Asp Val	
279 284 289 294	
gat aaa ctt tct ttg cct caa gac act ggc aca ttc att agc aag att	1146
Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly Thr Phe Ile Ser Lys Ile	
295 300 305 310	
ccc tgg agc ttt tat aag tta ttt ttg cta atc ctt ctg ctt ggc ctt	1194
Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu Ile Leu Leu Leu Gly Leu	
311 316 321 326	
gtc att gtc ttt ggt cct acc atg ttc cta gaa tgg tca tta ttt gat	1242
Val Ile Val Phe Gly Pro Thr Met Phe Leu Glu Trp Ser Leu Phe Asp	
327 332 337 342	
gac ctg gca act tgg aaa ggc tgt ctt tca aac ttc agt tcc tat ctg	1290
Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser Asn Phe Ser Ser Tyr Leu	
343 348 353 358	
act aaa aca gcc gat ttc ata gaa caa tca gtt ttt tac tgg gaa cag	1338
Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser Val Phe Tyr Trp Glu Gln	
359 364 369 374	
gtg aca gat ggg ttt ttc att ttc aat gaa aga ttc aag aat ttt act	1386
Val Thr Asp Gly Phe Phe Ile Phe Asn Glu Arg Phe Lys Asn Phe Thr	
375 380 385 390	
ttg gtg gta ctg aac aat gtg gca gaa ttt gtg tgc aaa tat aaa cta	1434
Leu Val Val Leu Asn Asn Val Ala Glu Phe Val Cys Lys Tyr Lys Leu	
391 396 401 406	
tta taa aatcaaaaaa aaaaaaagg ggggcccttt aaaaaaaca aattttaata	1490
Leu *	
407	
cccgggggtg ggaaagtaaa aatttttttt agggggcccc aaatttaatt tccggggccg	1550
ggtttttaaaa aggggggggg gggaaaaacc cggggggtcc ccaattaaac ccctttggca	1610
ccaaannnan nnnnnnnngn nnaantcttt ttaantctta tactcccagt acaatngcat	1670
atttatacta aacctatccc tgtccaacct ttttagtacc gaacttagac atacattggg	1730
taagcgctc gccgttattt gatattacta ataatttggt ccggcccttg ttttgtccca	1790
caccctggtc t	1801

<210> 405
 <211> 1786
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (263)..(1651)

<400> 405

```
cgaaaaaatt gaagccttac gcccgcggtta ccggtccgga attccccgggt cgacccacgc      60
gtccgcctcc ccttacctcc cttctcttct gaattctcca ttctgggctc tttcctgtga      120
aatctttctt tgctttcccc atcttttctt cgcatttttt caccatcttt ccctcaatct      180
ccaggagcca atgcgagact ttggctccga ttaagcgacg gcccgagact tgggggtgcgc      240
gaggaggatc gacagagtgg tg atg gag agc acc cct tca agg gga ctg aac      292
                Met Glu Ser Thr Pro Ser Arg Gly Leu Asn
                  1                      5

cga gta cac cta caa tgc agg aat ctg cag gaa ttc tta ggg ggc ctg      340
Arg Val His Leu Gln Cys Arg Asn Leu Gln Glu Phe Leu Gly Gly Leu
  11                      16                      21                      26

agc cct ggg gta ttg gac cga ttg tat ggg cac cct gcc aca tgt ctg      388
Ser Pro Gly Val Leu Asp Arg Leu Tyr Gly His Pro Ala Thr Cys Leu
  27                      32                      37                      42

gct gtc ttc agg gag ctc cca tcc ttg gct aag aac tgg gtg atg cgg      436
Ala Val Phe Arg Glu Leu Pro Ser Leu Ala Lys Asn Trp Val Met Arg
  43                      48                      53                      58

atg ctc ttt ctg gag cag cct ttg oca cag gct gct gta gct ctg tgg      484
Met Leu Phe Leu Glu Gln Pro Leu Pro Gln Ala Ala Val Ala Leu Trp
  59                      64                      69                      74

gta aag aag gaa ttc agc aag gct cag gag gaa agt aca ggg ctg ctg      532
Val Lys Lys Glu Phe Ser Lys Ala Gln Glu Glu Ser Thr Gly Leu Leu
  75                      80                      85                      90

agc ggc ctc cgg atc tgg cac acc cag ctg ctc cca ggc ggg ctc cag      580
Ser Gly Leu Arg Ile Trp His Thr Gln Leu Leu Pro Gly Gly Leu Gln
  91                      96                      101                      106

ggc ctc atc ctc aac ccc att ttc cgc cag aac ctc cgc att gcc ctt      628
Gly Leu Ile Leu Asn Pro Ile Phe Arg Gln Asn Leu Arg Ile Ala Leu
  107                      112                      117                      122

ctg ggt ggg ggg aag gcc tgg tct gat gac aca agt cag ctg gga cca      676
Leu Gly Gly Gly Lys Ala Trp Ser Asp Asp Thr Ser Gln Leu Gly Pro
  123                      128                      133                      138

gac aag cat gcc cgg gac gtt ccc tcc ctt gac aag tac gcc gag gag      724
Asp Lys His Ala Arg Asp Val Pro Ser Leu Asp Lys Tyr Ala Glu Glu
  139                      144                      149                      154

cga tgg gag gtg gtc ttg cac ttc atg gtg ggc tcc ccc agt gca gct      772
Arg Trp Glu Val Val Leu His Phe Met Val Gly Ser Pro Ser Ala Ala
```

155	160	165	170	
gtc agc cag gac ttg gct cag ctc ctc agc cag gct ggg ctc atg aag				820
Val Ser Gln Asp Leu Ala Gln Leu Leu Ser Gln Ala Gly Leu Met Lys				
171	176	181	186	
agt act gaa cct gga gag ccg ccc tgc att act tcc gct ggc ttc cag				868
Ser Thr Glu Pro Gly Glu Pro Pro Cys Ile Thr Ser Ala Gly Phe Gln				
187	192	197	202	
ttc ctg ttg ctg gac acc ccg gct cag ctc tgg tac ttt atg ttg cag				916
Phe Leu Leu Leu Asp Thr Pro Ala Gln Leu Trp Tyr Phe Met Leu Gln				
203	208	213	218	
tat ttg cag aca gcc cag agc cgg ggc atg gac ctg gta gag att ctc				964
Tyr Leu Gln Thr Ala Gln Ser Arg Gly Met Asp Leu Val Glu Ile Leu				
219	224	229	234	
tcc ttc ctc ttc cag ctc agc ttc tct act ctg ggc aag gat tac tct				1012
Ser Phe Leu Phe Gln Leu Ser Phe Ser Thr Leu Gly Lys Asp Tyr Ser				
235	240	245	250	
gtg gaa ggt atg agt gat tct ctg ttg aac ttc ctg caa cat ctg cgt				1060
Val Glu Gly Met Ser Asp Ser Leu Leu Asn Phe Leu Gln His Leu Arg				
251	256	261	266	
gag ttt ggg ctt gtt ttc cag agg aag agg aaa tct cgg cgt tac tac				1108
Glu Phe Gly Leu Val Phe Gln Arg Lys Arg Lys Ser Arg Arg Tyr Tyr				
267	272	277	282	
ccc aca cgc ctg gcc atc aat ctc tca tca ggt gtc tct gga gct ggg				1156
Pro Thr Arg Leu Ala Ile Asn Leu Ser Ser Gly Val Ser Gly Ala Gly				
283	288	293	298	
ggc act gtg cat cag cca ggt ttc att gtc gtg gaa acc aat tac cga				1204
Gly Thr Val His Gln Pro Gly Phe Ile Val Val Glu Thr Asn Tyr Arg				
299	304	309	314	
ctg tat gcc tac acg gag tgc gag ctg cag att gcc ctc att gcc ctc				1252
Leu Tyr Ala Tyr Thr Glu Ser Glu Leu Gln Ile Ala Leu Ile Ala Leu				
315	320	325	330	
ttc tct gag atg ctc tat cgg ttc ccc aac atg gtg gtg gcg cag gtg				1300
Phe Ser Glu Met Leu Tyr Arg Phe Pro Asn Met Val Val Ala Gln Val				
331	336	341	346	
acc cgg gag agt gtg cag cag gca atc gcc agt ggc atc aca gcc cag				1348
Thr Arg Glu Ser Val Gln Gln Ala Ile Ala Ser Gly Ile Thr Ala Gln				
347	352	357	362	
cag ata atc cat ttc cta agg aca aga gcc cac cca gtg atg ctc aaa				1396
Gln Ile Ile His Phe Leu Arg Thr Arg Ala His Pro Val Met Leu Lys				
363	368	373	378	
cag aca cct gtg ctg ccc ccc acc atc acc gac cag atc cgg ctc tgg				1444
Gln Thr Pro Val Leu Pro Pro Thr Ile Thr Asp Gln Ile Arg Leu Trp				
379	384	389	394	

gag ctg gaa agg gac aga ctc cgg ttc act gag ggt gtc ctg tat aac 1492
 Glu Leu Glu Arg Asp Arg Leu Arg Phe Thr Glu Gly Val Leu Tyr Asn
 395 400 405 410

cag ttc ctg tcg caa gtg gac ttt gag ctg ctg ctg gcc cac gcg cgg 1540
 Gln Phe Leu Ser Gln Val Asp Phe Glu Leu Leu Leu Ala His Ala Arg
 411 416 421 426

gag ctg ggc gtg ctc gtg ttc gag aac tcg gcc aag cgg ctc atg gtg 1588
 Glu Leu Gly Val Leu Val Phe Glu Asn Ser Ala Lys Arg Leu Met Val
 427 432 437 442

gtg acc ccg gcc ggg cac agc gac gtc aag cgc ttt tgg aag cgg cag 1636
 Val Thr Pro Ala Gly His Ser Asp Val Lys Arg Phe Trp Lys Arg Gln
 443 448 453 458

aaa cat agc tcc tga gagcgcgggga cttggacacg gacctcggcg ggcgggagct 1691
 Lys His Ser Ser *
 459

gggcggggcg gggcatcaga actcaggtgt tttttattta cgcgtcaggg cttttcttgt 1751

ttaataaagt tatgatagct agcaaaaaaa aaaaa 1786

<210> 406
 <211> 1113
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (11)..(913)

<400> 406
 ggaattcgcc atg gca gcc cag gca gct ggt gta tct agg cag cgg gca 49
 Met Ala Ala Gln Ala Ala Gly Val Ser Arg Gln Arg Ala
 1 5 10

gcc act caa ggt ctt ggc tcc aac caa aac gct ttg aag tac ttg ggc 97
 Ala Thr Gln Gly Leu Gly Ser Asn Gln Asn Ala Leu Lys Tyr Leu Gly
 14 19 24 29

cag gat ttc aag acc ctg agg caa cag tgc ttg gac tca ggg gtc cta 145
 Gln Asp Phe Lys Thr Leu Arg Gln Gln Cys Leu Asp Ser Gly Val Leu
 30 35 40 45

ttt aag gac cct gag ttc cca gca tgt cca tca gct ttg ggc tac aag 193
 Phe Lys Asp Pro Glu Phe Pro Ala Cys Pro Ser Ala Leu Gly Tyr Lys
 46 51 56 61

gat ctt gga cca ggc tct ccg caa act caa ggc atc atc tgg aag cgg 241
 Asp Leu Gly Pro Gly Ser Pro Gln Thr Gln Gly Ile Ile Trp Lys Arg
 62 67 72 77

ccc acg gag ttg tgt ccc agc cct cag ttt atc gtt ggt gga gcc acg	289
Pro Thr Glu Leu Cys Pro Ser Pro Gln Phe Ile Val Gly Gly Ala Thr	
78 83 88 93	
cgc aca gac att tgt cag ggt ggt cta ggt gac tgc tgg ctt ctg gct	337
Arg Thr Asp Ile Cys Gln Gly Gly Leu Gly Asp Cys Trp Leu Leu Ala	
94 99 104 109	
gcc att gcc tcc ctg acc ctg aat gaa gag ctg ctt tac cgg gtg gtc	385
Ala Ile Ala Ser Leu Thr Leu Asn Glu Glu Leu Leu Tyr Arg Val Val	
110 115 120 125	
ccc agg gac cag gac ttc cag gag aac tat gcg gga atc ttt cac ttt	433
Pro Arg Asp Gln Asp Phe Gln Glu Asn Tyr Ala Gly Ile Phe His Phe	
126 131 136 141	
cag ttc tgg cag tac gga gag tgg gtg gag gtg gtc att gac gac agg	481
Gln Phe Trp Gln Tyr Gly Glu Trp Val Glu Val Val Ile Asp Asp Arg	
142 147 152 157	
ctg ccc acc aag aat gga cag ctg ctc ttc cta cac tcg gaa caa ggc	529
Leu Pro Thr Lys Asn Gly Gln Leu Leu Phe Leu His Ser Glu Gln Gly	
158 163 168 173	
aat gaa ttc tgg agt gcc ctg ctg gag aaa gcc tat gcc aag ctt aat	577
Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala Tyr Ala Lys Leu Asn	
174 179 184 189	
ggt tgt tat gag gct ctc gct gga ggt tcc aca gtg gag ggg ttt gag	625
Gly Cys Tyr Glu Ala Leu Ala Gly Gly Ser Thr Val Glu Gly Phe Glu	
190 195 200 205	
gat ttc aca ggt ggc atc tct gag ttt tat gac ctg aag aaa cca cca	673
Asp Phe Thr Gly Gly Ile Ser Glu Phe Tyr Asp Leu Lys Lys Pro Pro	
206 211 216 221	
gcc aat cta tat cag atc atc cgg aag gcc ctc tgt gcg ggg tct ctg	721
Ala Asn Leu Tyr Gln Ile Ile Arg Lys Ala Leu Cys Ala Gly Ser Leu	
222 227 232 237	
ctg ggc tgc tcc att gat gtc tac agt gca gcc gaa gcc gaa gcc atc	769
Leu Gly Cys Ser Ile Asp Val Tyr Ser Ala Ala Glu Ala Glu Ala Ile	
238 243 248 253	
acc agc cag aag ctg gtt aag agt cat gcg tac tct gtc act gga gtc	817
Thr Ser Gln Lys Leu Val Lys Ser His Ala Tyr Ser Val Thr Gly Val	
254 259 264 269	
gaa gag gtg aat ttc cag ggc cat cca gag aag ctg atc aga ctc agg	865
Glu Glu Val Asn Phe Gln Gly His Pro Glu Lys Leu Ile Arg Leu Arg	
270 275 280 285	
aat cca tgg ggt gaa gtg gag tgg tcg gga gcc tgg agc gat gag tag	913
Asn Pro Trp Gly Glu Val Glu Trp Ser Gly Ala Trp Ser Asp Glu *	
286 291 296 301	

[illegible]

2711

[illegible][illegible]

gac atc ctc atc ccg gag ttc cta aag tct ggc cat ccc agc aac ctg	556
Asp Ile Leu Ile Pro Glu Phe Leu Lys Ser Gly His Pro Ser Asn Leu	
122 127 132 137	
acc tgc tct gtg ccc tgg gtc tgt gag cag gga aca ccc ccc atc ttc	604
Thr Cys Ser Val Pro Trp Val Cys Glu Gln Gly Thr Pro Pro Ile Phe	
138 143 148 153	
tcc tgg atg tca gct gcc ccc acc tcc ctg ggc ccc agg acc ctc cac	652
Ser Trp Met Ser Ala Ala Pro Thr Ser Leu Gly Pro Arg Thr Leu His	
154 159 164 169	
tcc tca gtg ctc acg atc atc cca cgg cct cag gac cac ggc acc aac	700
Ser Ser Val Leu Thr Ile Ile Pro Arg Pro Gln Asp His Gly Thr Asn	
170 175 180 185	
ctc atc tgt cag gtg acg ttc ccc gga gct ggt gtg acc acg gag aga	748
Leu Ile Cys Gln Val Thr Phe Pro Gly Ala Gly Val Thr Thr Glu Arg	
186 191 196 201	
acc atc cag ctc agt gtc tcc tgg aaa tca gga acc gtg gag gag gtg	796
Thr Ile Gln Leu Ser Val Ser Trp Lys Ser Gly Thr Val Glu Glu Val	
202 207 212 217	
gtt gtt ttg gcc gtg ggg gta gtg gct gtg aag atc ctg ctt ctc tgc	844
Val Val Leu Ala Val Gly Val Val Ala Val Lys Ile Leu Leu Leu Cys	
218 223 228 233	
ctt tgc ctc atc atc ctc agt ttc cac aag aag aag gcg gtg agg gca	892
Leu Cys Leu Ile Ile Leu Ser Phe His Lys Lys Lys Ala Val Arg Ala	
234 239 244 249	
gtg gag gtt gag gag aat gta tat gct gtc atg ggt taa tctctcaggc	941
Val Glu Val Glu Glu Asn Val Tyr Ala Val Met Gly *	
250 255 260	
ctccagactg tacttccaga tgtctcctca tccagttcct ccacagtctg aatggccatg	1001
ttttcttcttc attgctggag aatgaagtgc aaatgccact gcctggactg aaggcctttc	1061
acgatctgtc ttctgctgga ctctgctcct gatccccctt ctcttgcct caccggaagt	1121
ctccctacac ccaccaggcc aagccctctg tgattctgag actttgcatg ttagttact	1181
tctcctgaaa tggccttcct cccattcct gccaatccag gtccttatca tccttcaggt	1241
tgtcttaaat gtcattccagg tgtgtgtatt tttatgtaat ccttgatga tattaagcgg	1301
agatgtggca tttgttcatt aatttgtaga catattcagt aaccatactg aatacatata	1361
atgactatgt gccagcattt ccgtatgtgc aagaagttca tcaatagata tagactcaaa	1421
gagctctgtc atcaagctgt tgttctgaag agcagaagga taaaataaa aagaaatgaag	1481
taaaata	1488

<210> 408
 <211> 1457
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (253)..(1140)

<400> 408
 cgactcctga cctttcccag cctcctcggt ccgctgagga acccgagcc cggggcctcg 60
 agcagactgc tgggactgcg gggcgggccg gcgcggggcc agagggcggg cggggcggggt 120
 cgggtcgggg gcctttaaga ggcgcggtcg ccgggaccga cacagacgcg gacagcgccg 180
 ggactcgccg ccccgggact cgcgcagccc gcagcgctcc ggctcctcct ctgcgcaccg 240
 ccctccgcag cg atg gac gga gac ggt gac cca gag agc gtg ggc cag 288
 Met Asp Gly Asp Gly Asp Pro Glu Ser Val Gly Gln
 1 5 10
 ccc gag gag gca agc ccg gag gag cag cca gag gag gcg agt gct gag 336
 Pro Glu Glu Ala Ser Pro Glu Glu Gln Pro Glu Glu Ala Ser Ala Glu
 13 18 23 28
 gag gag cgg ccg gag gac cag cag gag gag gag gcg gcc gcc gcc gcg 384
 Glu Glu Arg Pro Glu Asp Gln Gln Glu Glu Glu Ala Ala Ala Ala Ala
 29 34 39 44
 tac ctg gac gag ctg ccc gag ccg ctg ctg ctg cgc gtg ctg gcc gca 432
 Tyr Leu Asp Glu Leu Pro Glu Pro Leu Leu Leu Arg Val Leu Ala Ala
 45 50 55 60
 ctg ccg gcc gcc gag ctg gtg cag gcc tgc cgc ctg gtg tgc ctg cgc 480
 Leu Pro Ala Ala Glu Leu Val Gln Ala Cys Arg Leu Val Cys Leu Arg
 61 66 71 76
 tgg aag gag ctg gtg gac ggc gcc ccg ctg tgg ctg ctc aag tgc cag 528
 Trp Lys Glu Leu Val Asp Gly Ala Pro Leu Trp Leu Leu Lys Cys Gln
 77 82 87 92
 cag gag ggg ctg gtg ccc gag ggc ggc gtg gag gag gag cgc gac cac 576
 Gln Glu Gly Leu Val Pro Glu Gly Gly Val Glu Glu Glu Arg Asp His
 93 98 103 108
 tgg cag cag ttc tac ttc ctg agc aag cgg cgc cgc aac ctt ctg cgt 624
 Trp Gln Gln Phe Tyr Phe Leu Ser Lys Arg Arg Arg Asn Leu Leu Arg
 109 114 119 124
 aac ccg tgt ggg gaa gag gac ttg gaa ggc tgg tgt gac gtg gag cat 672
 Asn Pro Cys Gly Glu Glu Asp Leu Glu Gly Trp Cys Asp Val Glu His
 125 130 135 140
 ggt ggg gac ggc tgg agg gtg gag gag ctg cct gga gac agt ggg gtg 720

Gly Gly Asp Gly Trp Arg Val Glu Glu Leu Pro Gly Asp Ser Gly Val	
141 146 151 156	
gag ttc acc cac gat gag agc gtc aag aag tac ttc gcc tcc tcc ttt	768
Glu Phe Thr His Asp Glu Ser Val Lys Lys Tyr Phe Ala Ser Ser Phe	
157 162 167 172	
gag tgg tgt cgc aaa gca cag gtc att gac ctg cag gct gag ggc tac	816
Glu Trp Cys Arg Lys Ala Gln Val Ile Asp Leu Gln Ala Glu Gly Tyr	
173 178 183 188	
tgg gag gag ctg ctg gac acg act cag ccg gcc atc gtg gtg aag gac	864
Trp Glu Glu Leu Leu Asp Thr Thr Gln Pro Ala Ile Val Val Lys Asp	
189 194 199 204	
tgg tac tcg ggc cgc agc gac gct ggt tgc ctc tac gag ctc acc gtt	912
Trp Tyr Ser Gly Arg Ser Asp Ala Gly Cys Leu Tyr Glu Leu Thr Val	
205 210 215 220	
aag cta ctg tcc gag cac gag aac gtg ctg gct gag ttc agc agc ggg	960
Lys Leu Leu Ser Glu His Glu Asn Val Leu Ala Glu Phe Ser Ser Gly	
221 226 231 236	
cag gtg gca gtg ccc caa gac agt gac ggc ggg ggc tgg atg gag atc	1008
Gln Val Ala Val Pro Gln Asp Ser Asp Gly Gly Gly Trp Met Glu Ile	
237 242 247 252	
tcc cac acc ttc acc gac tac ggg ccg ggc gtc cgc ttc gtc cgc ttc	1056
Ser His Thr Phe Thr Asp Tyr Gly Pro Gly Val Arg Phe Val Arg Phe	
253 258 263 268	
gag cac ggg ggg cag gac tcc gtc tac tgg aag ggc tgg ttc ggg gcc	1104
Glu His Gly Gly Gln Asp Ser Val Tyr Trp Lys Gly Trp Phe Gly Ala	
269 274 279 284	
cgg gtg acc aac agc agc gtg tgg gta gaa ccc tga gcga ccctgcctcc	1154
Arg Val Thr Asn Ser Ser Val Trp Val Glu Pro *	
285 290 295	
gctctcccc agctgcctgg aggggcaaag gtcgagggta gataggcctt aacttagtcc	1214
atagcgtcct caccttcccc aagccacaca tctcctccc atcccttgct ccgatcccag	1274
cccctgagca gggagagaga agttttgttg gcataggttt gcttaggtag ccggcttcta	1334
gaatgtagat ccgtgagggc gtgagcttgg actggaccca ctgctgattc cctgcaccta	1394
gcacagtgct tgccacaaaag tgggctctca ataaatatta tttgtccaag gaaaaaaaaa	1454
aaa	1457

<210> 409
 <211> 2188
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (400)..(1899)

<220>

<221> misc_feature

<222> (1)...(2188)

<223> n = a,t,c or g

<400> 409

```
ctaatacggg cacatagggga atttggccct cgacgggnata ttccggcacga ggccaatccc 60
tgcttaaagg ccttgctttc ttgtctaacg ccgcaaccag tcctctgagt tgccaacgtc 120
tttcttcttg tctcgacgcc ccgtgtcacg gccacagcga ttctctgctt agcaggatcg 180
gtccacagcg ggacgtgagt ctcttcctcc tcgaggctta ccgctctctc cgcctagtgc 240
caggtgctaa taaagttggt gtttcaaagc cggccaggaa catcgcgagc ggggaccaat 300
cagagagtag ctttgcctct ataacggcgc gagagtgaga cgtcatcggt gagcgactaa 360
cgctagaaac agtgggtgcgc ggagaggaga ggcctcggg atg tct ctg gca gat 414
Met Ser Leu Ala Asp
1
gag ctc tta gct gat ctc gaa gag gca gca gaa gag gag gaa gga gga 462
Glu Leu Leu Ala Asp Leu Glu Glu Ala Ala Glu Glu Glu Glu Gly Gly
6 11 16 21
agc tat ggg gag gaa gaa gag gag cca gcg atc gag gat gtg cag gag 510
Ser Tyr Gly Glu Glu Glu Glu Glu Pro Ala Ile Glu Asp Val Gln Glu
22 27 32 37
gag aca cag ctg gat ctt tcc ggg gat tca gtc aag acc atc gcc aag 558
Glu Thr Gln Leu Asp Leu Ser Gly Asp Ser Val Lys Thr Ile Ala Lys
38 43 48 53
cta tgg gat agt aag atg ttt gct gag att atg atg aag att gag gag 606
Leu Trp Asp Ser Lys Met Phe Ala Glu Ile Met Met Lys Ile Glu Glu
54 59 64 69
tat atc agc aag caa gcc aaa gct tca gaa gtg atg gga cca gtg gag 654
Tyr Ile Ser Lys Gln Ala Lys Ala Ser Glu Val Met Gly Pro Val Glu
70 75 80 85
gcc gcg cct gaa tac cgc gtc atc gtg gat gcc aac aac ctg acc gtg 702
Ala Ala Pro Glu Tyr Arg Val Ile Val Asp Ala Asn Asn Leu Thr Val
86 91 96 101
gag atc gaa aac gag ctg aac atc atc cat aag ttc atc cgg gat aag 750
Glu Ile Glu Asn Glu Leu Asn Ile Ile His Lys Phe Ile Arg Asp Lys
102 107 112 117
tac tca aag aga ttc cct gaa ctg gag tcc ttg gtc ccc aat gca ctg 798
```

Tyr	Ser	Lys	Arg	Phe	Pro	Glu	Leu	Glu	Ser	Leu	Val	Pro	Asn	Ala	Leu		
118					123					128					133		
gat	tac	atc	cgc	acg	gtc	aag	gag	ctg	ggc	aac	agc	ctg	gac	aag	tgc	846	
Asp	Tyr	Ile	Arg	Thr	Val	Lys	Glu	Leu	Gly	Asn	Ser	Leu	Asp	Lys	Cys		
134					139					144					149		
aag	aac	aat	gag	aac	ctg	cag	cag	atc	ctc	acc	aat	gcc	acc	atc	atg	894	
Lys	Asn	Asn	Glu	Asn	Leu	Gln	Gln	Ile	Leu	Thr	Asn	Ala	Thr	Ile	Met		
150					155					160					165		
gtc	gtc	agc	gtc	acc	gcc	tcc	acc	acc	cag	ggg	cag	cag	ctg	tcg	gag	942	
Val	Val	Ser	Val	Thr	Ala	Ser	Thr	Thr	Gln	Gly	Gln	Gln	Leu	Ser	Glu		
166					171					176					181		
gag	gag	ctg	gag	cgg	ctg	gag	gag	gcc	tgc	gac	atg	gcg	ctg	gag	ctg	990	
Glu	Glu	Leu	Glu	Arg	Leu	Glu	Glu	Ala	Cys	Asp	Met	Ala	Leu	Glu	Leu		
182					187					192					197		
aac	gcc	tcc	aag	cac	cgc	atc	tac	gag	tat	gtg	gag	tcc	cgg	atg	tcc	1038	
Asn	Ala	Ser	Lys	His	Arg	Ile	Tyr	Glu	Tyr	Val	Glu	Ser	Arg	Met	Ser		
198					203					208					213		
ttc	atc	gca	ccc	aac	ctg	tcc	atc	att	atc	ggg	gca	tcc	acg	gcc	gcc	1086	
Phe	Ile	Ala	Pro	Asn	Leu	Ser	Ile	Ile	Ile	Gly	Ala	Ser	Thr	Ala	Ala		
214					219					224					229		
aag	atc	atg	ggt	gtg	gcc	ggc	ggc	ctg	acc	aac	ctc	tcc	aag	atg	ccc	1134	
Lys	Ile	Met	Gly	Val	Ala	Gly	Gly	Leu	Thr	Asn	Leu	Ser	Lys	Met	Pro		
230					235					240					245		
gcc	tgc	aac	atc	atg	ctg	ctc	ggg	gcc	cag	cgc	aag	acg	ctg	tcg	ggc	1182	
Ala	Cys	Asn	Ile	Met	Leu	Leu	Gly	Ala	Gln	Arg	Lys	Thr	Leu	Ser	Gly		
246					251					256					261		
ttc	tcg	tct	acc	tca	gtg	ctg	ccc	cac	acc	ggc	tac	atc	tac	cac	agt	1230	
Phe	Ser	Ser	Thr	Ser	Val	Leu	Pro	His	Thr	Gly	Tyr	Ile	Tyr	His	Ser		
262					267					272					277		
gac	atc	gtg	cag	tcc	ctg	cca	ccg	gat	ctg	cgg	cgg	aaa	gcg	gcc	cgg	1278	
Asp	Ile	Val	Gln	Ser	Leu	Pro	Pro	Asp	Leu	Arg	Arg	Lys	Ala	Ala	Arg		
278					283					288					293		
ctg	gtg	gcc	gcc	aag	tgc	aca	ctg	gca	gcc	cgt	gtg	gac	agt	ttc	cac	1326	
Leu	Val	Ala	Ala	Lys	Cys	Thr	Leu	Ala	Ala	Arg	Val	Asp	Ser	Phe	His		
294					299					304					309		
gag	agc	aca	gaa	ggg	aag	gtg	ggc	tac	gaa	ctg	aag	gat	gag	atc	gag	1374	
Glu	Ser	Thr	Glu	Gly	Lys	Val	Gly	Tyr	Glu	Leu	Lys	Asp	Glu	Ile	Glu		
310					315					320					325		
cgc	aaa	ttc	gac	aag	tgg	cag	gag	ccg	ccg	cct	gtg	aag	cag	gtg	aag	1422	
Arg	Lys	Phe	Asp	Lys	Trp	Gln	Glu	Pro	Pro	Pro	Val	Lys	Gln	Val	Lys		
326					331					336					341		
ccg	ctg	cct	gcg	ccc	ctg	gat	gga	cag	cgg	aag	aag	cga	ggc	ggc	cgc	1470	
Pro	Leu	Pro	Ala	Pro	Leu	Asp	Gly	Gln	Arg	Lys	Lys	Arg	Gly	Gly	Arg		

342	347	352	357	
agg tac cgc aag atg aag gag cgg ctg ggg ctg acg gag atc cgg aag				1518
Arg Tyr Arg Lys Met Lys Glu Arg Leu Gly Leu Thr Glu Ile Arg Lys				
358	363	368	373	
cag gcc aac cgt atg agc ttc gga gag atc gag gag gac gcc tac cag				1566
Gln Ala Asn Arg Met Ser Phe Gly Glu Ile Glu Glu Asp Ala Tyr Gln				
374	379	384	389	
gag gac ctg gga ttc agc ctg ggc cac ctg ggc aag tcg ggc agt ggg				1614
Glu Asp Leu Gly Phe Ser Leu Gly His Leu Gly Lys Ser Gly Ser Gly				
390	395	400	405	
cgt gtg cgg cag aca cag gta aac gag gcc acc aag gcc agg atc tcc				1662
Arg Val Arg Gln Thr Gln Val Asn Glu Ala Thr Lys Ala Arg Ile Ser				
406	411	416	421	
aag acg ctg cag cgg acc ctg cag aag cag agc gtc gta tat ggc ggg				1710
Lys Thr Leu Gln Arg Thr Leu Gln Lys Gln Ser Val Val Tyr Gly Gly				
422	427	432	437	
aag tcc acc atc cgc gac cgc tcc tcg ggc acg gcc tcc agc gtg gcc				1758
Lys Ser Thr Ile Arg Asp Arg Ser Ser Gly Thr Ala Ser Ser Val Ala				
438	443	448	453	
ttc acc cca ctc cag ggc ctg gag att gtg aac cca cag gcg gca gag				1806
Phe Thr Pro Leu Gln Gly Leu Glu Ile Val Asn Pro Gln Ala Ala Glu				
454	459	464	469	
aag aag gtg gct gag gcc aac cag aag tat ttc tcc agc atg gct gag				1854
Lys Lys Val Ala Glu Ala Asn Gln Lys Tyr Phe Ser Ser Met Ala Glu				
470	475	480	485	
ttc ctc aag gtc aag ggc gag aag agt ggc ctt atg tcc acc tga atg				1902
Phe Leu Lys Val Lys Gly Glu Lys Ser Gly Leu Met Ser Thr *				
486	491	496		
actgogtgtg tccaaggtgg cttcccactg aagggacaca gaggtccagt ctttctgaag				1962
ggctaggatc gggttctggc agggagaacc tgccctgcc a ctggcccat tgctgggact				2022
gccaggaggag gaggccttgg aagagtcgg cctggcctcc cccaggaccg agatcacccg				2082
ccagtatggg ctagagcagg tcttcatcat gccttgtctt ttttaactga gaaaggagat				2142
tttttgaaaa gagtacaatt aaaaggacat tgtcaaaaaa aaaaaa				2188

<210> 410
 <211> 2275
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> (400)..(1986)

<220>
 <221> misc_feature
 <222> (1)...(2275)
 <223> n = a,t,c or g

<400> 410

ctaatacggg	cacatagggg	atttggccct	cgacgggnata	ttcggcacga	ggcgaatccc	60
tgcttaaagg	ccttgctttc	ttgtctaacg	ccgcaaccag	tcctctgagt	tgccaacgtc	120
tttcttcttg	tctcgacgcc	ccgtgtcacg	gccacagcga	ttctctgctt	agcaggatcg	180
gtccacagcg	ggacgtgagt	ctcttcctcc	tcgcggtta	ccgtctcttc	cgcctagtgc	240
caggtgctaa	taaagttggt	gtttcaaatz	cggccaggaa	catcgcgagc	ggggaccaat	300
cagagagtag	ctttgcctct	ataacggcgc	gagagtgaga	cgatcatcgt	gagcgactaa	360
cgctagaaac	agtgggtgcgc	ggagaggaga	ggcctcggg	atg tct ctg gca gat		414
				Met Ser Leu Ala Asp		
				1		
gag ctc tta gct gat ctc gaa gag gca gca gaa gag gag gaa gga gga						462
Glu Leu Leu Ala Asp Leu Glu Glu Ala Ala Glu Glu Glu Glu Gly Gly						
6 11 16 21						
agc tat ggg gag gaa gaa gag gag cca gcg atc gag gat gtg cag gag						510
Ser Tyr Gly Glu Glu Glu Glu Glu Pro Ala Ile Glu Asp Val Gln Glu						
22 27 32 37						
gag aca cag ctg gat ctt tcc ggg gat tca gtc aag acc atc gcc aag						558
Glu Thr Gln Leu Asp Leu Ser Gly Asp Ser Val Lys Thr Ile Ala Lys						
38 43 48 53						
cta tgg gat agt aag atg ttt gct gag att atg atg aag att gag gag						606
Leu Trp Asp Ser Lys Met Phe Ala Glu Ile Met Met Lys Ile Glu Glu						
54 59 64 69						
tat atc agc aag caa gcc aaa gct tca gaa gtg atg gga cca gtg gag						654
Tyr Ile Ser Lys Gln Ala Lys Ala Ser Glu Val Met Gly Pro Val Glu						
70 75 80 85						
gcc gcg cct gaa tac cgc gtc atc gtg gat gcc aac aac ctg acc gtg						702
Ala Ala Pro Glu Tyr Arg Val Ile Val Asp Ala Asn Asn Leu Thr Val						
86 91 96 101						
gag atc gaa aac gag ctg aac atc atc cat aag ttc atc cgg gat aag						750
Glu Ile Glu Asn Glu Leu Asn Ile Ile His Lys Phe Ile Arg Asp Lys						
102 107 112 117						
tac tca aag aga ttc cct gaa ctg gag tcc ttg gtc ccc aat gca ctg						798
Tyr Ser Lys Arg Phe Pro Glu Leu Glu Ser Leu Val Pro Asn Ala Leu						
118 123 128 133						

gat tac atc cgc acg gtc aag gag ctg ggc aac agc ctg gac aag tgc	846
Asp Tyr Ile Arg Thr Val Lys Glu Leu Gly Asn Ser Leu Asp Lys Cys	
134 139 144 149	
aag aac aat gag aac ctg cag cag atc ctc acc aat gcc acc atc atg	894
Lys Asn Asn Glu Asn Leu Gln Gln Ile Leu Thr Asn Ala Thr Ile Met	
150 155 160 165	
gtc gtc agc gtc acc gcc tcc acc acc cag ggg cag cag ctg tcg gag	942
Val Val Ser Val Thr Ala Ser Thr Thr Gln Gly Gln Gln Leu Ser Glu	
166 171 176 181	
gag gag ctg gag cgg ctg gag gag gcc tgc gac atg gcg ctg gag ctg	990
Glu Glu Leu Glu Arg Leu Glu Glu Ala Cys Asp Met Ala Leu Glu Leu	
182 187 192 197	
aac gcc tcc aag cac cgc atc tac gag tat gtg gag tcc cgg atg tcc	1038
Asn Ala Ser Lys His Arg Ile Tyr Glu Tyr Val Glu Ser Arg Met Ser	
198 203 208 213	
ttc atc gca ccc aac ctg tcc atc att atc ggg gca tcc acg gcc gcc	1086
Phe Ile Ala Pro Asn Leu Ser Ile Ile Ile Gly Ala Ser Thr Ala Ala	
214 219 224 229	
aag atc atg ggt gtg gcc ggc ggc ctg acc aac ctc tcc aag atg ccc	1134
Lys Ile Met Gly Val Ala Gly Gly Leu Thr Asn Leu Ser Lys Met Pro	
230 235 240 245	
gcc tgc aac atc atg ctg ctc ggg gcc cag cgc aag acg ctg tcg ggc	1182
Ala Cys Asn Ile Met Leu Leu Gly Ala Gln Arg Lys Thr Leu Ser Gly	
246 251 256 261	
ttc tcg tct acc tca gtg ctg ccc cac acc ggc tac atc tac cac agt	1230
Phe Ser Ser Thr Ser Val Leu Pro His Thr Gly Tyr Ile Tyr His Ser	
262 267 272 277	
gac atc gtg cag tcc ctg cca ccg gat ctg cgg cgg aaa gcg gcc cgg	1278
Asp Ile Val Gln Ser Leu Pro Pro Asp Leu Arg Arg Lys Ala Ala Arg	
278 283 288 293	
ctg gtg gcc gcc aag tgc aca ctg gca gcc cgt gtg gac agt ttc cac	1326
Leu Val Ala Ala Lys Cys Thr Leu Ala Ala Arg Val Asp Ser Phe His	
294 299 304 309	
gag agc aca gaa ggg aag gtg ggc tac gaa ctg aag gat gag atc gag	1374
Glu Ser Thr Glu Gly Lys Val Gly Tyr Glu Leu Lys Asp Glu Ile Glu	
310 315 320 325	
cgc aaa ttc gac aag tgg cag gag ccg ccg cct gtg aag cag gtg aag	1422
Arg Lys Phe Asp Lys Trp Gln Glu Pro Pro Pro Val Lys Gln Val Lys	
326 331 336 341	
ccg ctg cct gcg ccc ctg gat gga cag ccg aag aag cga ggc ggc cgc	1470
Pro Leu Pro Ala Pro Leu Asp Gly Gln Arg Lys Lys Arg Gly Gly Arg	
342 347 352 357	
agg tac cgc aag atg aag gag ccg ctg ggg ctg acg gag atc ccg aag	1518

Arg Tyr Arg Lys Met Lys Glu Arg Leu Gly Leu Thr Glu Ile Arg Lys
358 363 368 373

cag gcc aac cgt atg agc ttc gga gag atc gag gag gac gcc tac cag 1566
Gln Ala Asn Arg Met Ser Phe Gly Glu Ile Glu Glu Asp Ala Tyr Gln
374 379 384 389

gag gac ctg gga ttc agc ctg ggc cac ctg ggc aag tcg ggc agt ggg 1614
Glu Asp Leu Gly Phe Ser Leu Gly His Leu Gly Lys Ser Gly Ser Gly
390 395 400 405

cgt gtg cgg cag aca cag gta aac gag gcc acc aag gcc agg atc tcc 1662
Arg Val Arg Gln Thr Gln Val Asn Glu Ala Thr Lys Ala Arg Ile Ser
406 411 416 421

aag acg ctg cag gta tgg gcc aga ccc agg tgg ggc tgg gag acc gag 1710
Lys Thr Leu Gln Val Trp Ala Arg Pro Arg Trp Gly Trp Glu Thr Glu
422 427 432 437

gga cac aag gtg ggg gga gcc cag atc gca gcc tcc ctg tcc tcc cca 1758
Gly His Lys Val Gly Gly Ala Gln Ile Ala Ala Ser Leu Ser Ser Pro
438 443 448 453

cag cgg acc ctg cag aag cag agc gtc gta tat ggc ggg aag tcc acc 1806
Gln Arg Thr Leu Gln Lys Gln Ser Val Val Tyr Gly Gly Lys Ser Thr
454 459 464 469

atc cgc gac cgc tcc tcg ggc acg gcc tcc agc gtg gcc ttc acc cca 1854
Ile Arg Asp Arg Ser Ser Gly Thr Ala Ser Ser Val Ala Phe Thr Pro
470 475 480 485

ctc cag ggc ctg gag att gtg aac cca cag gcg gca gag aag aag gtg 1902
Leu Gln Gly Leu Glu Ile Val Asn Pro Gln Ala Ala Glu Lys Lys Val
486 491 496 501

gct gag gcc aac cag aag tat ttc tcc agc atg gct gag ttc ctc aag 1950
Ala Glu Ala Asn Gln Lys Tyr Phe Ser Ser Met Ala Glu Phe Leu Lys
502 507 512 517

gtc aag ggc gag aag agt ggc ctt atg tcc acc tga atga ctgcgtgtgt 2000
Val Lys Gly Glu Lys Ser Gly Leu Met Ser Thr *
518 523 528

ccaaggtggc ttccactga agggacacag aggtccagtc cttctgaagg gctaggatcg 2060

ggttctggca gggagaacct gccctgccac tggccccatt gctgggactg cccagggagg 2120

aggccttggga agagtccggc ctggcctccc ccaggaccga gatcaccgcc cagtatgggc 2180

tagagcaggt cttcatcatg ctttgtcttt tttaactgag aaaggagatt ttttgaaaag 2240

agtacaatta aaaggacatt gtcaaaaaaa aaaaa 2275

<210> 411

<211> 2338
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (115)..(1455)

<400> 411

tagcgggtccc aggagtttcc aaggtaacccg cgcagtaggg cggatctcat taggcggaaa	60
gcgaaaccgc gaagtgcgc tcttaccggg tgtcagcagc gagagggttc gaag atg	117
	Met
	1
gcg gcg cgc aag ggt cgg cgt cgc acg tgt gaa acc ggg gaa ccc atg	165
Ala Ala Arg Lys Gly Arg Arg Arg Thr Cys Glu Thr Gly Glu Pro Met	
2 7 12 17	
gaa gcc gag tcc ggc gac aca agt tcc gag ggc ccg gcc cag gtc tac	213
Glu Ala Glu Ser Gly Asp Thr Ser Ser Glu Gly Pro Ala Gln Val Tyr	
18 23 28 33	
ctg ccc ggc cgg ggg ccg ccg cta cgc gaa ggg gag gag ctg gtc atg	261
Leu Pro Gly Arg Gly Pro Pro Leu Arg Glu Gly Glu Glu Leu Val Met	
34 39 44 49	
gac gag gag gcc tat gtg ctc tac cac cga gcg cag act ggc gcc ccc	309
Asp Glu Glu Ala Tyr Val Leu Tyr His Arg Ala Gln Thr Gly Ala Pro	
50 55 60 65	
tgt ctc agc ttt gac ata gtc cgg gat cac ctg gga gac aac cgg aca	357
Cys Leu Ser Phe Asp Ile Val Arg Asp His Leu Gly Asp Asn Arg Thr	
66 71 76 81	
gag ctt cct ctt aca ctt tac ttg tgt gct ggg acc cag gct gag agc	405
Glu Leu Pro Leu Thr Leu Tyr Leu Cys Ala Gly Thr Gln Ala Glu Ser	
82 87 92 97	
gcc cag agc aac aga ctg atg atg ctt cgg atg cac aat ctg cat ggg	453
Ala Gln Ser Asn Arg Leu Met Met Leu Arg Met His Asn Leu His Gly	
98 103 108 113	
aca aag ccc cca ccc tca gag ggc agt gat gaa gaa gaa gag gag gaa	501
Thr Lys Pro Pro Pro Ser Glu Gly Ser Asp Glu Glu Glu Glu Glu Glu	
114 119 124 129	
gat gaa gag gat gaa gaa gag cgg aaa cct cag ctg gag ctg gcc atg	549
Asp Glu Glu Asp Glu Glu Glu Arg Lys Pro Gln Leu Glu Leu Ala Met	
130 135 140 145	
gtg ccc cac tat ggt ggc atc aac cga gtt cgg gtg tca tgg ctg ggt	597
Val Pro His Tyr Gly Gly Ile Asn Arg Val Arg Val Ser Trp Leu Gly	
146 151 156 161	
gaa gag cct gtg gct ggg gtg tgg tca gag aag ggc cag gtg gag gtg	645
Glu Glu Pro Val Ala Gly Val Trp Ser Glu Lys Gly Gln Val Glu Val	

162	167	172	177	
ttt gcg ctg cgg cgg ctt ctg cag gtg gtg gag gag ccc cag gcc ctg				693
Phe Ala Leu Arg Arg Leu Leu Gln Val Val Glu Glu Pro Gln Ala Leu				
178	183	188	193	
gca gcc ttc ctc cgg gat gag cag gcc caa atg aag ccc atc ttc tcc				741
Ala Ala Phe Leu Arg Asp Glu Gln Ala Gln Met Lys Pro Ile Phe Ser				
194	199	204	209	
ttc gct gga cac atg ggc gag ggc ttt gcc ctt gac tgg tcc ccc cgg				789
Phe Ala Gly His Met Gly Glu Gly Phe Ala Leu Asp Trp Ser Pro Arg				
210	215	220	225	
gtg acc ggt cgc ctg ctg acc ggt gac tgt caa aag aac atc cac ctc				837
Val Thr Gly Arg Leu Leu Thr Gly Asp Cys Gln Lys Asn Ile His Leu				
226	231	236	241	
tgg aca cct acg gac ggc ggc tcc tgg cac gtg gac cag cgg cca ttc				885
Trp Thr Pro Thr Asp Gly Gly Ser Trp His Val Asp Gln Arg Pro Phe				
242	247	252	257	
gtg ggc cac aca cgc tct gtg gag gac ctg cag tgg tca ccg act gag				933
Val Gly His Thr Arg Ser Val Glu Asp Leu Gln Trp Ser Pro Thr Glu				
258	263	268	273	
aac acg gtg ttt gcc tcc tgc tca gct gac gcc tcc atc cgc atc tgg				981
Asn Thr Val Phe Ala Ser Cys Ser Ala Asp Ala Ser Ile Arg Ile Trp				
274	279	284	289	
gac atc cgg gca gcc ccc agc aag gcc tgc atg ctc acc aca gcc acc				1029
Asp Ile Arg Ala Ala Pro Ser Lys Ala Cys Met Leu Thr Thr Ala Thr				
290	295	300	305	
gcc cat gat ggg gac gtc aat gtc atc agc tgg agc cgc cgg gag ccc				1077
Ala His Asp Gly Asp Val Asn Val Ile Ser Trp Ser Arg Arg Glu Pro				
306	311	316	321	
ttc ctg ctc agt ggc ggg gat gat ggg gcc ctc aag atc tgg gac ctt				1125
Phe Leu Leu Ser Gly Gly Asp Asp Gly Ala Leu Lys Ile Trp Asp Leu				
322	327	332	337	
cgg cag ttc aag tct ggt tcc cca gtg gcc acc ttc aag cag cac gtg				1173
Arg Gln Phe Lys Ser Gly Ser Pro Val Ala Thr Phe Lys Gln His Val				
338	343	348	353	
gcc ccc gtg acc tcc gtc gag tgg cac ccc cag gac agc ggg gtc ttt				1221
Ala Pro Val Thr Ser Val Glu Trp His Pro Gln Asp Ser Gly Val Phe				
354	359	364	369	
gca gcc tcg ggt gca gac cac cag atc aca cag tgg gac ctg gca gtg				1269
Ala Ala Ser Gly Ala Asp His Gln Ile Thr Gln Trp Asp Leu Ala Val				
370	375	380	385	
gag cgg gac cct gag gcg ggc gac gtg gag gcc gac ccc gga ctg gcc				1317
Glu Arg Asp Pro Glu Ala Gly Asp Val Glu Ala Asp Pro Gly Leu Ala				
386	391	396	401	

aagggaccag gccgccgtcc ccagcgagag gcatgcagcg ctgaggagcg gcgaccacgc 120
acggcgggcgc c atg aac ctc ctg ccg tgt aac cct cac ggc aac ggg ctg 170
Met Asn Leu Leu Pro Cys Asn Pro His Gly Asn Gly Leu
1 5 10
ctc tac gcc ggc ttc aac cag gac cac gga tgc ttt gcg tgt ggg atg 218
Leu Tyr Ala Gly Phe Asn Gln Asp His Gly Cys Phe Ala Cys Gly Met
14 19 24 29
gaa aat gga ttc cga gtc tat aac act gat cca cta aaa gaa aaa gag 266
Glu Asn Gly Phe Arg Val Tyr Asn Thr Asp Pro Leu Lys Glu Lys Glu
30 35 40 45
aaa caa gaa ttt cta gaa gga gga gtt ggc cat gtt gaa atg tta ttt 314
Lys Gln Glu Phe Leu Glu Gly Gly Val Gly His Val Glu Met Leu Phe
46 51 56 61
cgc tgc aac tat tta gct tta gtt ggt ggt gga aaa aag ccg aaa tac 362
Arg Cys Asn Tyr Leu Ala Leu Val Gly Gly Gly Lys Lys Pro Lys Tyr
62 67 72 77
cct ccc aac aaa gta atg atc tgg gat gac ctg aag aag aag act gtt 410
Pro Pro Asn Lys Val Met Ile Trp Asp Asp Leu Lys Lys Lys Thr Val
78 83 88 93
att gaa ata gaa ttt tct aca gaa gtc aag gca gtc aag ctg cgg cga 458
Ile Glu Ile Glu Phe Ser Thr Glu Val Lys Ala Val Lys Leu Arg Arg
94 99 104 109
gat aga att gtg gtg gtt ttg gac tcc atg att aag gtg ttc aca ttc 506
Asp Arg Ile Val Val Val Leu Asp Ser Met Ile Lys Val Phe Thr Phe
110 115 120 125
aca cac aat ccc cat cag ttg cac gtc ttc gaa acc tgc tat aac ccc 554
Thr His Asn Pro His Gln Leu His Val Phe Glu Thr Cys Tyr Asn Pro
126 131 136 141
aaa ggc ctc tgt gtc ctt tgt ccc aat agt aac aac tcc ctc ctg gcc 602
Lys Gly Leu Cys Val Leu Cys Pro Asn Ser Asn Asn Ser Leu Leu Ala
142 147 152 157
ttt ccg ggc acg cac acg ggc cat gtg cag ctt gtg gac ctg gcc agc 650
Phe Pro Gly Thr His Thr Gly His Val Gln Leu Val Asp Leu Ala Ser
158 163 168 173
acg gag aag cca ccc gtg gac att cct gca cac gag ggt gtc ctg agc 698
Thr Glu Lys Pro Pro Val Asp Ile Pro Ala His Glu Gly Val Leu Ser
174 179 184 189
tgc att gca ctc aac ctg cag gga aca aga att gca act gca tcc gag 746
Cys Ile Ala Leu Asn Leu Gln Gly Thr Arg Ile Ala Thr Ala Ser Glu
190 195 200 205
aaa ggg acg ctt ata aga ata ttt gat act tca tca ggg cat tta atc 794
Lys Gly Thr Leu Ile Arg Ile Phe Asp Thr Ser Ser Gly His Leu Ile

206	211	216	221	
cag gaa ctg cga aga gga tct caa gca gcc aat att tac tgc atc aac				842
Gln Glu Leu Arg Arg Gly Ser Gln Ala Ala Asn Ile Tyr Cys Ile Asn				
222	227	232	237	
ttc aat cag gat gcg tcc ctc atc tgc gta tcc agc gac cac ggc aca				890
Phe Asn Gln Asp Ala Ser Leu Ile Cys Val Ser Ser Asp His Gly Thr				
238	243	248	253	
gtg cat att ttt gca gct gaa gat cca aaa agg aat aaa cag tcc agt				938
Val His Ile Phe Ala Ala Glu Asp Pro Lys Arg Asn Lys Gln Ser Ser				
254	259	264	269	
ttg gcc tca gcc agt ttc ctt cca aaa tac ttc agt tcc aag tgg agt				986
Leu Ala Ser Ala Ser Phe Leu Pro Lys Tyr Phe Ser Ser Lys Trp Ser				
270	275	280	285	
ttc tcc aag ttt cag gtt ccc tca ggc tct ccg tgc att tgt gcc ttt				1034
Phe Ser Lys Phe Gln Val Pro Ser Gly Ser Pro Cys Ile Cys Ala Phe				
286	291	296	301	
gga aca gag cca aac gcc gtc att gca att tgt gca gac ggc agc tac				1082
Gly Thr Glu Pro Asn Ala Val Ile Ala Ile Cys Ala Asp Gly Ser Tyr				
302	307	312	317	
tac aaa ttc ctg ttc aac ccc aag ggg gag tgc atc cga gat gtc tac				1130
Tyr Lys Phe Leu Phe Asn Pro Lys Gly Glu Cys Ile Arg Asp Val Tyr				
318	323	328	333	
gcg cag ttt cta gag atg acc gat gac aag ctg tga ctcc agctgggggc				1180
Ala Gln Phe Leu Glu Met Thr Asp Asp Lys Leu *				
334	339	344		
gccacagcac ccaccacctg ccgccttcag actctcgggg ctggtgccag tgccccaggg				1240
gcctcctgagg ccacggggctg gaggggctgc ccagggaacct tgggtctcgaa gccatacgtg				1300
gttgtctgct ttctaagga ctccatttc cagtattaaa gagagaatca tcatcaaggc				1360
accgtaggta actcagtggc tgtgaccagc tcgactggcg gccactggct gttcccatga				1420
gttcagctgt gacgttagct tcagtggctc cgccgcatcc tcacactgac gggggctcca				1480
tacggacctg gggactgggc tgagaggggtg gacgagttca ggtttgtttt tgcagcagat				1540
tccgtcgttc ttactgagtc tgcagcgggg gagtgaacaa gtgtgcagat gtaagttctt				1600
acatgataag cagattgaat acaacaccag cagcttgccct tagaaaagga gaaaggaatt				1660
ccttttcccg ccgaacatg aagaaaaacg acctgacctt gtagagagaa cacagtgtga				1720
atgtttcccc tcgtgtgagc ccagcctgtg gtcttctccg taccgcgaac gtggtcacct				1780
gtgcccgtga cgtcacctgt gcccgctgct ggcgtccccg tctccgttgg ggccattaga				1840
atgaggcaga caccaggcca ctctagaagc cgagccgtca cacctcaggc gtgtgcgggg				1900

cggggacggg ggggtctcctg gttacatddd ggattaaacc tgtttcccgg ttatgtgtag 1960
 ggaacagcag agtgatgcac gaactttgaa cattcgttat ggggaaaaca tcctttaact 2020
 tcggggtcgt ctgccagagc aggggtctggg aggggtccatg cagttcccgc tgggtgtggag 2080
 ggaaatgcc tgggtctggcc tccgagcccc cagggtccacc gtctcccctc ccctcatttg 2140
 taagaatagc tacacactaa cattttggga aggagaggca cataactddd tttaacattt 2200
 ggtaactagg ttatgggctc tacattgtca gctacttggg atatatatddd aatdddctta 2260
 aattcccgtt aaactctatt ttatggtdttt gatttcagat tgcaaactg taaaacctgc 2320
 atagcagcga gtcctcgggt ttgccggttt ctttagttct ttactgtcac tgtcatgtaa 2380
 tcagctaatt ctctgtggat gttgctgtaa agtatgcag ttcccttccat gtgtatttaa 2440
 tcatgatgtt taatdddgca cacttatddd taatgttdct tttaaataaa agtgactaat 2500
 tttgttgtag tctggaaaaa aaaaaa 2527

<210> 413
 <211> 2488
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (617) .. (1933)

<400> 413
 tttgaatgca gatgctgttg cgctgccgg accggaccgg aattcccggg tcgacgattt 60
 cgctccttggg ttccgctgta ggggaggtcc cgtgcgaaag aatgaggaga tcctggggcc 120
 ttacctacta gcggaatcga ctgaagagac gcctgccagt gcgggaggta ggaagctcga 180
 tccccaaaga aaagagcgag tgggcaggca gctgcgagac agaaccggag tgtgcagggt 240
 ccctagaggc cggttcctgg tctgtgctgc tctcctggaa gccatggtac aggcagagct 300
 cagggcgatc ccaggtgag ggcagcggct ctgcctggga ttccaccgca gtacaaccgg 360
 gtagatgcgg ggtggagaag aaaggatgtt gcctgcactg ctcgccaata gcaccctgag 420
 aggctacatt tgcagaagca gcagcagcag aagacacagc gccggtccag gaggcgggtc 480
 gagctgttcg taaagtgcgc cgacagcttd ttctccgtag tatgcgagtt gacaaaacag 540
 ccagagaaca gggctcccca ttacaatctt ttcgagatct tttcccttgc taaccggatc 600
 tgatttgtgc gaaaac atg cct tgc act tgt acc tgg agg aac tgg aga 649

Met Pro Cys Thr Cys Thr Trp Arg Asn Trp Arg
1 5

cag tgg att cga cct tta gta gcg gtc atc tac ctg gtg tca ata gtg Gln Trp Ile Arg Pro Leu Val Ala Val Ile Tyr Leu Val Ser Ile Val 12 17 22 27	697
gtt gcg gtt ccc cta tgc gtg tgg gaa tta cag aaa ctg gag gtt gga Val Ala Val Pro Leu Cys Val Trp Glu Leu Gln Lys Leu Glu Val Gly 28 33 38 43	745
ata cac acc aag gct tgg ttt att gct gga atc ttt ttg ctg ttg act Ile His Thr Lys Ala Trp Phe Ile Ala Gly Ile Phe Leu Leu Leu Thr 44 49 54 59	793
att cct ata tca ctg tgg gtg ata ttg caa cac tta gtg cat tat aca Ile Pro Ile Ser Leu Trp Val Ile Leu Gln His Leu Val His Tyr Thr 60 65 70 75	841
caa cct gaa cta caa aaa cca ata ata agg att ctt tgg atg gta cct Gln Pro Glu Leu Gln Lys Pro Ile Ile Arg Ile Leu Trp Met Val Pro 76 81 86 91	889
att tac agt tta gat agt tgg ata gct ttg aaa tat ccc gga att gca Ile Tyr Ser Leu Asp Ser Trp Ile Ala Leu Lys Tyr Pro Gly Ile Ala 92 97 102 107	937
ata tat gtg gat acc tgc aga gaa tgc tat gaa gct tat gta att tac Ile Tyr Val Asp Thr Cys Arg Glu Cys Tyr Glu Ala Tyr Val Ile Tyr 108 113 118 123	985
aac ttt atg gga ttc ctt acc aat tat cta act aac cgg tat cca aat Asn Phe Met Gly Phe Leu Thr Asn Tyr Leu Thr Asn Arg Tyr Pro Asn 124 129 134 139	1033
ctg gta tta atc ctt gaa gcc aaa gat caa cag aaa cat ttc cct cct Leu Val Leu Ile Leu Glu Ala Lys Asp Gln Gln Lys His Phe Pro Pro 140 145 150 155	1081
tta tgt tgc tgt cca cca tgg gct atg gga gaa gta ttg ctg ttt agg Leu Cys Cys Cys Pro Pro Trp Ala Met Gly Glu Val Leu Leu Phe Arg 156 161 166 171	1129
tgc aaa cta ggt gta tta cag tac aca gtt gtc aga cct ttc acc acc Cys Lys Leu Gly Val Leu Gln Tyr Thr Val Val Arg Pro Phe Thr Thr 172 177 182 187	1177
atc gtt gct tta atc tgt gag ctg ctt ggt ata tat gac gaa ggg aac Ile Val Ala Leu Ile Cys Glu Leu Leu Gly Ile Tyr Asp Glu Gly Asn 188 193 198 203	1225
ttt agc ttt tca aat gct tgg act tat ttg gtt ata ata aac aac atg Phe Ser Phe Ser Asn Ala Trp Thr Tyr Leu Val Ile Ile Asn Asn Met 204 209 214 219	1273
tca cag ttg ttt gcc atg tat tgt ctc ctg ctc ttt tat aaa gta cta Ser Gln Leu Phe Ala Met Tyr Cys Leu Leu Leu Phe Tyr Lys Val Leu	1321

220	225	230	235
aaa gaa gaa ctg agc cca atc caa cct gtt ggc aaa ttt ctt tgt gta Lys Glu Glu Leu Ser Pro Ile Gln Pro Val Gly Lys Phe Leu Cys Val 236 241 246 251			1369
aag ctg gtg gtt ttt gtt tct ttt tgg caa gca gta gtt att gct ttg Lys Leu Val Val Phe Val Ser Phe Trp Gln Ala Val Val Ile Ala Leu 252 257 262 267			1417
ttg gta aaa gtt ggc gtt att tct gaa aag cat acg tgg gaa tgg caa Leu Val Lys Val Gly Val Ile Ser Glu Lys His Thr Trp Glu Trp Gln 268 273 278 283			1465
act gta gaa gct gtg gcc acc gga ctc cag gat ttt att atc tgt att Thr Val Glu Ala Val Ala Thr Gly Leu Gln Asp Phe Ile Ile Cys Ile 284 289 294 299			1513
gag atg ttc ctc gct gcc att gct cat cat tac aca ttc tca tat aaa Glu Met Phe Leu Ala Ala Ile Ala His His Tyr Thr Phe Ser Tyr Lys 300 305 310 315			1561
cca tat gtc caa gaa gca gaa gag ggc tca tgc ttt gat tcc ttt ctt Pro Tyr Val Gln Glu Ala Glu Glu Gly Ser Cys Phe Asp Ser Phe Leu 316 321 326 331			1609
gcc atg tgg gat gtc tca gat att aga gat gat att tct gaa caa gta Ala Met Trp Asp Val Ser Asp Ile Arg Asp Asp Ile Ser Glu Gln Val 332 337 342 347			1657
agg cat gtt gga cgg aca gtc agg gga cat ccc agg aaa aaa ttg ttt Arg His Val Gly Arg Thr Val Arg Gly His Pro Arg Lys Lys Leu Phe 348 353 358 363			1705
ccc gag gat caa gat caa aat gaa cat aca agt tta tta tca tca tca Pro Glu Asp Gln Asp Gln Asn Glu His Thr Ser Leu Leu Ser Ser Ser 364 369 374 379			1753
tca caa gat gca att tcc att gct tct tct atg cca cct tca ccc atg Ser Gln Asp Ala Ile Ser Ile Ala Ser Ser Met Pro Pro Ser Pro Met 380 385 390 395			1801
ggt cac tac caa ggg ttt gga cac act gtg act ccc cag act aca cct Gly His Tyr Gln Gly Phe Gly His Thr Val Thr Pro Gln Thr Thr Pro 396 401 406 411			1849
acc aca gct aag ata tct gat gaa atc ctt agt gat act ata gga gag Thr Thr Ala Lys Ile Ser Asp Glu Ile Leu Ser Asp Thr Ile Gly Glu 412 417 422 427			1897
aaa aaa gaa cct tca gat aaa tcc gtg gat tcc tga acag tatggaaaag Lys Lys Glu Pro Ser Asp Lys Ser Val Asp Ser *			1947
428 433 438			
caaactgtgc aactactaca ttatatcatt acctggtatc ccatggattt tgtgcttggg			2007
acagaccata aatgatggaa aatgtcaaca caaaaatagc tgaaagccag gtacaactac			2067

tgcatttata tatgtaagtt ttgtatatca aaaataattg gtctaaattt cctagactta 2127
 gacttgattt cttaacatta gggatcgca tactcaaagtg gtagacaatg accccaacta 2187
 aatcttcctg atgttacact gctttatcaa gaggatggac tttttttttt tgagacagac 2247
 agagtcttgc totgtcaccc aggggtggagt gcagggggccc aatctcgggt cactgcaagc 2307
 tctgcctccc aagttcatgc cattctcctg cctaaccctc ccaagaagtt ggggactaca 2367
 ggcacctgcc accatgcccga gttaattttt tttttttaag aaaaaagggg gtctccctt 2427
 ttggcccaga agggttttta ttaaccttg gaacccccca acctcgccct cccaaagggt 2487
 g 2488

<210> 414
 <211> 1240
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (82)..(1080)

<400> 414
 atttggccct cgaggccaag aattcggcac gagactggcc cgactacttt cgttcggtct 60
 tccatcgtgg gctctcgtgc a atg gcg tcc ggg ctg gta aga ttg ctg cag 111
 Met Ala Ser Gly Leu Val Arg Leu Leu Gln
 1 5
 cag gga cat cgc tgc ctc ctg gct cca gtc gcc ccc aag ctg gtc cct 159
 Gln Gly His Arg Cys Leu Leu Ala Pro Val Ala Pro Lys Leu Val Pro
 11 16 21 26
 ccg gtt cgg gga gtg aag aag gga ttc cgc gcc gcc ttc cgc ttc cag 207
 Pro Val Arg Gly Val Lys Lys Gly Phe Arg Ala Ala Phe Arg Phe Gln
 27 32 37 42
 aag gag tta gag cgg cag cgc ctt ctg cgg tgc ccg ccg ccg ccc gtg 255
 Lys Glu Leu Glu Arg Gln Arg Leu Leu Arg Cys Pro Pro Pro Pro Val
 43 48 53 58
 cgc cgt tca gag aag ccg aac tgg gat tac cat gca gaa ata caa gct 303
 Arg Arg Ser Glu Lys Pro Asn Trp Asp Tyr His Ala Glu Ile Gln Ala
 59 64 69 74
 ttt gga cat cgg tta cag gaa aac ttt tcc tta gat ctt ctc aaa act 351
 Phe Gly His Arg Leu Gln Glu Asn Phe Ser Leu Asp Leu Leu Lys Thr
 75 80 85 90
 gca ttt gtt aat agc tgc tat att aaa agt gag gag gcc aaa cgc caa 399

Ala Phe Val Asn Ser Cys Tyr Ile Lys Ser Glu Glu Ala Lys Arg Gln	
91 96 101 106	
caa ctt ggg ata gag aaa gaa gct gtt ctt ctg aat ctt aaa agt aat	447
Gln Leu Gly Ile Glu Lys Glu Ala Val Leu Leu Asn Leu Lys Ser Asn	
107 112 117 122	
caa gaa cta tcc gaa caa ggg aca tct ttt tca cag act tgc ctt aca	495
Gln Glu Leu Ser Glu Gln Gly Thr Ser Phe Ser Gln Thr Cys Leu Thr	
123 128 133 138	
cag ttt ctt gaa gac gag tac cca gac atg ccc act gaa ggc ata aaa	543
Gln Phe Leu Glu Asp Glu Tyr Pro Asp Met Pro Thr Glu Gly Ile Lys	
139 144 149 154	
aat ctt gtt gac ttt ctc act ggt gag gaa gtc gtg tgt cac gtg gct	591
Asn Leu Val Asp Phe Leu Thr Gly Glu Glu Val Val Cys His Val Ala	
155 160 165 170	
aga aac ttg gct gtg gag cag tta aca ctg agt gaa gaa ttc cca gtg	639
Arg Asn Leu Ala Val Glu Gln Leu Thr Leu Ser Glu Glu Phe Pro Val	
171 176 181 186	
ccc cca gct gtg tta cag cag act ttc ttt gca gtt att gga gcc ctg	687
Pro Pro Ala Val Leu Gln Gln Thr Phe Phe Ala Val Ile Gly Ala Leu	
187 192 197 202	
tta cag agc agt gga cct gag agg act gca ctt ttc atc agg gac ttc	735
Leu Gln Ser Ser Gly Pro Glu Arg Thr Ala Leu Phe Ile Arg Asp Phe	
203 208 213 218	
tta att act caa atg act gga aaa gag ctc ttt gag atg tgg aag ata	783
Leu Ile Thr Gln Met Thr Gly Lys Glu Leu Phe Glu Met Trp Lys Ile	
219 224 229 234	
ata aat ccc atg ggg cta ttg gta gaa gaa ctg aag aaa agg aat gtt	831
Ile Asn Pro Met Gly Leu Leu Val Glu Glu Leu Lys Lys Arg Asn Val	
235 240 245 250	
tca gct cct gaa tca aga ctt act agg cag tct ggt ggc acc aca gct	879
Ser Ala Pro Glu Ser Arg Leu Thr Arg Gln Ser Gly Gly Thr Thr Ala	
251 256 261 266	
ttg cct ttg tat ttt gtt ggc tta tac tgt gat aaa aag ttg att gca	927
Leu Pro Leu Tyr Phe Val Gly Leu Tyr Cys Asp Lys Lys Leu Ile Ala	
267 272 277 282	
gaa gga cct ggg gaa aca gta ttg gtt gca gaa gaa gag gct gct cga	975
Glu Gly Pro Gly Glu Thr Val Leu Val Ala Glu Glu Glu Ala Ala Arg	
283 288 293 298	
gtg gcc ctt aga aaa ctt tat gga ttc aca gaa aat aga cgg ccg tgg	1023
Val Ala Leu Arg Lys Leu Tyr Gly Phe Thr Glu Asn Arg Arg Pro Trp	
299 304 309 314	
aac tat tcc aag ccc aaa gaa acc ttg aga gca gaa aag agc atc act	1071
Asn Tyr Ser Lys Pro Lys Glu Thr Leu Arg Ala Glu Lys Ser Ile Thr	

315	320	325	330	
gcc agc tag cgcgccat ggatgcagca gcctgaaact tgagagcgaa agtgagataa				1127
Ala Ser *				
331				
atgtcaaagg tgtttcaagc cagacatttt cacaattgtg aagaaataga tgttttgttt				1187
ctgtttttta ctgtgttccc aaaattaaat aaatgttaac caaaaaaaaaaaa aaa				1240

<210> 415
 <211> 6082
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (262)..(3144)

<400> 415	
accgctccgg aattcccgagg tcgacgattt cgtcccgccct agaaagggtg aagtgggtgt	60
ttccgtgacg gactgagtac ggggtgcctgt caggctcttg cggaagtcca tgcgccattg	120
ggagggcctc ggccgcgggt ctgtgccctt gctgctgagg gccacttccct gggtcattcc	180
tggaccggga gccgggctgg ggctcacacg ggggctcccg cgtggccgctc tcggcgccctg	240
cgtgacctcc ccgcggcgagg g atg tgg cga cta cgt cgg gcc gct gtg gcc	291
Met Trp Arg Leu Arg Arg Ala Ala Val Ala	
1 5	
tgt gag gtc tgc cag tct tta gtg aaa cac agc tct gga ata aaa gga	339
Cys Glu Val Cys Gln Ser Leu Val Lys His Ser Ser Gly Ile Lys Gly	
11 16 21 26	
agt tta cca cta caa aaa cta cat ctg gct tca cga agc att tat cat	387
Ser Leu Pro Leu Gln Lys Leu His Leu Ala Ser Arg Ser Ile Tyr His	
27 32 37 42	
tca cat cat cct acc tta aag ctt caa cga ccc caa tta agg aca tcc	435
Ser His His Pro Thr Leu Lys Leu Gln Arg Pro Gln Leu Arg Thr Ser	
43 48 53 58	
ttt cag cag ttc tct tct ctg aca aac ctt cct tta cgt aaa ctg aaa	483
Phe Gln Gln Phe Ser Ser Leu Thr Asn Leu Pro Leu Arg Lys Leu Lys	
59 64 69 74	
ttc tct cca att aaa tat ggc tac cag cct cgc agg aat ttt tgg cca	531
Phe Ser Pro Ile Lys Tyr Gly Tyr Gln Pro Arg Arg Asn Phe Trp Pro	
75 80 85 90	
gca aga tta gct acg aga ctc tta aaa ctt cgc tat ctc ata cta gga	579
Ala Arg Leu Ala Thr Arg Leu Leu Lys Leu Arg Tyr Leu Ile Leu Gly	

91	96	101	106	
tcg gct gtt ggg ggt ggc tac aca gcc aaa aag act ttt gat cag tgg				627
Ser Ala Val Gly Gly Gly Tyr Thr Ala Lys Lys Thr Phe Asp Gln Trp				
107	112	117	122	
aaa gat atg ata ccg gac ctt agt gaa tat aaa tgg att gtg cct gac				675
Lys Asp Met Ile Pro Asp Leu Ser Glu Tyr Lys Trp Ile Val Pro Asp				
123	128	133	138	
att gtg tgg gaa att gat gag tat atc gat ttt gag aaa att aga aaa				723
Ile Val Trp Glu Ile Asp Glu Tyr Ile Asp Phe Glu Lys Ile Arg Lys				
139	144	149	154	
gcc ctt cct aat tca gaa gac ctt gta aag tta gca cca gac ttt gac				771
Ala Leu Pro Asn Ser Glu Asp Leu Val Lys Leu Ala Pro Asp Phe Asp				
155	160	165	170	
aag att gtt gaa agc ctt agc tta ttg aag gac ttt ttt acc tca ggt				819
Lys Ile Val Glu Ser Leu Ser Leu Leu Lys Asp Phe Phe Thr Ser Gly				
171	176	181	186	
tct ccg gaa gaa acg gcg ttt aga gca aca gat cgt gga tct gaa agt				867
Ser Pro Glu Glu Thr Ala Phe Arg Ala Thr Asp Arg Gly Ser Glu Ser				
187	192	197	202	
gac aag cat ttt aga aag gtg tca gac aaa gag aaa att gac caa ctt				915
Asp Lys His Phe Arg Lys Val Ser Asp Lys Glu Lys Ile Asp Gln Leu				
203	208	213	218	
cag gaa gaa ctt ctg cac act cag ttg aag tat cag aga atc ttg gaa				963
Gln Glu Glu Leu Leu His Thr Gln Leu Lys Tyr Gln Arg Ile Leu Glu				
219	224	229	234	
cga tta gaa aag gag aac aaa gaa ttg aga aaa tta gta ttg cag aaa				1011
Arg Leu Glu Lys Glu Asn Lys Glu Leu Arg Lys Leu Val Leu Gln Lys				
235	240	245	250	
gat gac aaa ggc att cat cat aga aag ctt aag aaa tct ttg att gac				1059
Asp Asp Lys Gly Ile His His Arg Lys Leu Lys Lys Ser Leu Ile Asp				
251	256	261	266	
atg tat tct gaa gtt ctt gat gtt ctc tct gat tat gat gcc agt tat				1107
Met Tyr Ser Glu Val Leu Asp Val Leu Ser Asp Tyr Asp Ala Ser Tyr				
267	272	277	282	
aat acg caa gat cat ctg cca cgg gtt gtt gtg gtt gga gat cag agt				1155
Asn Thr Gln Asp His Leu Pro Arg Val Val Val Val Gly Asp Gln Ser				
283	288	293	298	
gct gga aag act agt gtg ttg gaa atg att gcc caa gct cga ata ttc				1203
Ala Gly Lys Thr Ser Val Leu Glu Met Ile Ala Gln Ala Arg Ile Phe				
299	304	309	314	
cca aga gga tct ggg gag atg atg aca cgt tct cca gtt aag gtg act				1251
Pro Arg Gly Ser Gly Glu Met Met Thr Arg Ser Pro Val Lys Val Thr				
315	320	325	330	

ctg agt gaa ggt cct cac cat gtg gcc cta ttt aaa gat agt tct cgg	1299
Leu Ser Glu Gly Pro His His Val Ala Leu Phe Lys Asp Ser Ser Arg	
331 336 341 346	
gag ttt gat ctt acc aaa gaa gaa gat ctt gca gca tta aga cat gaa	1347
Glu Phe Asp Leu Thr Lys Glu Glu Asp Leu Ala Ala Leu Arg His Glu	
347 352 357 362	
ata gaa ctt cga atg agg aaa aat gtg aaa gaa ggc tgt acc gtt agc	1395
Ile Glu Leu Arg Met Arg Lys Asn Val Lys Glu Gly Cys Thr Val Ser	
363 368 373 378	
cct gag acc ata tcc tta aat gta aaa ggc cct gga cta cag agg atg	1443
Pro Glu Thr Ile Ser Leu Asn Val Lys Gly Pro Gly Leu Gln Arg Met	
379 384 389 394	
gtg ctt gtt gac tta cca ggt gtg att aat act gtg aca tca ggc atg	1491
Val Leu Val Asp Leu Pro Gly Val Ile Asn Thr Val Thr Ser Gly Met	
395 400 405 410	
gct cct gac aca aag gaa act att ttc agt atc agc aaa gct tac atg	1539
Ala Pro Asp Thr Lys Glu Thr Ile Phe Ser Ile Ser Lys Ala Tyr Met	
411 416 421 426	
cag aat cct aat gcc atc ata ctg tgt att caa gat gga tct gtg gat	1587
Gln Asn Pro Asn Ala Ile Ile Leu Cys Ile Gln Asp Gly Ser Val Asp	
427 432 437 442	
gct gaa cgc agt att gtt aca gac ttg gtc agt caa atg gac cct cat	1635
Ala Glu Arg Ser Ile Val Thr Asp Leu Val Ser Gln Met Asp Pro His	
443 448 453 458	
gga agg aga acc ata ttc gtt ttg acc aaa gta gac ctg gca gag aaa	1683
Gly Arg Arg Thr Ile Phe Val Leu Thr Lys Val Asp Leu Ala Glu Lys	
459 464 469 474	
aat gta gcc agt cca agc agg att cag cag ata att gaa gga aag ctc	1731
Asn Val Ala Ser Pro Ser Arg Ile Gln Gln Ile Ile Glu Gly Lys Leu	
475 480 485 490	
ttc cca atg aaa gct tta ggt tat ttt gct gtt gta aca gga aaa ggg	1779
Phe Pro Met Lys Ala Leu Gly Tyr Phe Ala Val Val Thr Gly Lys Gly	
491 496 501 506	
aac agc tct gaa agc att gaa gct ata aga gaa tat gaa gaa gag ttt	1827
Asn Ser Ser Glu Ser Ile Glu Ala Ile Arg Glu Tyr Glu Glu Glu Phe	
507 512 517 522	
ttt cag aat tca aag ctc cta aag aca agc atg cta aag gca cac caa	1875
Phe Gln Asn Ser Lys Leu Leu Lys Thr Ser Met Leu Lys Ala His Gln	
523 528 533 538	
gtg act aca aga aat tta agc ctt gca gta tca gac tgc ttt tgg aaa	1923
Val Thr Thr Arg Asn Leu Ser Leu Ala Val Ser Asp Cys Phe Trp Lys	
539 544 549 554	

atg gta cga gag tct gtt gaa caa cag gct gat agt ttc aaa gca aca	1971
Met Val Arg Glu Ser Val Glu Gln Gln Ala Asp Ser Phe Lys Ala Thr	
555 560 565 570	
cgt ttt aac ctt gaa act gaa tgg aag aat aac tat cct cgc ctg cgg	2019
Arg Phe Asn Leu Glu Thr Glu Trp Lys Asn Asn Tyr Pro Arg Leu Arg	
571 576 581 586	
gaa ctt gac cgg aat gaa cta ttt gaa aaa gct aaa aat gaa atc ctt	2067
Glu Leu Asp Arg Asn Glu Leu Phe Glu Lys Ala Lys Asn Glu Ile Leu	
587 592 597 602	
gat gaa gtt atc agt ctg agc cag gtt aca cca aaa cat tgg gag gaa	2115
Asp Glu Val Ile Ser Leu Ser Gln Val Thr Pro Lys His Trp Glu Glu	
603 608 613 618	
atc ctt caa caa tct ttg tgg gaa aga gta tca act cat gtg att gaa	2163
Ile Leu Gln Gln Ser Leu Trp Glu Arg Val Ser Thr His Val Ile Glu	
619 624 629 634	
aac atc tac ctt cca gct gcg cag acc atg aat tca gga act ttt aac	2211
Asn Ile Tyr Leu Pro Ala Ala Gln Thr Met Asn Ser Gly Thr Phe Asn	
635 640 645 650	
acc aca gtg gat atc aag ctt aaa cag tgg act gat aaa caa ctt cct	2259
Thr Thr Val Asp Ile Lys Leu Lys Gln Trp Thr Asp Lys Gln Leu Pro	
651 656 661 666	
aat aaa gca gta gag gtt gct tgg gag acc cta caa gaa gaa ttt tcc	2307
Asn Lys Ala Val Glu Val Ala Trp Glu Thr Leu Gln Glu Glu Phe Ser	
667 672 677 682	
cgc ttt atg aca gaa ccg aaa ggg aaa gag cat gat gac ata ttt gat	2355
Arg Phe Met Thr Glu Pro Lys Gly Lys Glu His Asp Asp Ile Phe Asp	
683 688 693 698	
aaa ctt aaa gag gcc gtt aag gaa gaa agt att aaa cga cac aag tgg	2403
Lys Leu Lys Glu Ala Val Lys Glu Glu Ser Ile Lys Arg His Lys Trp	
699 704 709 714	
aat gac ttt gcg gag gac agc ttg agg gtt att caa cac aat gct ttg	2451
Asn Asp Phe Ala Glu Asp Ser Leu Arg Val Ile Gln His Asn Ala Leu	
715 720 725 730	
gaa gac cga tcc ata tct gat aaa cag caa tgg gat gca gct att tat	2499
Glu Asp Arg Ser Ile Ser Asp Lys Gln Gln Trp Asp Ala Ala Ile Tyr	
731 736 741 746	
ttt atg gaa gag gct ctg cag gct cgt ctc aag gat act gaa aat gca	2547
Phe Met Glu Glu Ala Leu Gln Ala Arg Leu Lys Asp Thr Glu Asn Ala	
747 752 757 762	
att gaa aac atg gtg ggt cca gac tgg aaa aag agg tgg tta tac tgg	2595
Ile Glu Asn Met Val Gly Pro Asp Trp Lys Lys Arg Trp Leu Tyr Trp	
763 768 773 778	
aag aat cgg acc caa gaa cag tgt gtt cac aat gaa acc aag aat gaa	2643

Lys Asn Arg Thr Gln Glu Gln Cys Val His Asn Glu Thr Lys Asn Glu	
779 784 789 794	
ttg gag aag atg ttg aaa tgt aat gag gag cac cca gct tat ctt gca	2691
Leu Glu Lys Met Leu Lys Cys Asn Glu Glu His Pro Ala Tyr Leu Ala	
795 800 805 810	
agt gat gaa ata acc aca gtc cgg aag aac ctt gaa tcc cga gga gta	2739
Ser Asp Glu Ile Thr Thr Val Arg Lys Asn Leu Glu Ser Arg Gly Val	
811 816 821 826	
gaa gta gat cca agc ttg att aag gat act tgg cat caa gtt tat aga	2787
Glu Val Asp Pro Ser Leu Ile Lys Asp Thr Trp His Gln Val Tyr Arg	
827 832 837 842	
aga cat ttt tta aaa aca gct cta aac cat tgt aac ctt tgt cga aga	2835
Arg His Phe Leu Lys Thr Ala Leu Asn His Cys Asn Leu Cys Arg Arg	
843 848 853 858	
ggg ttt tat tac tac caa agg cat ttt gta gat tct gag ttg gaa tgc	2883
Gly Phe Tyr Tyr Tyr Gln Arg His Phe Val Asp Ser Glu Leu Glu Cys	
859 864 869 874	
aat gat gtg gtc ttg ttt tgg cgt ata cag cgc atg ctt gct atc acc	2931
Asn Asp Val Val Leu Phe Trp Arg Ile Gln Arg Met Leu Ala Ile Thr	
875 880 885 890	
gca aat act tta agg caa caa ctt aca aat act gaa gtt agg cga tta	2979
Ala Asn Thr Leu Arg Gln Gln Leu Thr Asn Thr Glu Val Arg Arg Leu	
891 896 901 906	
gag aaa aat gtt aaa gag gta ttg gaa gat ttt gct gaa gat ggt gag	3027
Glu Lys Asn Val Lys Glu Val Leu Glu Asp Phe Ala Glu Asp Gly Glu	
907 912 917 922	
aag aag att aaa ttg ctt act ggt aaa cgc gtt caa ctg gcg gaa gac	3075
Lys Lys Ile Lys Leu Leu Thr Gly Lys Arg Val Gln Leu Ala Glu Asp	
923 928 933 938	
ctc aag aaa gtt aga gaa att caa gaa aaa ctt gat gct ttc att gaa	3123
Leu Lys Lys Val Arg Glu Ile Gln Glu Lys Leu Asp Ala Phe Ile Glu	
939 944 949 954	
gct ctt cat cag gag aaa taa at taaaatcgta ctcataatca gctctgcata	3176
Ala Leu His Gln Glu Lys *	
955 960	
catctgaaga acaaaaaacat caacgtcttt tgtccagcct cttttttcttc tgctgttcca	3236
ccttttctaaa catacaataa agtcatggga taaaaataat cgatgtatgt tacgggcgct	3296
ttaaccatca gctgcctctc gaatggaaga acagtggtaa tggattaaca tcctattttg	3356
ttgtactaaa gtgacaaatc ggaataatat aattggatg gccattaggt tcagtccttg	3416
aagataagaa gcttgttctc tgtttgttgt cttatttgtg gtggcactcg tttaatggat	3476

taactgaggt tgctcaatgt tcagtttctt ttccagaaat acaatgctag gtgttttgaa	3536
ataaaactta tatagcaatt gtttaaagtt atcaattgta tataaaatca cagtagcctg	3596
ctaaatcatt gtatgtgtct gtagtattct attcccagaa actatttgac catgataatt	3656
cagtttatat tcaccacatg aaagaaaaat gggtaacaga agaacccta aaacagggtta	3716
atttggattg taacgttcag tgaaagaaat ttcaaccctt catagccagc gaagaaattt	3776
gccttggaag ccaagtcagt accagcttac ctatttgatt cagttgctgt tttctcactc	3836
tctatatcca ttgaaattg atttatttta gatgttgat acttacgtta ggctttctgt	3896
taatagtggg tttctcctg ttgacagagc caccggatta tgacacagga tgaggaagat	3956
taaggataat caattgacta atttcattta gaatattatc aaacatttca actaggatc	4016
agaaaaaggc tttctttcat aagactattt taaatagaaa ttatttcaac aattaaagta	4076
atgttgacca tccccctctc agctgaataa agaaaaattt agttcaattt attgcaattt	4136
aattacaata ctaccttcac aacattttca tgtgttttaa ataaatattt ttttaattggc	4196
taaaggacat tcaagcaaag aaatgctttc tttactttaa atgtctatct catttgctgc	4256
tttttacta agcctttact ttgttaataa aagtgtccat tgtgtgatgt ttttgatttt	4316
acagtttgct aaatcttatt ttcttgaggt tgccttttgg taacagcccc attgctactc	4376
cccattttat tgttttacat caatgcatgc ttcggttgta tccctcaaga tgtaacactt	4436
ggtatgctcg gttgaggata tgaaaaaata cttccgaaac caggaattca gtgtatgttt	4496
gttttatact gtttgataag aaaagtaggt ccagccttaa gcagcacaga tgcgctggta	4556
gatgcatagt caggaacttt ttttatttct tttaggtcta gggacaggag tgaatagaaa	4616
gggaggagag ctctattatg ttctatacac agattaggag atgaccttac tgggtacacc	4676
cctctaacca gtgcttacag gttaatgcat gttaatgaat atttttgcag ttgtaaagca	4736
taacaattac aactacacat ctatttctaa agaataaaac aggaccatat ttatttactt	4796
ctgtcaacta tagaaagaaa gaccttcagc tgtatttcca cagatttctc ccaaggaaaa	4856
ggctaataatt agtcactact gttatcacat ccctttgtat aagtttttaa aagagatgga	4916
gggagatctt catttctttg aggagatcag tattgtaacg tatgtgaata gatgataaca	4976
attaatatta ctaaaagtcc cacatgagag tcttgacgcc ctctccatgc cccacagtaa	5036
tgtggcttct ttcattgggtt ttttttctt ctttttagct gatctcatcc taagcatgct	5096
ttatttttcc ttgaaagcta ggtatttatc aactgcagat gttattgaaa gaaaataaaa	5156
ttcagtctca agagtaaacc ctgtgtcttg tgtctgtagt tcaaaagtca gaaatgatcc	5216

taattttaaac aaaaagatat taaatataca gaagttaaata tcgaactagc cacagaatca 5276
 tttgttttta tgtcagaatt tgcaaagagt ggagtggaca aagctctgta tggaagactg 5336
 aacaactgta aatagatgat atccaaactt aatttggtta ggacttcaat tttaaaaatc 5396
 agtgtacctta ggcagtgcac agcacgaaat aagtggccct tgcagcttcc ccgtttaacc 5456
 cactgtgcta tagttgcggg tggaacagtc agcctttcta gtagtttatg atattgccct 5516
 ctttgtattc ccattttcca cagttttttc cgcagacttc tttctgcaaa ttattcagcc 5576
 tccaaatgca aatgaatgat ataaaaataa gtaggggaaca tggcagagag tgggtgcttcc 5636
 cagcctcaca atgtgggaat ttgacatagg atgagagtca gagtataggt ttaaaagata 5696
 aaatcttttag ttaataattht tgtatttatt tattctagat gtatgtatct gaggaagaa 5756
 atctggtatt tttgctttcc aataaagggg atcaaagtaa tggtttttct ctcagttctc 5816
 taagctggtc tatgttatag ctctagcagt atggaaatgt gctttaaaat atgcttacct 5876
 tttgaatgat catggctata tgttggtgag atatttgaaa cttaccttgt tttcacttgt 5936
 gcactgtgaa tgaactttgt attatttttt taaaaccttc acattacgtg tagatattat 5996
 tgcaacttat attttgccctg tgcttgatca aaggtcattt gtgtagatga gtaattaaaa 6056
 aatattttaa tcacaaaaaa aaaaaa 6082

<210> 416
 <211> 1782
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (101)..(1579)

<400> 416
 ctgcggtacc ggtccggaat tcccgggtcg acccacgct ccgccgacat attgcccgca 60
 ggagctgcgg cggcgaagcg gagagcaccg gggggaggag atg gga gga cga aga 115
 Met Gly Gly Arg Arg
 1
 ggt ccc aac agg aca tct tac tgt cga aat ccg ctc tgt gag ccg gga 163
 Gly Pro Asn Arg Thr Ser Tyr Cys Arg Asn Pro Leu Cys Glu Pro Gly
 6 11 16 21
 tcc tcg ggg ggc tct agt gga agc cac act tcc agt gca tcg gtg acc 211
 Ser Ser Gly Gly Ser Ser Gly Ser His Thr Ser Ser Ala Ser Val Thr
 22 27 32 37

agt gtt cgt tcc cgc acc agg agc agt tct gga aca ggc ctc tcc agc	259
Ser Val Arg Ser Arg Thr Arg Ser Ser Ser Gly Thr Gly Leu Ser Ser	
38 43 48 53	
cct cct ctg gcc acc caa act gtt gtg cct cta cag cac tgc aag atc	307
Pro Pro Leu Ala Thr Gln Thr Val Val Pro Leu Gln His Cys Lys Ile	
54 59 64 69	
ccc gag ctg cca gtc cag gcc agc att ctg ttt gag ttg cag ctc ttc	355
Pro Glu Leu Pro Val Gln Ala Ser Ile Leu Phe Glu Leu Gln Leu Phe	
70 75 80 85	
ttc tgc cag ctc ata gca ctc ttc gtc cac tac atc aac atc tac aag	403
Phe Cys Gln Leu Ile Ala Leu Phe Val His Tyr Ile Asn Ile Tyr Lys	
86 91 96 101	
aca gtg tgg tgg tat cca cct tcc cac cca ccc tcc cac acc tcc ctg	451
Thr Val Trp Trp Tyr Pro Pro Ser His Pro Pro Ser His Thr Ser Leu	
102 107 112 117	
aac ttc cat ctg atc gac ttc aac ttg ctg atg gtg acc acc atc gtt	499
Asn Phe His Leu Ile Asp Phe Asn Leu Leu Met Val Thr Thr Ile Val	
118 123 128 133	
ctg ggc cgc cgc ttc att ggg tcc atc gtg aag gag gcc tct cag agg	547
Leu Gly Arg Arg Phe Ile Gly Ser Ile Val Lys Glu Ala Ser Gln Arg	
134 139 144 149	
ggg aag gtc tcc ctc ttt cgc tcc atc ctg ctg ttc ctc act cgc ttc	595
Gly Lys Val Ser Leu Phe Arg Ser Ile Leu Leu Phe Leu Thr Arg Phe	
150 155 160 165	
acc gtt ctc acg gca aca ggc tgg agt ctg tgc cga tcc ctc atc cac	643
Thr Val Leu Thr Ala Thr Gly Trp Ser Leu Cys Arg Ser Leu Ile His	
166 171 176 181	
ctc ttc agg acc tac tcc ttc ctg aac ctc ctg ttc ctc tgc tat ccg	691
Leu Phe Arg Thr Tyr Ser Phe Leu Asn Leu Leu Phe Leu Cys Tyr Pro	
182 187 192 197	
ttt ggg atg tac att ccg ttc ctg cag ctg aat tgc gac ctc cgc aag	739
Phe Gly Met Tyr Ile Pro Phe Leu Gln Leu Asn Cys Asp Leu Arg Lys	
198 203 208 213	
aca agc ctc ttc aac cac atg gcc tcc atg ggg ccc cgg gag gcg gtc	787
Thr Ser Leu Phe Asn His Met Ala Ser Met Gly Pro Arg Glu Ala Val	
214 219 224 229	
agt ggc ctg gca aag agc cgg gac tac ctc ctg aca ctg cgg gag acg	835
Ser Gly Leu Ala Lys Ser Arg Asp Tyr Leu Leu Thr Leu Arg Glu Thr	
230 235 240 245	
tgg aag cag cac aca aga cag ctg tat ggc ccg gac gcc atg ccc acc	883
Trp Lys Gln His Thr Arg Gln Leu Tyr Gly Pro Asp Ala Met Pro Thr	
246 251 256 261	

cat gcc tgc tgc ctg tca ccc agc ctc atc cgc agt gag gtg gag ttc	931
His Ala Cys Cys Leu Ser Pro Ser Leu Ile Arg Ser Glu Val Glu Phe	
262 267 272 277	
ctc aag atg gac ttc aac tgg cgc atg aag gaa gtg ctc gtc agc tcc	979
Leu Lys Met Asp Phe Asn Trp Arg Met Lys Glu Val Leu Val Ser Ser	
278 283 288 293	
atg ctg agc gcc tac tat gtg gcc ttt gtg cct gtc tgg ttc gtg aag	1027
Met Leu Ser Ala Tyr Tyr Val Ala Phe Val Pro Val Trp Phe Val Lys	
294 299 304 309	
aac aca cat tac tat gac aag cgc tgg tcc tgt gaa ctc ttc ctg ctg	1075
Asn Thr His Tyr Tyr Asp Lys Arg Trp Ser Cys Glu Leu Phe Leu Leu	
310 315 320 325	
gtg tcc atc agc acc tcc gtg atc ctc atg cag cac ctg ctg cct gcc	1123
Val Ser Ile Ser Thr Ser Val Ile Leu Met Gln His Leu Leu Pro Ala	
326 331 336 341	
agc tac tgt gac ctg ctg cac aag gcc gcc gcc cat ctg ggc tgt tgg	1171
Ser Tyr Cys Asp Leu Leu His Lys Ala Ala Ala His Leu Gly Cys Trp	
342 347 352 357	
cag aag gtg gac cca gcg ctg tgc tcc aac gtg ctg cag cac ccg tgg	1219
Gln Lys Val Asp Pro Ala Leu Cys Ser Asn Val Leu Gln His Pro Trp	
358 363 368 373	
act gaa gaa tgc atg tgg ccg cag ggc gtg ctg gtg aag cac agc aag	1267
Thr Glu Glu Cys Met Trp Pro Gln Gly Val Leu Val Lys His Ser Lys	
374 379 384 389	
aac gtc tac aaa gcc gta ggc cac tac aac gtg gct atc ccc tct gac	1315
Asn Val Tyr Lys Ala Val Gly His Tyr Asn Val Ala Ile Pro Ser Asp	
390 395 400 405	
gtc tcc cac ttc cgc ttc cat ttc ttt ttc agc aaa ccc ctg cgg atc	1363
Val Ser His Phe Arg Phe His Phe Phe Phe Ser Lys Pro Leu Arg Ile	
406 411 416 421	
ctc aac atc ctc ctg ctg ctg gag ggc gct gtc att gtc tat cag ctg	1411
Leu Asn Ile Leu Leu Leu Leu Glu Gly Ala Val Ile Val Tyr Gln Leu	
422 427 432 437	
tac tcc cta atg tcc tct gaa aag tgg cac cag acc atc tcg ctg gcc	1459
Tyr Ser Leu Met Ser Ser Glu Lys Trp His Gln Thr Ile Ser Leu Ala	
438 443 448 453	
ctc atc ctc ttc agc aac tac tat gcc ttc ttc aag ctg ctc cgg gac	1507
Leu Ile Leu Phe Ser Asn Tyr Tyr Ala Phe Phe Lys Leu Leu Arg Asp	
454 459 464 469	
cgc ttg gta ttg ggc aag gcc tac tca tac tct gct agc ccc cag aga	1555
Arg Leu Val Leu Gly Lys Ala Tyr Ser Tyr Ser Ala Ser Pro Gln Arg	
470 475 480 485	
gac ctg gac cac cgt ttc tcc tga gccctgggggt cacctcaggg acagcgtcca	1609

Asp Leu Asp His Arg Phe Ser *
486 491

ggcttcagcc aagggctccc tggcaagggg ctgttgggta gaagtgggtg tggggggggac 1669
aaaagacaaa aaaatccacc agagctttgt atttttgtta cgtactgttt ctttgataat 1729
tgatgtgata aggaaaaaag tcctatTTTT atactoccaa caaaaaaaaaaaa aaa 1782

<210> 417
<211> 3297
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (44) .. (2890)

<400> 417

gtcgaagatt tcgtggcctg gccggccgtc gcggaactcgg gag atg gag gaa aag 55
Met Glu Glu Lys
1

gag ata tta cgg cgg cag atc cgc cta ctg cag ggt ctg att gat gac 103
Glu Ile Leu Arg Arg Gln Ile Arg Leu Leu Gln Gly Leu Ile Asp Asp
5 10 15 20

tac aaa acc ctc cac ggc aat gcc ccg gcc cct ggt acc cca gca gct 151
Tyr Lys Thr Leu His Gly Asn Ala Pro Ala Pro Gly Thr Pro Ala Ala
21 26 31 36

tct ggg tgg cag cca ccc act tac cac agt ggc aga gcc ttt agt gcc 199
Ser Gly Trp Gln Pro Pro Thr Tyr His Ser Gly Arg Ala Phe Ser Ala
37 42 47 52

cgc tac cct cgt cca agc cgg agg ggc tac tct tcc cac cat ggg cct 247
Arg Tyr Pro Arg Pro Ser Arg Arg Gly Tyr Ser Ser His His Gly Pro
53 58 63 68

tcg tgg cgc aag aaa tac tcc ctc gtg aat cgg ccc ccg gga ccc tca 295
Ser Trp Arg Lys Lys Tyr Ser Leu Val Asn Arg Pro Pro Gly Pro Ser
69 74 79 84

gac cct cct gcc gac cat gct gtg cgg ccg ttg cac ggg gcc cgg ggg 343
Asp Pro Pro Ala Asp His Ala Val Arg Pro Leu His Gly Ala Arg Gly
85 90 95 100

ggc cag cct cct gtc ccg cag cag cat gtc ctt gag aga cag gtc cag 391
Gly Gln Pro Pro Val Pro Gln Gln His Val Leu Glu Arg Gln Val Gln
101 106 111 116

ctc agt cag ggt cag aac gtg gtc atc aaa gtt aaa ccg cca tca aag 439
Leu Ser Gln Gly Gln Asn Val Val Ile Lys Val Lys Pro Pro Ser Lys
117 122 127 132

tct ggc tct gcc agt gcc tca ggg gcc cag cgg ggc tct ttg gaa gaa	487
Ser Gly Ser Ala Ser Ala Ser Gly Ala Gln Arg Gly Ser Leu Glu Glu	
133 138 143 148	
ttt gag gac acc ccc tgg agt gac caa agg ccc cgg gaa ggt gaa ggt	535
Phe Glu Asp Thr Pro Trp Ser Asp Gln Arg Pro Arg Glu Gly Glu Gly	
149 154 159 164	
gag ccc cct cgg gga cag ctg cag ccc tcg agg cca aca aga gcc agg	583
Glu Pro Pro Arg Gly Gln Leu Gln Pro Ser Arg Pro Thr Arg Ala Arg	
165 170 175 180	
ggg acc tgc agt gtg gaa gat cct ctt ctg gtc tgc cag aag gag cct	631
Gly Thr Cys Ser Val Glu Asp Pro Leu Leu Val Cys Gln Lys Glu Pro	
181 186 191 196	
ggg aag ccc agg atg gtg aag tca gtg ggc agt gtg ggc gac agc ccc	679
Gly Lys Pro Arg Met Val Lys Ser Val Gly Ser Val Gly Asp Ser Pro	
197 202 207 212	
cgg gag ccc cgc cgg aca gtc agt gag agt gtg att gcc gtc aag gcg	727
Arg Glu Pro Arg Arg Thr Val Ser Glu Ser Val Ile Ala Val Lys Ala	
213 218 223 228	
agc ttc cca tcc tcc gct ctg ccc cca cgc act ggc gtg gcc ctg ggc	775
Ser Phe Pro Ser Ser Ala Leu Pro Pro Arg Thr Gly Val Ala Leu Gly	
229 234 239 244	
cgg aag ctg ggt tct cat tcc gtg gcc agc tgt gct cca cag ctc ctt	823
Arg Lys Leu Gly Ser His Ser Val Ala Ser Cys Ala Pro Gln Leu Leu	
245 250 255 260	
ggg gac agg aga gta gat gct ggc cac aca gat cag cca gtt ccg tct	871
Gly Asp Arg Arg Val Asp Ala Gly His Thr Asp Gln Pro Val Pro Ser	
261 266 271 276	
ggc tca gtg ggg ggc ccc gcc aga ccg gcc tca gga ccc agg cag gcc	919
Gly Ser Val Gly Gly Pro Ala Arg Pro Ala Ser Gly Pro Arg Gln Ala	
277 282 287 292	
cgg gag gcc tcg ctg gtt gtg acc tgt cga act aac aag ttc cgg aaa	967
Arg Glu Ala Ser Leu Val Thr Cys Arg Thr Asn Lys Phe Arg Lys	
293 298 303 308	
aac aac tac aaa tgg gtg gct gcc tcc tcg aag agt ccc cgg gtt gct	1015
Asn Asn Tyr Lys Trp Val Ala Ala Ser Ser Lys Ser Pro Arg Val Ala	
309 314 319 324	
cgg agg gcc ctc agt ccc aga gtg gct gca gag aat gtg tgc aag gcc	1063
Arg Arg Ala Leu Ser Pro Arg Val Ala Ala Glu Asn Val Cys Lys Ala	
325 330 335 340	
tct gct ggc atg gca aac aag gtg gag aag ccg cag ctc ata gct gac	1111
Ser Ala Gly Met Ala Asn Lys Val Glu Lys Pro Gln Leu Ile Ala Asp	
341 346 351 356	

cca gag ccc aag ccc agg aag cca gcc acg tcc tcc aag cca ggg tct	1159
Pro Glu Pro Lys Pro Arg Lys Pro Ala Thr Ser Ser Lys Pro Gly Ser	
357 362 367 372	
gcc ccc agc aag tac aag tgg aag gcc tcc agc ccc tct gcc tcc tcc	1207
Ala Pro Ser Lys Tyr Lys Trp Lys Ala Ser Ser Pro Ser Ala Ser Ser	
373 378 383 388	
tct tcc tcc ttc cgt tgg cag tcg gag gcc ggc agc aag gac cat gcc	1255
Ser Ser Ser Phe Arg Trp Gln Ser Glu Ala Gly Ser Lys Asp His Ala	
389 394 399 404	
tcc cag ctc tcc cca gtc ctg tct agg tcc ccg tcg ggg gac aga cca	1303
Ser Gln Leu Ser Pro Val Leu Ser Arg Ser Pro Ser Gly Asp Arg Pro	
405 410 415 420	
gca gta gga cac agt ggc ttg aag ccc ctc tct ggg gag acc ccg ctc	1351
Ala Val Gly His Ser Gly Leu Lys Pro Leu Ser Gly Glu Thr Pro Leu	
421 426 431 436	
tcg gct tac aaa gtg aag agc cgc acc aag atc atc cgg aga cgc ggc	1399
Ser Ala Tyr Lys Val Lys Ser Arg Thr Lys Ile Ile Arg Arg Arg Gly	
437 442 447 452	
agc aca agc ctt cct gga gac aag aaa agc ggc acc tca cct gcc gcc	1447
Ser Thr Ser Leu Pro Gly Asp Lys Lys Ser Gly Thr Ser Pro Ala Ala	
453 458 463 468	
acc gcc aag agc cac ctc agc ctc cgg cgg aga cag gcc ctc agg ggg	1495
Thr Ala Lys Ser His Leu Ser Leu Arg Arg Arg Gln Ala Leu Arg Gly	
469 474 479 484	
aag agc agc cct gtc ctg aag aag acc ccc aac aag ggc ctg gta cag	1543
Lys Ser Ser Pro Val Leu Lys Lys Thr Pro Asn Lys Gly Leu Val Gln	
485 490 495 500	
gtc acc aag cac cga cta tgt cgc ctg cca ccg agc cgg gcc cac ctc	1591
Val Thr Lys His Arg Leu Cys Arg Leu Pro Pro Ser Arg Ala His Leu	
501 506 511 516	
ccc acc aag gaa gcg tcc agc ctg cat gcc gtg cgg act gca ccc acc	1639
Pro Thr Lys Glu Ala Ser Ser Leu His Ala Val Arg Thr Ala Pro Thr	
517 522 527 532	
agc aag gtg atc aag acc cgc tac cgc att gtc aag aag acg ccg gcc	1687
Ser Lys Val Ile Lys Thr Arg Tyr Arg Ile Val Lys Lys Thr Pro Ala	
533 538 543 548	
tcg cct ctc agc gcc ccg ccc ttc ccc ctg tct ctg ccc tcc tgg cgg	1735
Ser Pro Leu Ser Ala Pro Pro Phe Pro Leu Ser Leu Pro Ser Trp Arg	
549 554 559 564	
gcc cgg cgg ctc tca cta tcc agg tcc ctg gtg ctg aac cgc ctg cgt	1783
Ala Arg Arg Leu Ser Leu Ser Arg Ser Leu Val Leu Asn Arg Leu Arg	
565 570 575 580	
cca gtt gcc agc ggg ggt ggg aaa gcc caa ccg ggc tcc cct tgg tgg	1831

Pro Val Ala Ser Gly Gly Gly Lys Ala Gln Pro Gly Ser Pro Trp Trp	
581 586 591 596	
cgg agc aaa ggc tac cgc tgc atc gga ggg gtc ctc tac aaa gta tct	1879
Arg Ser Lys Gly Tyr Arg Cys Ile Gly Gly Val Leu Tyr Lys Val Ser	
597 602 607 612	
gcc aac aag ctc tcc aag acc tcc ggc cag ccc agt gat gcg ggc agc	1927
Ala Asn Lys Leu Ser Lys Thr Ser Gly Gln Pro Ser Asp Ala Gly Ser	
613 618 623 628	
agg ccc ctc ctg cgc aca ggc cgg ctg gat cct gca ggc agc tgt agc	1975
Arg Pro Leu Leu Arg Thr Gly Arg Leu Asp Pro Ala Gly Ser Cys Ser	
629 634 639 644	
cgt tcc ctg gcc agc cgg gca gtg cag cgc agc ctg gcc atc atc cgg	2023
Arg Ser Leu Ala Ser Arg Ala Val Gln Arg Ser Leu Ala Ile Ile Arg	
645 650 655 660	
cag gcg cgg cag cgc agg gag aag agg aag gag tac tgc atg tac tac	2071
Gln Ala Arg Gln Arg Arg Glu Lys Arg Lys Glu Tyr Cys Met Tyr Tyr	
661 666 671 676	
aac cgc ttc ggc agg tgc aac cgt ggc gag cgc tgc ccc tac atc cac	2119
Asn Arg Phe Gly Arg Cys Asn Arg Gly Glu Arg Cys Pro Tyr Ile His	
677 682 687 692	
gat ccc gag aag gtg gcc gtg tgc acc agg ttt gtc cgg ggc acc tgc	2167
Asp Pro Glu Lys Val Ala Val Cys Thr Arg Phe Val Arg Gly Thr Cys	
693 698 703 708	
aag aaa acg gat ggg acc tgc ccc ttc tcc cac cat gtg tcc aag gag	2215
Lys Lys Thr Asp Gly Thr Cys Pro Phe Ser His His Val Ser Lys Glu	
709 714 719 724	
aag atg ccg gtg tgc tcc tac ttc ctg aag ggc atc tgc agc aac agc	2263
Lys Met Pro Val Cys Ser Tyr Phe Leu Lys Gly Ile Cys Ser Asn Ser	
725 730 735 740	
aac tgt ccc tat agc cac gtg tac gtg tcc cgc aag gcc gag gtc tgc	2311
Asn Cys Pro Tyr Ser His Val Tyr Val Ser Arg Lys Ala Glu Val Cys	
741 746 751 756	
agc gac ttc ctc aaa ggc tac tgc ccc ctg ggt gca aag tgc aag aag	2359
Ser Asp Phe Leu Lys Gly Tyr Cys Pro Leu Gly Ala Lys Cys Lys Lys	
757 762 767 772	
aaa cac acg ctg ctg tgc ccc gac ttt gcc cgc agg ggg gcg tgt ccc	2407
Lys His Thr Leu Leu Cys Pro Asp Phe Ala Arg Arg Gly Ala Cys Pro	
773 778 783 788	
cgc ggc gcc cag tgc cag ctg ctc cac cgt acc cag aaa cgc cac agt	2455
Arg Gly Ala Gln Cys Gln Leu Leu His Arg Thr Gln Lys Arg His Ser	
789 794 799 804	
cgg cgg gca gcc acg tcc ccc gcc cca ggg ccc agc gac gca acc gcc	2503
Arg Arg Ala Ala Thr Ser Pro Ala Pro Gly Pro Ser Asp Ala Thr Ala	

805	810	815	820	
agg agc agg gtc tcg gcc agc cac ggg ccc agg aag cct tca gca tcc				2551
Arg Ser Arg Val Ser Ala Ser His Gly Pro Arg Lys Pro Ser Ala Ser				
821	826	831	836	
cag cgc ccc acc agg cag acg ccc agc tcg gct gcc ctc act gcg gct				2599
Gln Arg Pro Thr Arg Gln Thr Pro Ser Ser Ala Ala Leu Thr Ala Ala				
837	842	847	852	
gcc gtg gct gca cct ccc cac tgc cca ggg ggg tca gcc tct ccc tca				2647
Ala Val Ala Ala Pro Pro His Cys Pro Gly Gly Ser Ala Ser Pro Ser				
853	858	863	868	
tcc tcg aag gct tcc tcc tcc tcc tcc tcc tcc tca tcc cct ccc gct				2695
Ser Ser Lys Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Pro Pro Ala				
869	874	879	884	
tcc ttg gac cac gag gca cca tct ctc cag gag gct gcc tta gca gca				2743
Ser Leu Asp His Glu Ala Pro Ser Leu Gln Glu Ala Ala Leu Ala Ala				
885	890	895	900	
gcg tgc tcc aac agg ctc tgc aag ctg cct tcc ttc atc tcc ctg cag				2791
Ala Cys Ser Asn Arg Leu Cys Lys Leu Pro Ser Phe Ile Ser Leu Gln				
901	906	911	916	
tcc tcg ccg agc cca gga gcc cag ccc agg gtc cgg gcc cct agg gcc				2839
Ser Ser Pro Ser Pro Gly Ala Gln Pro Arg Val Arg Ala Pro Arg Ala				
917	922	927	932	
ccc ctc acc aag gac tca ggg aag cct ctg cac atc aaa cca cgt ctg				2887
Pro Leu Thr Lys Asp Ser Gly Lys Pro Leu His Ile Lys Pro Arg Leu				
933	938	943	948	
tga ggac ccagggacc ggccctgcacc tacctcagac cctcatcctt ggagaggaaa				2944
*				
949				
gaggctctgt ccaccactct accccacagg agggccgccc gccaccaagc ctcacctggg				3004
ggccacaggg acaactgctct gectgcctgg cctcaacct tccatgacca gcgtgtgcgc				3064
agggcctggg cttcctcccc caagccaggc cctgtcccc accccaccac cttccagggt				3124
gccaggcagg gctggcctcc aggcctgtcc ccgactgcca ttggcaacag tggccctgca				3184
gccccagcc ctccccaccc aggttttcgg ccagtggaag agggccactgg ccaggcctcc				3244
caggcagggt ttttatgttc agcaataaag gttctatccg taaaaaaaaaaa aaa				3297

<210> 418
 <211> 4562
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (139)..(3189)

<400> 418

gctctggagt tccccgggtcg acgatttcgt agggccgggtg gcgccggcgg ctgcggctac 60

ggccggagac ggcagtgttg gcggtagtgg tgggtggcag gggcctgtga ccgggagctg 120

cccccgacc cgggcacc atg agc caa ggc ccc ccc aca ggg gag agc agc 171
Met Ser Gln Gly Pro Pro Thr Gly Glu Ser Ser

1

5

gag ccc gaa gca aaa gtc ctc cac act aag cgg ctt tac cgg gct gtg 219
Glu Pro Glu Ala Lys Val Leu His Thr Lys Arg Leu Tyr Arg Ala Val
12 17 22 27

gtg gag gct gtg cat cga ctt gac ctc atc ctt tgc aac aaa act gct 267
Val Glu Ala Val His Arg Leu Asp Leu Ile Leu Cys Asn Lys Thr Ala
28 33 38 43

tat caa gaa gta ttc aaa cca gaa aac att agc ctg agg aac aag ctg 315
Tyr Gln Glu Val Phe Lys Pro Glu Asn Ile Ser Leu Arg Asn Lys Leu
44 49 54 59

cgt gag ctc tgc gtc aag ctt atg ttc ctg cac cca gtg gac tat ggg 363
Arg Glu Leu Cys Val Lys Leu Met Phe Leu His Pro Val Asp Tyr Gly
60 65 70 75

aga aag gct gag gag ctg ctg tgg aga aag gta tac tat gaa gtt atc 411
Arg Lys Ala Glu Glu Leu Leu Trp Arg Lys Val Tyr Tyr Glu Val Ile
76 81 86 91

cag ctt atc aag act aac aaa aag cac atc cac agc cgg agc act ttg 459
Gln Leu Ile Lys Thr Asn Lys Lys His Ile His Ser Arg Ser Thr Leu
92 97 102 107

gaa tgt gcc tac agg acg cac ctg gtt gct ggt att ggc ttc tac cag 507
Glu Cys Ala Tyr Arg Thr His Leu Val Ala Gly Ile Gly Phe Tyr Gln
108 113 118 123

cat ctc ctt ctc tat atc cag tcc cac tac cag ctg gaa ctg cag tgc 555
His Leu Leu Leu Tyr Ile Gln Ser His Tyr Gln Leu Glu Leu Gln Cys
124 129 134 139

tgc atc gac tgg acc cat gtc act gac ccc ctc ata gga tgc aag aag 603
Cys Ile Asp Trp Thr His Val Thr Asp Pro Leu Ile Gly Cys Lys Lys
140 145 150 155

cca gtg tct gcc tca ggg aag gag atg gat tgg gca cag atg gca tgt 651
Pro Val Ser Ala Ser Gly Lys Glu Met Asp Trp Ala Gln Met Ala Cys
156 161 166 171

cac cga tgt ctg gtg tat ctg ggg gat ttg tcc cga tat cag aat gaa 699
His Arg Cys Leu Val Tyr Leu Gly Asp Leu Ser Arg Tyr Gln Asn Glu
172 177 182 187

tta gct ggc gta gat acc gag ctg cta gcc gag aga ttt tac tac caa	747
Leu Ala Gly Val Asp Thr Glu Leu Leu Ala Glu Arg Phe Tyr Tyr Gln	
188 193 198 203	
gcc ctg tca gta gct cct cag att gga atg ccc ttc aat cag ctg ggc	795
Ala Leu Ser Val Ala Pro Gln Ile Gly Met Pro Phe Asn Gln Leu Gly	
204 209 214 219	
acc ctg gca ggc agc aag tac tat aat gtg gaa gcc atg tat tgc tac	843
Thr Leu Ala Gly Ser Lys Tyr Tyr Asn Val Glu Ala Met Tyr Cys Tyr	
220 225 230 235	
ctg cgc tgc atc cag tca gaa gtg tcc ttt gag gga gcc tat ggg aac	891
Leu Arg Cys Ile Gln Ser Glu Val Ser Phe Glu Gly Ala Tyr Gly Asn	
236 241 246 251	
ctc aag cgg ctg tat gac aag gca gcc aaa atg tac cac caa ctg aag	939
Leu Lys Arg Leu Tyr Asp Lys Ala Ala Lys Met Tyr His Gln Leu Lys	
252 257 262 267	
aag tgt gag act cgg aaa ctg tct cct ggc aaa aag cga tgt aaa gac	987
Lys Cys Glu Thr Arg Lys Leu Ser Pro Gly Lys Lys Arg Cys Lys Asp	
268 273 278 283	
att aaa agg ttg cta gtg aac ttt atg tat ctg caa agc ctc cta cag	1035
Ile Lys Arg Leu Leu Val Asn Phe Met Tyr Leu Gln Ser Leu Leu Gln	
284 289 294 299	
ccc aaa agc agc tcc gtg gac tca gag ctg acc tca ctt tgc cag tca	1083
Pro Lys Ser Ser Ser Val Asp Ser Glu Leu Thr Ser Leu Cys Gln Ser	
300 305 310 315	
gtc ctg gag gac ttc aac ctc tgc ctc ttc tac ctg ccc tcc tca ccc	1131
Val Leu Glu Asp Phe Asn Leu Cys Leu Phe Tyr Leu Pro Ser Ser Pro	
316 321 326 331	
aac ctc agc ctg gcc agt gag gat gag gag gag tat gag agt gga tat	1179
Asn Leu Ser Leu Ala Ser Glu Asp Glu Glu Glu Tyr Glu Ser Gly Tyr	
332 337 342 347	
gct ttc ctc ccg gac ctt ctc atc ttt caa atg gtc atc atc tgc ctt	1227
Ala Phe Leu Pro Asp Leu Leu Ile Phe Gln Met Val Ile Ile Cys Leu	
348 353 358 363	
atg tgt gtg cac agc ttg gag aga gca gga tcc aag cag tac agt gca	1275
Met Cys Val His Ser Leu Glu Arg Ala Gly Ser Lys Gln Tyr Ser Ala	
364 369 374 379	
gcc att gcc ttc acc ctg gcc ctc ttt tcc cac ctc gtc aat cat gtc	1323
Ala Ile Ala Phe Thr Leu Ala Leu Phe Ser His Leu Val Asn His Val	
380 385 390 395	
aac ata cgg ctg cag gct gag ctg gaa gag ggc gag aat ccc gtc ccg	1371
Asn Ile Arg Leu Gln Ala Glu Leu Glu Glu Gly Glu Asn Pro Val Pro	
396 401 406 411	

gca ttc cag agt gat ggc aca gat gaa cca gag tcc aag gaa cct gtg	1419
Ala Phe Gln Ser Asp Gly Thr Asp Glu Pro Glu Ser Lys Glu Pro Val	
412 417 422 427	
gag aaa gag gag gag cca gat cct gag cct cct cct gta aca ccc caa	1467
Glu Lys Glu Glu Glu Pro Asp Pro Glu Pro Pro Pro Val Thr Pro Gln	
428 433 438 443	
gtg ggt gag ggc aga aag agc cgt aag ttc tct cgc ctc tcc tgt ctc	1515
Val Gly Glu Gly Arg Lys Ser Arg Lys Phe Ser Arg Leu Ser Cys Leu	
444 449 454 459	
cgc cgt cgc cgc cac cca ccc aaa gtt ggt gat gac agt gac ctg agt	1563
Arg Arg Arg Arg His Pro Pro Lys Val Gly Asp Asp Ser Asp Leu Ser	
460 465 470 475	
gaa ggc ttt gaa tcg gac tca agc cat gac tca gcc cgg gcc agt gag	1611
Glu Gly Phe Glu Ser Asp Ser Ser His Asp Ser Ala Arg Ala Ser Glu	
476 481 486 491	
ggc tca gac agt ggc tct gac aag agt ctt gaa ggt ggg gga acg gcc	1659
Gly Ser Asp Ser Gly Ser Asp Lys Ser Leu Glu Gly Gly Gly Thr Ala	
492 497 502 507	
ttt gat gct gaa aca gac tcg gaa atg aat agc cag gag tcc cga tca	1707
Phe Asp Ala Glu Thr Asp Ser Glu Met Asn Ser Gln Glu Ser Arg Ser	
508 513 518 523	
gac ttg gaa gat atg gag gaa gag gag ggg aca cgg tca cca acc ctg	1755
Asp Leu Glu Asp Met Glu Glu Glu Glu Gly Thr Arg Ser Pro Thr Leu	
524 529 534 539	
gag ccc cct cgg ggc aga tca gag gct ccc gat tcc ctc aat ggc cca	1803
Glu Pro Pro Arg Gly Arg Ser Glu Ala Pro Asp Ser Leu Asn Gly Pro	
540 545 550 555	
ctg ggc ccc agt gag gct agc att gcc agc aat cta caa gcc atg tcc	1851
Leu Gly Pro Ser Glu Ala Ser Ile Ala Ser Asn Leu Gln Ala Met Ser	
556 561 566 571	
acc cag atg ttc cag act aag cgc tgc ttc cga ctg gcc ccc acc ttt	1899
Thr Gln Met Phe Gln Thr Lys Arg Cys Phe Arg Leu Ala Pro Thr Phe	
572 577 582 587	
agc aac ctg ctc ctc cag ccc acc acc aac cct cat acc tcg gcc agc	1947
Ser Asn Leu Leu Leu Gln Pro Thr Thr Asn Pro His Thr Ser Ala Ser	
588 593 598 603	
cac agg cct tgc gtc aat ggg gat gta gac aag cct tca gag cca gcc	1995
His Arg Pro Cys Val Asn Gly Asp Val Asp Lys Pro Ser Glu Pro Ala	
604 609 614 619	
tct gag gag ggc tct gag tcg gag ggg agt gag tcc agt gga cgc tcc	2043
Ser Glu Glu Gly Ser Glu Ser Glu Gly Ser Glu Ser Ser Gly Arg Ser	
620 625 630 635	
tgt cgg aat gag cgc agc atc cag gag aag ctt cag gtc ctg atg gcc	2091

Cys	Arg	Asn	Glu	Arg	Ser	Ile	Gln	Glu	Lys	Leu	Gln	Val	Leu	Met	Ala		
636					641					646					651		
gaa	ggt	ctg	ctt	cct	gct	gtg	aaa	gtc	ttc	ctg	gac	tgg	ctt	cgg	acc		2139
Glu	Gly	Leu	Leu	Pro	Ala	Val	Lys	Val	Phe	Leu	Asp	Trp	Leu	Arg	Thr		
652					657					662					667		
aac	ccc	gac	ctc	atc	atc	gtg	tgt	gca	cag	agc	tct	caa	agt	ctg	tgg		2187
Asn	Pro	Asp	Leu	Ile	Ile	Val	Cys	Ala	Gln	Ser	Ser	Gln	Ser	Leu	Trp		
668					673					678					683		
aac	cgc	ctg	tct	gtg	ttg	ctg	aat	ctg	ttg	cct	gct	gct	ggt	gaa	ctc		2235
Asn	Arg	Leu	Ser	Val	Leu	Leu	Asn	Leu	Leu	Pro	Ala	Ala	Gly	Glu	Leu		
684					689					694					699		
cag	gag	tct	ggc	ctg	gcc	ttg	tgt	cct	gag	gtc	caa	gat	ctt	ctt	gaa		2283
Gln	Glu	Ser	Gly	Leu	Ala	Leu	Cys	Pro	Glu	Val	Gln	Asp	Leu	Leu	Glu		
700					705					710					715		
ggt	tgt	gaa	ctg	cct	gac	ctc	ccc	tct	agc	ctt	ctg	ctc	cca	gag	gac		2331
Gly	Cys	Glu	Leu	Pro	Asp	Leu	Pro	Ser	Ser	Leu	Leu	Leu	Pro	Glu	Asp		
716					721					726					731		
atg	gct	ctt	cgt	aac	ctg	ccc	ccg	ctc	cga	gct	gcc	cac	aga	cgc	ttt		2379
Met	Ala	Leu	Arg	Asn	Leu	Pro	Pro	Leu	Arg	Ala	Ala	His	Arg	Arg	Phe		
732					737					742					747		
aac	ttt	gac	acg	gat	cgg	ccc	ctg	ctc	agc	acc	tta	gag	gag	tca	gtg		2427
Asn	Phe	Asp	Thr	Asp	Arg	Pro	Leu	Leu	Ser	Thr	Leu	Glu	Glu	Ser	Val		
748					753					758					763		
gtg	cgc	atc	tgc	tgc	atc	cgc	agc	ttt	ggt	cat	ttc	atc	gcc	cgc	ctg		2475
Val	Arg	Ile	Cys	Cys	Ile	Arg	Ser	Phe	Gly	His	Phe	Ile	Ala	Arg	Leu		
764					769					774					779		
caa	ggc	agc	atc	ctg	cag	ttc	aac	cca	gag	gtt	ggc	atc	ttc	gtc	agc		2523
Gln	Gly	Ser	Ile	Leu	Gln	Phe	Asn	Pro	Glu	Val	Gly	Ile	Phe	Val	Ser		
780					785					790					795		
att	gcc	cag	tct	gag	cag	gag	agc	ctg	ctg	cag	cag	gcc	cag	gca	cag		2571
Ile	Ala	Gln	Ser	Glu	Gln	Glu	Ser	Leu	Leu	Gln	Gln	Ala	Gln	Ala	Gln		
796					801					806					811		
ttc	cga	atg	gca	cag	gag	gaa	gct	cgt	cgg	aac	agg	ctc	atg	aga	gac		2619
Phe	Arg	Met	Ala	Gln	Glu	Glu	Ala	Arg	Arg	Asn	Arg	Leu	Met	Arg	Asp		
812					817					822					827		
atg	gct	cag	cta	cga	ctt	cag	ctc	gaa	gtg	tct	cag	ctg	gag	ggc	agc		2667
Met	Ala	Gln	Leu	Arg	Leu	Gln	Leu	Glu	Val	Ser	Gln	Leu	Glu	Gly	Ser		
828					833					838					843		
ctg	cag	cag	ccc	aag	gcc	cag	tca	gcc	atg	tct	ccc	tac	ctc	gtc	cct		2715
Leu	Gln	Gln	Pro	Lys	Ala	Gln	Ser	Ala	Met	Ser	Pro	Tyr	Leu	Val	Pro		
844					849					854					859		
gac	acc	cag	gcc	ctc	tgc	cac	cat	ctc	cct	gtc	atc	cgc	caa	ctg	gcc		2763
Asp	Thr	Gln	Ala	Leu	Cys	His	His	Leu	Pro	Val	Ile	Arg	Gln	Leu	Ala		

860	865	870	875			
acc agt ggc cgc ttc	att gtc atc atc cca	agg aca gtg atc gat	ggc	2811		
Thr Ser Gly Arg Phe	Ile Val Ile Ile Pro	Arg Thr Val Ile Asp	Gly			
876	881	886	891			
ctg gat ttg ctg aag	aag gaa cac cca ggg	gcc cgg gat ggg att	cgg	2859		
Leu Asp Leu Leu Lys	Lys Glu His Pro Gly	Ala Arg Asp Gly Ile	Arg			
892	897	902	907			
tac ctg gag gca gag	ttt aaa aaa gga aac	agg tac att cgc tgc	cag	2907		
Tyr Leu Glu Ala Glu	Phe Lys Lys Gly Asn	Arg Tyr Ile Arg Cys	Gln			
908	913	918	923			
aaa gag gtg gga aag	agc ttt gag cgg cat	aag ctg aag agg cag	gat	2955		
Lys Glu Val Gly Lys	Ser Phe Glu Arg His	Lys Leu Lys Arg Gln	Asp			
924	929	934	939			
gca gat gcc tgg act	ctc tat aag atc cta	gac agc tgc aaa cag	ctg	3003		
Ala Asp Ala Trp Thr	Leu Tyr Lys Ile Leu	Asp Ser Cys Lys Gln	Leu			
940	945	950	955			
act ctg gcc cag ggg	gca ggt gag gag gat	ccg agt ggc atg gtg	acc	3051		
Thr Leu Ala Gln Gly	Ala Gly Glu Glu Asp	Pro Ser Gly Met Val	Thr			
956	961	966	971			
atc atc aca ggc ctt	cca ctg gac aac ccc	agc gtg ctt tca ggc	ccc	3099		
Ile Ile Thr Gly Leu	Pro Leu Asp Asn Pro	Ser Val Leu Ser Gly	Pro			
972	977	982	987			
atg cag gca gcc ctg	cag gcc gct gcc cac	gcc agt gtg gac atc	aag	3147		
Met Gln Ala Ala Leu	Gln Ala Ala Ala His	Ala Ser Val Asp Ile	Lys			
988	993	998	1003			
aat gtt ctg gac ttc	tac aag cag tgg aag	gaa att ggt tga tact	gac	3196		
Asn Val Leu Asp Phe	Tyr Lys Gln Trp Lys	Glu Ile Gly *				
1004	1009	1014				
ccccaggccc	tgcaagtgggg	ctgactccag	atctctcctg	ccctccctgg	cagccaggac	3256
cagcacctgt	agtcacccca	ccacacgcag	actcatgcac	gcacacagga	gggaggccta	3316
gctgctcaga	ggctgcaggg	agggcccagg	agccggctgg	gaggggtggg	tccctttgtt	3376
gccaagacgt	taggaaagcg	aggaaagtgc	ttggattagg	agagtottgt	gggcccctgg	3436
ccagccttcc	tgccctcagct	cccctgctgt	ctccaggggc	aggtggtagg	catgggtacc	3496
tgcatttcac	tggagtgggt	tcttgatct	ctgaggggaa	ggaacagcaa	aagaggccct	3556
tcttcctcac	ccaagatgca	gggtggttgg	ggccaggagt	ttggaccctc	taggtcttgg	3616
gggaagagct	gggtaatacc	tgggtgtctga	gtgattctct	gcagaccctt	cccctoctca	3676
aggatcaccc	atcctccttt	cagccccctt	tatggggacc	aggcagctct	ggagccagcc	3736
acaggggctg	ttagagaagc	aaggcctgga	gtggcctgca	ccgagtagca	gggtcagggt	3796

tcgtgtgctc ctctctctgc tgcaggggct gcacatccca ttgccccact tctgctttgt 3856
gtctccctct gtctagcttc cagggcaggg agcaggcccc acctagggct gcaggcagtc 3916
tggcctgtgc cagcacgggc tcctgtgccc accagcccca caggtgctgt gctttgtgct 3976
cttggtgtgt gtgctgggac agaattgggat gccaggaaga gaagaaaggg ggtgcagtct 4036
gaggccacca ccccccttcc tatctaaggg agggctgaag acaagggggc ggcattcagt 4096
gggcagcaga aaggagaggg tccttgaagc tgctcagtca gaggcccccg tccctccttt 4156
tgccctccgc aggactgaag acctgaaggg gctggctttt ggagtgttga ggtgaatatc 4216
tgggagcaga gatcatgaat agctcagggc agtgaatggc gcaccaagag cagggctgtg 4276
tgtgggaggg tgcagccagg attgcctcag ctctccccc tcaggctggg aggatagcac 4336
aggctagggg ctgggggtgg agggctctcag ctctgtgtcc cccacccag tactagccta 4396
gcttcccaag ctgtggctta gaggatagtt ggcttcctgc ctctctctc taaaatagca 4456
agtctgggaa atcctggggg gagtggagtc accccactcc cagttgctgg cagagactga 4516
gactaaagca tcacttaata aaccccccaa gcccaaaaaa aaaaaa 4562

<210> 419
<211> 1237
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (75)..(992)

<400> 419
ccactttgta caagaaagct gggtacgcgt aagcttgggc cctcagagg atactctaga 60
gcggccgcag ggcc atg cta gcc ttg cgc gtg gcg cgc ggc tcg tgg ggg 110
Met Leu Ala Leu Arg Val Ala Arg Gly Ser Trp Gly
1 5 10
gcc ctg cgc ggc gcc gct tgg gct ccg gga acg cgg ccg agt aag cga 158
Ala Leu Arg Gly Ala Ala Trp Ala Pro Gly Thr Arg Pro Ser Lys Arg
13 18 23 28
cgc gcc tgc tgg gcc ctg ctg ccg ccc gtg ccc tgc tgc ttg ggc tgc 206
Arg Ala Cys Trp Ala Leu Leu Pro Pro Val Pro Cys Cys Leu Gly Cys
29 34 39 44
ctg gcc gaa cgc tgg agg ctg cgt ccg gcc gct ctt ggc ttg cgg ctg 254
Leu Ala Glu Arg Trp Arg Leu Arg Pro Ala Ala Leu Gly Leu Arg Leu
45 50 55 60

ccc ggg atc ggc cag cgg aac cac tgt tgc ggc gcg ggg aag gcg gct	302
Pro Gly Ile Gly Gln Arg Asn His Cys Ser Gly Ala Gly Lys Ala Ala	
61 66 71 76	
ccc agg cca gcg gcc gga gcg ggc gcc gct gcc gaa gcc ccg ggc ggc	350
Pro Arg Pro Ala Ala Gly Ala Gly Ala Ala Ala Glu Ala Pro Gly Gly	
77 82 87 92	
cag tgg ggc ccg gcg agc acc ccc agc ctg tat gaa aac cca tgg aca	398
Gln Trp Gly Pro Ala Ser Thr Pro Ser Leu Tyr Glu Asn Pro Trp Thr	
93 98 103 108	
atc ccg aat atg ttg tca atg acg aga att ggc ttg gcc cca gtt ctg	446
Ile Pro Asn Met Leu Ser Met Thr Arg Ile Gly Leu Ala Pro Val Leu	
109 114 119 124	
ggc tat ttg att att gaa gaa gat ttt aat att gca cta gga gtt ttt	494
Gly Tyr Leu Ile Ile Glu Glu Asp Phe Asn Ile Ala Leu Gly Val Phe	
125 130 135 140	
gct tta gct gga cta aca gat ttg ttg gat gga ttt att gct cga aac	542
Ala Leu Ala Gly Leu Thr Asp Leu Leu Asp Gly Phe Ile Ala Arg Asn	
141 146 151 156	
tgg gcc aat caa aga tca gct ttg gga agt gct ctt gat cca ctt gct	590
Trp Ala Asn Gln Arg Ser Ala Leu Gly Ser Ala Leu Asp Pro Leu Ala	
157 162 167 172	
gat aaa ata ctt atc agt atc tta tat gtt agc ttg acc tat gca gat	638
Asp Lys Ile Leu Ile Ser Ile Leu Tyr Val Ser Leu Thr Tyr Ala Asp	
173 178 183 188	
ctt att cca gtt cca ctt act tac atg atc att tgc aga gat gta atg	686
Leu Ile Pro Val Pro Leu Thr Tyr Met Ile Ile Ser Arg Asp Val Met	
189 194 199 204	
ttg att gct gct gtt ttt tat gtc aga tac cga act ctt cca aca cca	734
Leu Ile Ala Ala Val Phe Tyr Val Arg Tyr Arg Thr Leu Pro Thr Pro	
205 210 215 220	
gtc ctc tgc cag cga aca ctt gcc aag tat ttc aat cct tgc tat gcc	782
Val Leu Cys Gln Arg Thr Leu Ala Lys Tyr Phe Asn Pro Cys Tyr Ala	
221 226 231 236	
act gct agg tta aaa cca aca ttc atc agc aag gtg aat aca gca gtc	830
Thr Ala Arg Leu Lys Pro Thr Phe Ile Ser Lys Val Asn Thr Ala Val	
237 242 247 252	
cag tta atc ttg gtg gca gct tct ttg gca gct cca gtt ttc aac tat	878
Gln Leu Ile Leu Val Ala Ala Ser Leu Ala Ala Pro Val Phe Asn Tyr	
253 258 263 268	
gct gac agc att tat ctt cag ata cta tgg tgt ttt aca gct ttc acc	926
Ala Asp Ser Ile Tyr Leu Gln Ile Leu Trp Cys Phe Thr Ala Phe Thr	
269 274 279 284	

```

aca gct gca tca gct tat agt tac tat cat tat ggc cgg aag act gtt      974
Thr Ala Ala Ser Ala Tyr Ser Tyr Tyr His Tyr Gly Arg Lys Thr Val
285                290                295                300

cag gtg ata aaa gac tga tgaaag tcatccctca ctgttagtaa ggaagcagta      1028
Gln Val Ile Lys Asp *
301                306

tacatcaatg ggaacagggc ccatggaaat gtacaggagt ttccctatatt tggtgttcag      1088

cttgaaaaag gacttgctcag aatcaactgt gtcacaaaaa tttaagtaat gtgcattgaa      1148

aataagggtg atcatgggaa tatgcagaat ttccaatgta tttttaaata caaataaaat      1208

tgtaatttag aatttttaaa aaaaaaaaaa      1237

```

```

<210> 420
<211> 1432
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (59)..(1030)

```

```

<400> 420
gcacgaggac ccagcctaac catttctcag gtgcttgcca ggtgatcaga aggcaaag      58
atg tcg gag cga aaa gta tta aac aaa tac tac ccg ccg gac ttt gac      106
Met Ser Glu Arg Lys Val Leu Asn Lys Tyr Tyr Pro Pro Asp Phe Asp
1          5          10          15

cca tca aag atc ccc aaa ctc aag ctc ccc aaa gac cgg cag tac gtg      154
Pro Ser Lys Ile Pro Lys Leu Lys Leu Pro Lys Asp Arg Gln Tyr Val
17          22          27          32

gtg cgg ctg atg gcc ccc ttc aac atg agg tgt aag acg tgc gga gaa      202
Val Arg Leu Met Ala Pro Phe Asn Met Arg Cys Lys Thr Cys Gly Glu
33          38          43          48

tac atc tac aag ggg aag aaa ttc aat gct cgg aag gag acg gtg cag      250
Tyr Ile Tyr Lys Gly Lys Lys Phe Asn Ala Arg Lys Glu Thr Val Gln
49          54          59          64

aac gag gtc tac ctg ggc ctg ccc atc ttc cgc ttt tac atc aag tgc      298
Asn Glu Val Tyr Leu Gly Leu Pro Ile Phe Arg Phe Tyr Ile Lys Cys
65          70          75          80

acg cgc tgc ctg gca gag atc acc ttc aag aca gac cct gaa aac aca      346
Thr Arg Cys Leu Ala Glu Ile Thr Phe Lys Thr Asp Pro Glu Asn Thr
81          86          91          96

gac tac acc atg gag cat gga gcc acg cgg aat ttc cag gct gag aag      394
Asp Tyr Thr Met Glu His Gly Ala Thr Arg Asn Phe Gln Ala Glu Lys
97          102          107          112

```

ctc ctg gag gag gag gag aag agg gtg cag aag gag cgg gag gac gag	442
Leu Leu Glu Glu Glu Glu Lys Arg Val Gln Lys Glu Arg Glu Asp Glu	
113 118 123 128	
gag ctg aac aac ccc atg aag gtg ctg gag aac cgg acc aag gac tcc	490
Glu Leu Asn Asn Pro Met Lys Val Leu Glu Asn Arg Thr Lys Asp Ser	
129 134 139 144	
aag ctg gag atg gag gtg ctg gag aac ctc cag gag ctg aaa gac ctg	538
Lys Leu Glu Met Glu Val Leu Glu Asn Leu Gln Glu Leu Lys Asp Leu	
145 150 155 160	
aac cag cgg cag gcg cac gtg gac ttc gag gct atg ctg agg cag cac	586
Asn Gln Arg Gln Ala His Val Asp Phe Glu Ala Met Leu Arg Gln His	
161 166 171 176	
cgc ctg tcg gag gag gag cgg cgg agg cag cag cag gag gag gac gag	634
Arg Leu Ser Glu Glu Glu Arg Arg Arg Gln Gln Gln Glu Glu Asp Glu	
177 182 187 192	
cag gag acc gcg gcc ctg ttg gag gaa gcc aga aag cga aga ctg ctg	682
Gln Glu Thr Ala Ala Leu Leu Glu Glu Ala Arg Lys Arg Arg Leu Leu	
193 198 203 208	
gag gac tcc gac tca gag gat gag gct gct ccc tcg ccc ctg cag cca	730
Glu Asp Ser Asp Ser Glu Asp Glu Ala Ala Pro Ser Pro Leu Gln Pro	
209 214 219 224	
gcc ctt cgg ccc aac ccc acc gcc atc ctg gat gag gcc cca aag ccc	778
Ala Leu Arg Pro Asn Pro Thr Ala Ile Leu Asp Glu Ala Pro Lys Pro	
225 230 235 240	
aag agg aag gtg gag gtc tgg gag cag agc gtt ggc agc ctg ggc agc	826
Lys Arg Lys Val Glu Val Trp Glu Gln Ser Val Gly Ser Leu Gly Ser	
241 246 251 256	
cgg ccc ccg ctg tcg agg ctg gtc gtg gtg aag aag gca aag gcc gac	874
Arg Pro Pro Leu Ser Arg Leu Val Val Val Lys Lys Ala Lys Ala Asp	
257 262 267 272	
ccg gac tgc agc aac ggg cag cct cag gcg gcc ccc acc cca gga gcc	922
Pro Asp Cys Ser Asn Gly Gln Pro Gln Ala Ala Pro Thr Pro Gly Ala	
273 278 283 288	
ccg cag aac agg aag gag gcc aac cct aca ccc ctg acg cct ggc gcg	970
Pro Gln Asn Arg Lys Glu Ala Asn Pro Thr Pro Leu Thr Pro Gly Ala	
289 294 299 304	
tcc tcc ctg agc caa ctg ggt gca tac ctg gac agt gac gac agc aac	1018
Ser Ser Leu Ser Gln Leu Gly Ala Tyr Leu Asp Ser Asp Asp Ser Asn	
305 310 315 320	
ggc agc aac tga gcc ctcccaggac cccctcacgg ggtcaaagtc acacgtccag	1073
Gly Ser Asn *	
321	

cttcagccac attgaggcca gcattgctgg tggtcagggc aggaggcctt ggcgtgactg 1133
gaggccggac agacaagcgc cagcgtgctc caacacatag ggccaccagg ggcctcagcc 1193
ccaggaggtc ccttctctgt gccctcacca gcctotcaac acctcgggga cccctgctgc 1253
tcctgcccc acctgtcact gtgcttaggg ctgcaacatc cctggagcag cttccaacac 1313
tacttcaggg tggcagtgtt tggggcactg ggcgagcctg ccggcctcta gatggcctca 1373
tctcttcctt ccacaaactg tctagaacca ataaaaggaa acctgccaaa aaaaaaaaaa 1432

<210> 421
<211> 2145
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (105)..(1661)

<220>
<221> misc_feature
<222> (1)...(2145)
<223> n = a,t,c or g

<400> 421
gcattgaagc cgtacgcctg caggtaccgg tccggaattc ccgggtcgac ccacgcgtcc 60
ggcgacgcgg ggccggggcg ctgagcgttc gcggggccga ggcc atg gct ttc tgg 116
Met Ala Phe Trp
1
gcg ggg ggt tcg ccc agc gtc gtg gac tat ttc cct agc gag gac ttc 164
Ala Gly Gly Ser Pro Ser Val Val Asp Tyr Phe Pro Ser Glu Asp Phe
5 10 15 20
tac cgc tgc ggc tac tgc aag aac gag tcg ggc agc cgc tcc aat ggc 212
Tyr Arg Cys Gly Tyr Cys Lys Asn Glu Ser Gly Ser Arg Ser Asn Gly
21 26 31 36
atg tgg gca cat tcc atg aca gta cag gat tat cag gat ctc ata gac 260
Met Trp Ala His Ser Met Thr Val Gln Asp Tyr Gln Asp Leu Ile Asp
37 42 47 52
cga gga tgg cga aga agt gga aaa tat gtg tac aaa cct gtc atg aat 308
Arg Gly Trp Arg Arg Ser Gly Lys Tyr Val Tyr Lys Pro Val Met Asn
53 58 63 68
caa aca tgt tgt cct cag tac aca ata agg tgc cga cct tta caa ttt 356
Gln Thr Cys Cys Pro Gln Tyr Thr Ile Arg Cys Arg Pro Leu Gln Phe
69 74 79 84
cag cct tca aaa tct cac aag aag gtt ttg aaa aaa atg ttg aaa ttt 404

Gln	Pro	Ser	Lys	Ser	His	Lys	Lys	Val	Leu	Lys	Lys	Met	Leu	Lys	Phe	
85					90					95					100	
ctg	gct	aaa	ggg	gag	gtt	ccc	aaa	gga	agt	tgt	gag	gat	gag	ccc	atg	452
Leu	Ala	Lys	Gly	Glu	Val	Pro	Lys	Gly	Ser	Cys	Glu	Asp	Glu	Pro	Met	
101					106					111					116	
gat	tcc	aca	atg	gat	gat	gct	gtt	gcg	ggg	gac	ttt	gca	ttg	ata	aat	500
Asp	Ser	Thr	Met	Asp	Asp	Ala	Val	Ala	Gly	Asp	Phe	Ala	Leu	Ile	Asn	
117					122					127					132	
aaa	ctg	gat	ata	cag	tgt	gat	ctt	aaa	aca	ctc	agt	gat	gac	atc	aaa	548
Lys	Leu	Asp	Ile	Gln	Cys	Asp	Leu	Lys	Thr	Leu	Ser	Asp	Asp	Ile	Lys	
133					138					143					148	
gag	agt	tta	gag	agt	gaa	gga	aaa	aat	tca	aag	aaa	gaa	gaa	cct	cag	596
Glu	Ser	Leu	Glu	Ser	Glu	Gly	Lys	Asn	Ser	Lys	Lys	Glu	Glu	Pro	Gln	
149					154					159					164	
gaa	tta	ctt	cag	tca	caa	gat	ttc	gta	gga	gag	aag	ttg	ggc	tct	ggg	644
Glu	Leu	Leu	Gln	Ser	Gln	Asp	Phe	Val	Gly	Glu	Lys	Leu	Gly	Ser	Gly	
165					170					175					180	
gaa	ccg	tca	cat	tca	gtt	aaa	gtt	cac	aca	gtt	cct	aag	cca	ggc	aaa	692
Glu	Pro	Ser	His	Ser	Val	Lys	Val	His	Thr	Val	Pro	Lys	Pro	Gly	Lys	
181					186					191					196	
ggg	gct	gat	ttg	agt	aag	cct	cca	tgt	cga	aaa	gca	aag	gaa	atc	cgg	740
Gly	Ala	Asp	Leu	Ser	Lys	Pro	Pro	Cys	Arg	Lys	Ala	Lys	Glu	Ile	Arg	
197					202					207					212	
aaa	gaa	agg	aaa	agg	tta	aaa	cta	atg	cag	cag	aac	cca	gct	gga	gaa	788
Lys	Glu	Arg	Lys	Arg	Leu	Lys	Leu	Met	Gln	Gln	Asn	Pro	Ala	Gly	Glu	
213					218					223					228	
ctt	gag	ggg	ttc	cag	gct	caa	ggg	cac	cca	cca	tct	ttg	ttt	cca	cca	836
Leu	Glu	Gly	Phe	Gln	Ala	Gln	Gly	His	Pro	Pro	Ser	Leu	Phe	Pro	Pro	
229					234					239					244	
aag	gct	aaa	tcc	aac	cag	cca	aaa	tca	ctc	gaa	gat	tta	att	ttt	gag	884
Lys	Ala	Lys	Ser	Asn	Gln	Pro	Lys	Ser	Leu	Glu	Asp	Leu	Ile	Phe	Glu	
245					250					255					260	
tct	tta	cca	gag	aat	gca	tca	cac	aag	tta	gag	gtg	agg	gtg	gtg	aga	932
Ser	Leu	Pro	Glu	Asn	Ala	Ser	His	Lys	Leu	Glu	Val	Arg	Val	Val	Arg	
261					266					271					276	
tca	tct	cca	cca	agt	tcg	cag	ttc	aaa	gcc	aca	ctt	ctg	gag	tct	tac	980
Ser	Ser	Pro	Pro	Ser	Ser	Gln	Phe	Lys	Ala	Thr	Leu	Leu	Glu	Ser	Tyr	
277					282					287					292	
cag	gtc	tat	aaa	cgt	tac	cag	atg	gtt	att	cac	aag	aac	cca	cct	gat	1028
Gln	Val	Tyr	Lys	Arg	Tyr	Gln	Met	Val	Ile	His	Lys	Asn	Pro	Pro	Asp	
293					298					303					308	
acg	cca	acc	gaa	agc	cag	ttc	aca	aga	ttc	ctt	tgc	agt	tca	ccc	ttg	1076
Thr	Pro	Thr	Glu	Ser	Gln	Phe	Thr	Arg	Phe	Leu	Cys	Ser	Ser	Pro	Leu	

309	314	319	324	
gag gca gag act ccc cct aat ggg cca gat tgt ggc tat ggc tcc ttt				1124
Glu Ala Glu Thr Pro Pro Asn Gly Pro Asp Cys Gly Tyr Gly Ser Phe				
325	330	335	340	
cac cag cag tac tgg ctt gac gga aag atc att gct gtg ggg gtg att				1172
His Gln Gln Tyr Trp Leu Asp Gly Lys Ile Ile Ala Val Gly Val Ile				
341	346	351	356	
gac atc ctc cca aac tgt gta tca tct gtg tat ttg tac tac gat cct				1220
Asp Ile Leu Pro Asn Cys Val Ser Ser Val Tyr Leu Tyr Tyr Asp Pro				
357	362	367	372	
gat tat tcg ttt ttg tct ttg ggc gtc tac tct gca cta cga gaa att				1268
Asp Tyr Ser Phe Leu Ser Leu Gly Val Tyr Ser Ala Leu Arg Glu Ile				
373	378	383	388	
gct ttt act agg cag ctt cat gag aaa act tct caa ctc agc tat tat				1316
Ala Phe Thr Arg Gln Leu His Glu Lys Thr Ser Gln Leu Ser Tyr Tyr				
389	394	399	404	
tat atg ggt ttc tac att cat tca tgt ccc aag atg aaa tat aag ggt				1364
Tyr Met Gly Phe Tyr Ile His Ser Cys Pro Lys Met Lys Tyr Lys Gly				
405	410	415	420	
cag tat aga cct tct gat ttg ctg tgc cct gag aca tat gtt tgg gta				1412
Gln Tyr Arg Pro Ser Asp Leu Leu Cys Pro Glu Thr Tyr Val Trp Val				
421	426	431	436	
ccc att gag caa tgc ctg cct tca ctt gaa aac tcc aag tac tgc cgt				1460
Pro Ile Glu Gln Cys Leu Pro Ser Leu Glu Asn Ser Lys Tyr Cys Arg				
437	442	447	452	
ttc aac cag gac cca gaa gca gtg gat gag gat cgc agt acg gaa cct				1508
Phe Asn Gln Asp Pro Glu Ala Val Asp Glu Asp Arg Ser Thr Glu Pro				
453	458	463	468	
gac cga ttg cag gtg ttt cac aag aga gcc atc atg cct tac ggt gtt				1556
Asp Arg Leu Gln Val Phe His Lys Arg Ala Ile Met Pro Tyr Gly Val				
469	474	479	484	
tat aag aaa cag cag aaa gac cca agt gag gag gct gct gtt ctg cag				1604
Tyr Lys Lys Gln Gln Lys Asp Pro Ser Glu Glu Ala Ala Val Leu Gln				
485	490	495	500	
tac gcc agc ctg gtg ggg cag aag tgc tcc gag cgg atg ctg ctg ttc				1652
Tyr Ala Ser Leu Val Gly Gln Lys Cys Ser Glu Arg Met Leu Leu Phe				
501	506	511	516	
aga aac tga cctgttc goctctgccg ggaagttcct gtgttggtgt gatgatttgt				1708
Arg Asn *				
517				
gccaggatac atattcagta cctgtgggga aataactgtc accacccaca aattagacat				1768
ttttatttttg actatctatg gcttttaaaa aatattttgt ggcaatgtat ctgtgagaat				1828

ctcatagtta atataaagat tttaaaactg cattatgacc tagcccccac aattgggatt 1888
tatcattttg gaggattctt tctagagcaa gatatgctca aattctcctg tttgtatttt 1948
gtaaaatgaa gaagtgaatc taagtaactt aatcacagtt gtgcattttt tttgggttctg 2008
ttagagaaaat taaaacagac tgtttcctca ggcccatttt aaactgaact tatgctagga 2068
aaccttaagt atggggaagg tagaaagttc atttcatcac ttagaaaata tgtcttctca 2128
agancaaaac tgtgctg 2145

<210> 422
<211> 1966
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (115)..(1758)

<400> 422
cttggccatc gatatccgta gaccagctg gctagcgttt aaacttaagc ttggtaccga 60
gctcggatcc actagtccag tgtggtggaa ttcgctgcgc tactgagcag cgcc atg 117
Met
1
gag gac tct gaa gca ctg ggc ttc gaa cac atg ggc ctc gat ccc cgg 165
Glu Asp Ser Glu Ala Leu Gly Phe Glu His Met Gly Leu Asp Pro Arg
2 7 12 17
ctc ctt cag gct gtc acc gat ctg ggc tgg tgc cga cct acg ctg atc 213
Leu Leu Gln Ala Val Thr Asp Leu Gly Trp Ser Arg Pro Thr Leu Ile
18 23 28 33
cag gag aag gcc atc cca ctg gcc cta gaa ggg aag gac ctc ctg gct 261
Gln Glu Lys Ala Ile Pro Leu Ala Leu Glu Gly Lys Asp Leu Leu Ala
34 39 44 49
cgg gcc cgc acg ggc tcc ggg aag acg gcc gct tat gct att ccg atg 309
Arg Ala Arg Thr Gly Ser Gly Lys Thr Ala Ala Tyr Ala Ile Pro Met
50 55 60 65
ctg cag ctg ttg ctc cat agg aag gcg aca ggt ccg gtg gta gaa cag 357
Leu Gln Leu Leu Leu His Arg Lys Ala Thr Gly Pro Val Val Glu Gln
66 71 76 81
gca gtg aga ggc ctt gtt ctt gtt cct acc aag gag ctg gca cgg caa 405
Ala Val Arg Gly Leu Val Leu Val Pro Thr Lys Glu Leu Ala Arg Gln
82 87 92 97
gca cag tcc atg att cag cag ctg gct acc tac tgt gct cgg gat gtc 453

Ala Gln Ser Met Ile Gln Gln Leu Ala Thr Tyr Cys Ala Arg Asp Val
98 103 108 113

cga gtg gcc aat gtc tca gct gct gaa gac tca gtc tct cag aga gct 501
Arg Val Ala Asn Val Ser Ala Ala Glu Asp Ser Val Ser Gln Arg Ala
114 119 124 129

gtg ctg atg gag aag cca gat gtg gta gta ggg acc cca tct cgc ata 549
Val Leu Met Glu Lys Pro Asp Val Val Val Gly Thr Pro Ser Arg Ile
130 135 140 145

tta agc cac ttg cag caa gac agc ctg aaa ctt cgt gac tcc ctg gag 597
Leu Ser His Leu Gln Gln Asp Ser Leu Lys Leu Arg Asp Ser Leu Glu
146 151 156 161

ctt ttg gtg gtg gac gaa gct gac ctt ctt ttt tcc ttt ggc ttt gaa 645
Leu Leu Val Val Asp Glu Ala Asp Leu Leu Phe Ser Phe Gly Phe Glu
162 167 172 177

gaa gag ctc aag agt ctc ctc tgt cac ttg ccc cgg att tac cag gct 693
Glu Glu Leu Lys Ser Leu Leu Cys His Leu Pro Arg Ile Tyr Gln Ala
178 183 188 193

ttt ctc atg tca gct act ttt aac gag gac gta caa gca ctc aag gag 741
Phe Leu Met Ser Ala Thr Phe Asn Glu Asp Val Gln Ala Leu Lys Glu
194 199 204 209

ctg ata tta cat aac ccg gtt acc ctt aag tta cag gag tcc cag ctg 789
Leu Ile Leu His Asn Pro Val Thr Leu Lys Leu Gln Glu Ser Gln Leu
210 215 220 225

cct ggg cca gac cag tta cag cag ttt cag gtg gtc tgt gag act gag 837
Pro Gly Pro Asp Gln Leu Gln Gln Phe Gln Val Val Cys Glu Thr Glu
226 231 236 241

gaa gac aaa ttc ctc ctg ctg tat gcc ctg ctc aag ctg tca ttg att 885
Glu Asp Lys Phe Leu Leu Leu Tyr Ala Leu Leu Lys Leu Ser Leu Ile
242 247 252 257

cgg ggc aag tct ctg ctc ttt gtc aac act cta gaa cgg agt tac cgg 933
Arg Gly Lys Ser Leu Leu Phe Val Asn Thr Leu Glu Arg Ser Tyr Arg
258 263 268 273

cta cgc ctg ttc ttg gaa cag ttc agc atc ccc acc tgt gtg ctc aat 981
Leu Arg Leu Phe Leu Glu Gln Phe Ser Ile Pro Thr Cys Val Leu Asn
274 279 284 289

gga gag ctt cca ctg cgc tcc agg tgc cac atc atc tca cag ttc aac 1029
Gly Glu Leu Pro Leu Arg Ser Arg Cys His Ile Ile Ser Gln Phe Asn
290 295 300 305

caa ggc ttc tac gac tgt gtc ata gca act gat gct gaa gtc ctg ggg 1077
Gln Gly Phe Tyr Asp Cys Val Ile Ala Thr Asp Ala Glu Val Leu Gly
306 311 316 321

gcc cca gtc aag ggc aag cgt cgg ggc cga ggg ccc aaa ggg gac aag 1125
Ala Pro Val Lys Gly Lys Arg Arg Gly Arg Gly Pro Lys Gly Asp Lys

322	327	332	337	
gcc tct gat ccg gaa gca ggt gtg gcc cgg ggc ata gac ttc cac cat				1173
Ala Ser Asp Pro Glu Ala Gly Val Ala Arg Gly Ile Asp Phe His His				
338	343	348	353	
gtg tct gct gtg ctc aac ttt gat ctt ccc cca acc cct gag gcc tac				1221
Val Ser Ala Val Leu Asn Phe Asp Leu Pro Pro Thr Pro Glu Ala Tyr				
354	359	364	369	
atc cat cga gct ggc agg aca gca cgc gct aac aac cca ggc ata gtc				1269
Ile His Arg Ala Gly Arg Thr Ala Arg Ala Asn Asn Pro Gly Ile Val				
370	375	380	385	
tta acc ttt gtg ctt ccc acg gag cag ttc cac tta ggc aag att gag				1317
Leu Thr Phe Val Leu Pro Thr Glu Gln Phe His Leu Gly Lys Ile Glu				
386	391	396	401	
gag ctt ctc agt gga gag aac agg ggc ccc att ctg ctc ccc tac cag				1365
Glu Leu Leu Ser Gly Glu Asn Arg Gly Pro Ile Leu Leu Pro Tyr Gln				
402	407	412	417	
ttc cgg atg gag gag atc gag ggc ttc cgc tat cgc tgc agg gat gcc				1413
Phe Arg Met Glu Glu Ile Glu Gly Phe Arg Tyr Arg Cys Arg Asp Ala				
418	423	428	433	
atg cgc tca gtg act aag cag gcc att cgg gag gca aga ttg aag gag				1461
Met Arg Ser Val Thr Lys Gln Ala Ile Arg Glu Ala Arg Leu Lys Glu				
434	439	444	449	
atc aag gaa gag ctt ctg cat tct gag aag ctt aag aca tac ttt gaa				1509
Ile Lys Glu Glu Leu Leu His Ser Glu Lys Leu Lys Thr Tyr Phe Glu				
450	455	460	465	
gac aac cct agg gac ctc cag ctg ctg cgg cat gac cta cct ttg cac				1557
Asp Asn Pro Arg Asp Leu Gln Leu Leu Arg His Asp Leu Pro Leu His				
466	471	476	481	
ccc gca gtg gtg aag ccc cac ctg ggc cat gtt cct gac tac ctg gtt				1605
Pro Ala Val Val Lys Pro His Leu Gly His Val Pro Asp Tyr Leu Val				
482	487	492	497	
cct cct gct ctc cgt ggc ctg gtg cgc cct cac aag aag cgg aag aag				1653
Pro Pro Ala Leu Arg Gly Leu Val Arg Pro His Lys Lys Arg Lys Lys				
498	503	508	513	
ctg tct tcc tct tgt agg aag gcc aag aga gca aag tcc cag aac cca				1701
Leu Ser Ser Ser Cys Arg Lys Ala Lys Arg Ala Lys Ser Gln Asn Pro				
514	519	524	529	
ctg cgc agc ttc aag cac aaa gga aag aaa ttc aga ccc aca gcc aag				1749
Leu Arg Ser Phe Lys His Lys Gly Lys Lys Phe Arg Pro Thr Ala Lys				
530	535	540	545	
ccc tcc tga gggtgtt gggcctctt ggagctgagc acattgtgga gcacaggctt				1805
Pro Ser *				
546				

acacccttcg tggacaggcg aggcctctggt gcttactgca cagcctgaac agacagttct 1865
 ggggccggca gtgctgggcc ctttagctcc ttggcacttc caagctggca tcttgccct 1925
 tgacaacaga ataaaaattt tagctgcccc aaaaaaaaaa a 1966

<210> 423
 <211> 2341
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (704)..(1891)

<400> 423
 acccctgcgg taccggtccg gaattcccgg gtcgacgatt tcgtagaggc agagaccag 60
 gggagccgag gagcggagac acggaccag cagggctcag cgggaggaga ctggggacac 120
 ccactcgtg gctgccaccg ggagcagagg ggggctcggc cgccccctcc cacatcagtc 180
 tccagaccct tggggcttca gaggccgctc ctaggctcct cggaggaggc gcgggttctc 240
 tcttttccgg agagcaaact ttctcggag atgcctggca ggatgagccg cggcccccg 300
 agaggacggg acagcctctg atgcgcctt gcgtgccccg ccactgcca tggccaggag 360
 gccccaggga acggacagcc cgacctctta ggccgcggga ccctcaggct cagatcagtg 420
 gccgaggccc cagagtttgc aaactcagct ctggagtcca gcagcaacag cagcaggaaa 480
 aacctgcccc tgctcccccc tcccgccacc tccctctctc tcttctcccc tcaccagca 540
 ggcacccccg gttcccgcca ggccctcttg ccatgtcgga ccagacgtc ccaggggct 600
 cggatgtccc cgccatgtgg ccccttgctc caggggtgcc tgagcccctt caaggagccc 660
 caaccacccc ccaaccttgg ccagccctg agcccaggg acc atg agc ggg ggc 715
 Met Ser Gly Gly

1

aag aag aag agt agt ttc caa atc acc agc gtc acc acg gac tat gag 763
 Lys Lys Lys Ser Ser Phe Gln Ile Thr Ser Val Thr Thr Asp Tyr Glu
 5 10 15 20

ggc cct ggg agc cca ggg gct tcg gat ccc cct acc cca cag ccc cca 811
 Gly Pro Gly Ser Pro Gly Ala Ser Asp Pro Pro Thr Pro Gln Pro Pro
 21 26 31 36

acc ggg ccc ccg ccc cgc ctg ccc aat ggg gag ccc agc ccc gat ccg 859
 Thr Gly Pro Pro Pro Arg Leu Pro Asn Gly Glu Pro Ser Pro Asp Pro
 37 42 47 52

ggg ggc aag ggc acc ccc cgg aat ggc tcc cca cca cct ggg gcc cct	907
Gly Gly Lys Gly Thr Pro Arg Asn Gly Ser Pro Pro Pro Gly Ala Pro	
53 58 63 68	
tcc tcc cgt ttc cgg gtg gtg aag ctg ccc cac ggc ctg gga gag cct	955
Ser Ser Arg Phe Arg Val Val Lys Leu Pro His Gly Leu Gly Glu Pro	
69 74 79 84	
tat cgc cgc ggt cgc tgg acg tgt gtg gat gtt tat gag cga gac ctg	1003
Tyr Arg Arg Gly Arg Trp Thr Cys Val Asp Val Tyr Glu Arg Asp Leu	
85 90 95 100	
gag ccc cac agc ttc ggc gga ctc ctg gag gga att cga ggg gcc tca	1051
Glu Pro His Ser Phe Gly Gly Leu Leu Glu Gly Ile Arg Gly Ala Ser	
101 106 111 116	
ggg ggc gcc ggg ggc aga tct ttg gat tcc agg ttg gag ctg gcc agc	1099
Gly Gly Ala Gly Gly Arg Ser Leu Asp Ser Arg Leu Glu Leu Ala Ser	
117 122 127 132	
ctc ggc ctg ggc gcc ccc acc cca ccg tca ggc ctg tct cag ggc ccc	1147
Leu Gly Leu Gly Ala Pro Thr Pro Pro Ser Gly Leu Ser Gln Gly Pro	
133 138 143 148	
acc tcc tgg ctc cgt cca ccc ccc acc tct cct gga cct cag gcc cgc	1195
Thr Ser Trp Leu Arg Pro Pro Pro Thr Ser Pro Gly Pro Gln Ala Arg	
149 154 159 164	
tcc ttc act ggg gga ctg ggc cag ctg gtg gtg ccc agc aaa gcc aag	1243
Ser Phe Thr Gly Gly Leu Gly Gln Leu Val Val Pro Ser Lys Ala Lys	
165 170 175 180	
gca gag aaa ccc cca ctg tcg gcc tcc tca ccc cag cag cgc ccc cca	1291
Ala Glu Lys Pro Pro Leu Ser Ala Ser Ser Pro Gln Gln Arg Pro Pro	
181 186 191 196	
gag cct gag acc ggt gag agt gcg ggc aca tcc cgg gct gcc acg ccc	1339
Glu Pro Glu Thr Gly Glu Ser Ala Gly Thr Ser Arg Ala Ala Thr Pro	
197 202 207 212	
ctg ccc tct ctg agg gtg gaa gcg gag gct ggg ggc tca ggg gcc agg	1387
Leu Pro Ser Leu Arg Val Glu Ala Glu Ala Gly Gly Ser Gly Ala Arg	
213 218 223 228	
acc cct cca ctg tcc cgg agg aaa gct gta gac atg cgg ctg cgg atg	1435
Thr Pro Pro Leu Ser Arg Arg Lys Ala Val Asp Met Arg Leu Arg Met	
229 234 239 244	
gag ttg ggt gct cca gaa gag atg ggg cag gtg ccc cca ctt gac tct	1483
Glu Leu Gly Ala Pro Glu Glu Met Gly Gln Val Pro Pro Leu Asp Ser	
245 250 255 260	
cgc ccc agc tcc cca gcc ctc tac ttc acc cac gat gcc agc ctg gtt	1531
Arg Pro Ser Ser Pro Ala Leu Tyr Phe Thr His Asp Ala Ser Leu Val	
261 266 271 276	

cac aaa tct cca gac ccc ttc gga gca gta gca gct cag aag ttc agc	1579
His Lys Ser Pro Asp Pro Phe Gly Ala Val Ala Ala Gln Lys Phe Ser	
277 282 287 292	
ctg gcc cac tcc atg ttg gcc atc agt ggt cac cta gac agc gac gat	1627
Leu Ala His Ser Met Leu Ala Ile Ser Gly His Leu Asp Ser Asp Asp	
293 298 303 308	
gat agt ggc tcc gga agc ctg gtt ggc att gac aac aaa atc gag caa	1675
Asp Ser Gly Ser Gly Ser Leu Val Gly Ile Asp Asn Lys Ile Glu Gln	
309 314 319 324	
gcc atg gac ttg gtg aag tcc cac ctc atg ttt gcg gtc cgg gag gag	1723
Ala Met Asp Leu Val Lys Ser His Leu Met Phe Ala Val Arg Glu Glu	
325 330 335 340	
gtg gag gtg ctg aag gag cag atc cgg gaa ttg gcg gag cgg aac gct	1771
Val Glu Val Leu Lys Glu Gln Ile Arg Glu Leu Ala Glu Arg Asn Ala	
341 346 351 356	
gcg ctg gag cag gag aat ggg ctg ctg cgc gcc ctg gcc agc ccg gag	1819
Ala Leu Glu Gln Glu Asn Gly Leu Leu Arg Ala Leu Ala Ser Pro Glu	
357 362 367 372	
cag ctg gct cag ctg ccc tcc tcg ggg gtc cca cgg ctt ggg ccc cct	1867
Gln Leu Ala Gln Leu Pro Ser Ser Gly Val Pro Arg Leu Gly Pro Pro	
373 378 383 388	
gcg ccc aat ggg ccc tcc gtc tga gcctcccttc ccttacaatg tgcctttggg	1921
Ala Pro Asn Gly Pro Ser Val *	
389 394	
gctgcccggc cttgcgtcag ccgcctgccc cctcttcta tgcagcttta atgtccccgt	1981
gtccccgggg tgggagttca aggtcagta atggcctggg cccccggccc ctgccccatc	2041
tcctcatcat cccagcctt gatggaggag ggagggcttc aggacggggc gtcagaggga	2101
gccccctctg ggagggaaacc aacccccacc ctccctcctg ggacccccca gcagtagacg	2161
gcttggggga gtcggaggct ccccggcaga cccccaccc ccatcttggt cccttgaggt	2221
gcctcctctc ctctgccag gggagggagt gtggacagta tctggaagtt ctgggattca	2281
ggttggttatt aaaataataa taataattaa aaactctgaa gaaacttgaa aaaaaaaaaa	2341

<210> 424
 <211> 1593
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (301)..(1167)

<400> 424

atttggccct cgaggccaag aattcggcac gagggaggct tcaccctcat gacctcatcc 60

aaccctaatt acctcgtaaa gacccacact ccacacacca tcacattgaa gattagggct 120

tcaacatgta tgtttggtgt gggggcgggg ggcaagatac agacatttag tccatagcac 180

tgtatgtctt aaaattattg tttaaggcac cgttcacctc tggaaaagga ttcttcacct 240

ggaagttcat caacaagctt gttgataaaa aagcaaagag agacttcaga cacgccgac 300

atg aga gct tta aaa gaa ctt gat gag gga aaa ata ttt aaa aat tgg 348
Met Arg Ala Leu Lys Glu Leu Asp Glu Gly Lys Ile Phe Lys Asn Trp
1 5 10 15

ggg aca cag aca gag aaa gag gac acc tca aat ata aat cct cgg caa 396
Gly Thr Gln Thr Glu Lys Glu Asp Thr Ser Asn Ile Asn Pro Arg Gln
17 22 27 32

act gaa act tca gtt aat gca agt cgt tct cca gaa aag tgt gcc caa 444
Thr Glu Thr Ser Val Asn Ala Ser Arg Ser Pro Glu Lys Cys Ala Gln
33 38 43 48

cag aga caa aag aga ctt aat tcg gcc tca cag aga tca tca tct tta 492
Gln Arg Gln Lys Arg Leu Asn Ser Ala Ser Gln Arg Ser Ser Ser Leu
49 54 59 64

cca cct tca aat cgt aaa tca agt act cca aca aaa aga gag att atg 540
Pro Pro Ser Asn Arg Lys Ser Ser Thr Pro Thr Lys Arg Glu Ile Met
65 70 75 80

cta aca cca gtg act gtg gct tat agt cca aag cga tcc cct aaa gaa 588
Leu Thr Pro Val Thr Val Ala Tyr Ser Pro Lys Arg Ser Pro Lys Glu
81 86 91 96

aac ttg tcc cca gga ttt agt cat ctg ctt agc aaa aat gag agc agt 636
Asn Leu Ser Pro Gly Phe Ser His Leu Leu Ser Lys Asn Glu Ser Ser
97 102 107 112

cca att cga ttt gat ata ctt ttg gat gat tta gat act gtt cct gtg 684
Pro Ile Arg Phe Asp Ile Leu Leu Asp Asp Leu Asp Thr Val Pro Val
113 118 123 128

tct aca tta caa cgt acc aat cca aga aag caa ctc cag ttt ctt cct 732
Ser Thr Leu Gln Arg Thr Asn Pro Arg Lys Gln Leu Gln Phe Leu Pro
129 134 139 144

cta gat gac tcg gaa gaa aaa act tat tct gag aaa gcc acc gat aac 780
Leu Asp Asp Ser Glu Glu Lys Thr Tyr Ser Glu Lys Ala Thr Asp Asn
145 150 155 160

cat gtt aat cat agc tct tgc cct gaa ccg gtg cca aat gga gtg aag 828
His Val Asn His Ser Ser Cys Pro Glu Pro Val Pro Asn Gly Val Lys
161 166 171 176

aaa gta tct gtg aga aca gcc tgg gag aag aat aaa tca gtt agc tac 876

Lys Val Ser Val Arg Thr Ala Trp Glu Lys Asn Lys Ser Val Ser Tyr	
177	182 187 192
gaa cag tgt aag ccg gtt tca gtc act cca cag ggg aat gat ttt gaa	924
Glu Gln Cys Lys Pro Val Ser Val Thr Pro Gln Gly Asn Asp Phe Glu	
193	198 203 208
tat aca gca aaa att cgg acc cta gct gaa aca gaa cga ttt ttt gat	972
Tyr Thr Ala Lys Ile Arg Thr Leu Ala Glu Thr Glu Arg Phe Phe Asp	
209	214 219 224
gaa ctt aca aaa gaa aag gac cag att gag gca gca cta agc agg atg	1020
Glu Leu Thr Lys Glu Lys Asp Gln Ile Glu Ala Ala Leu Ser Arg Met	
225	230 235 240
cct tct cct gga gga cga atc act tta cag aca aga tta aat cag gaa	1068
Pro Ser Pro Gly Gly Arg Ile Thr Leu Gln Thr Arg Leu Asn Gln Glu	
241	246 251 256
gcc ttg gaa gat cgt ttg gaa agg att aat cga gaa ctg ggt tca gtt	1116
Ala Leu Glu Asp Arg Leu Glu Arg Ile Asn Arg Glu Leu Gly Ser Val	
257	262 267 272
cgc atg acg cta aag aaa ttc cat gtt ttg cgc acc tct gca aat ctt	1164
Arg Met Thr Leu Lys Lys Phe His Val Leu Arg Thr Ser Ala Asn Leu	
273	278 283 288
tga gatt tgtagccatt aaattttgag acatttttgt ttgcactaat gtataattat	1221
*	
289	
gcagtcagaa aaggcaaact attttgtact gtttataagc cttcaaacag tagttttaca	1281
atcatgctat tcttacactt gctattttat acttcaaata gccacatatt ttcaagatat	1341
ttttgttatg ctcaggaatc tcttgatat tttactatatt aaaaagcatt atttttaaat	1401
agtatctgtc tccaatttat atcaagaata aggaaatata aacagaggaa gcagcttggt	1461
tctaaacaaa tagtggtatc cttttacaat taactgcaca tcaattttat agacttgttc	1521
tacattgtaa atacaattca gtttttaaaa aataaagctt actagcttca cataaatgaa	1581
aaaaaaaaaa aa	1593

<210> 425
 <211> 1491
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (301)..(1065)

<400> 425

atttggccct cgaggccaag aattcggcac gagggaggct tcaccctcat gacctcatcc	60
aaccctaatt acctcgtaaa gacccacact ccacacacca tcacattgaa gattagggct	120
tcaacatgta tgtttggtgt gggggcgggg ggcaagatac agacatttag tccatagcac	180
tgtatgtctt aaaattattg tttaaggcac cgttcacctc tggaaaagga ttcttcacct	240
ggaagttcat caacaagctt gttgataaaa aagcaaagag agacttcaga cacgccgac	300
atg aga gct tta aaa gaa ctt gat gag gga aaa ata ttt aaa aat tgg	348
Met Arg Ala Leu Lys Glu Leu Asp Glu Gly Lys Ile Phe Lys Asn Trp	
1 5 10 15	
ggg aca cag aca gag aaa gag gac acc tca aat ata aat cct cgg caa	396
Gly Thr Gln Thr Glu Lys Glu Asp Thr Ser Asn Ile Asn Pro Arg Gln	
17 22 27 32	
act gaa act tca gtt aat gca agt cgt tct cca gaa aag tgt gcc caa	444
Thr Glu Thr Ser Val Asn Ala Ser Arg Ser Pro Glu Lys Cys Ala Gln	
33 38 43 48	
cag aga caa aag aga ctt aat tcg gcc tca cag aga tca tca tct tta	492
Gln Arg Gln Lys Arg Leu Asn Ser Ala Ser Gln Arg Ser Ser Ser Leu	
49 54 59 64	
cca cct tca aat cgt aaa tca agt act cca aca aaa aga gag att atg	540
Pro Pro Ser Asn Arg Lys Ser Ser Thr Pro Thr Lys Arg Glu Ile Met	
65 70 75 80	
cta aca cca gtg act gtg gct tat agt cca aag cga tcc cct aaa gaa	588
Leu Thr Pro Val Thr Val Ala Tyr Ser Pro Lys Arg Ser Pro Lys Glu	
81 86 91 96	
aac ttg tcc cca gga ttt agt cat ctg ctt agc aaa aat gag agc agt	636
Asn Leu Ser Pro Gly Phe Ser His Leu Leu Ser Lys Asn Glu Ser Ser	
97 102 107 112	
cca att cga gaa aaa act tat tct gag aaa gcc acc gat aac cat gtt	684
Pro Ile Arg Glu Lys Thr Tyr Ser Glu Lys Ala Thr Asp Asn His Val	
113 118 123 128	
aat cat agc tct tgc cct gaa ccg gtg cca aat gga gtg aag aaa gta	732
Asn His Ser Ser Cys Pro Glu Pro Val Pro Asn Gly Val Lys Lys Val	
129 134 139 144	
tct gtg aga aca gcc tgg gag aag aat aaa tca gtt agc tac gaa cag	780
Ser Val Arg Thr Ala Trp Glu Lys Asn Lys Ser Val Ser Tyr Glu Gln	
145 150 155 160	
tgt aag ccg gtt tca gtc act cca cag ggg aat gat ttt gaa tat aca	828
Cys Lys Pro Val Ser Val Thr Pro Gln Gly Asn Asp Phe Glu Tyr Thr	
161 166 171 176	
gca aaa att cgg acc cta gct gaa aca gaa cga ttt ttt gat gaa ctt	876
Ala Lys Ile Arg Thr Leu Ala Glu Thr Glu Arg Phe Phe Asp Glu Leu	

177	182	187	192	
aca aaa gaa aag gac	cag att gag gca gca cta	agc agg atg cct tct	924	
Thr Lys Glu Lys Asp	Gln Ile Glu Ala Ala	Leu Ser Arg Met Pro Ser		
193	198	203	208	
cct gga gga cga atc	act tta cag aca aga tta	aat cag gaa gcc ttg	972	
Pro Gly Gly Arg Ile	Thr Leu Gln Thr Arg	Leu Asn Gln Glu Ala Leu		
209	214	219	224	
gaa gat cgt ttg gaa	agg att aat cga gaa ctg	ggg tca gtt cgc atg	1020	
Glu Asp Arg Leu Glu	Arg Ile Asn Arg Glu	Leu Gly Ser Val Arg Met		
225	230	235	240	
acg cta aag aaa ttc	cat gtt ttg cgc acc tct	gca aat ctt tga gat	1068	
Thr Leu Lys Lys Phe	His Val Leu Arg Thr	Ser Ala Asn Leu *		
241	246	251		
ttgtagccat taaat	tttga gacatttttg	tttgcactaa tgtataatta	1128	
aaaggcaaac tatttt	gttac tggtttataag	ccttcaaaca gtagttttac	1188	
ttcttacact tgctat	tttta tacttcaa	aat agccacatat tttcaagata	1248	
gctcaggaat ctctt	gtata ttttactatt	taaaaagcat tattttttaa	1308	
tagtatctgt				
ctccaattta tatca	agaat aaggaaat	at aaacagagga agcagctt	1368	
gtt ttctaaacaa				
atagtggttat ccttt	tacaa ttaactgcac	atcaatttta tagacttg	1428	
gtt ctacattgta				
aatacaattc agttt	ttaaa aaataaagct	tactagcttc acataaatga	1488	
aaaaaaaaa				
aaa			1491	

<210> 426
 <211> 833
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (95)..(745)

<400> 426	
agacgcactg gtccggaatt cccgggtcga cgatttcgtg	gaggtaagtg gctatagaag 60
tcgggpcggac ccggaaccca gaggacgcga cacc	atg act tat gct tat ctc 112
	Met Thr Tyr Ala Tyr Leu
	1
ttc aag tat atc atc atc gga gac aca ggt gtg	ggg aag tca tgt ctc 160
Phe Lys Tyr Ile Ile Ile Gly Asp Thr Gly Val	Gly Lys Ser Cys Leu
7	12 17 22

ctc ctg cag ttt aca gat aag cgg ttc cag cct gtc cac gac ctc aca Leu Leu Gln Phe Thr Asp Lys Arg Phe Gln Pro Val His Asp Leu Thr 23 28 33 38	208
ata ggt gtg gag ttt gga gct cgt atg gtc aac att gat gga aaa caa Ile Gly Val Glu Phe Gly Ala Arg Met Val Asn Ile Asp Gly Lys Gln 39 44 49 54	256
atc aaa ctg caa atc tgg gat acg gct ggg caa gaa tcc ttc cgt tct Ile Lys Leu Gln Ile Trp Asp Thr Ala Gly Gln Glu Ser Phe Arg Ser 55 60 65 70	304
atc acc cgt tcc tac tac agg gga gca gct gga gca ctg ctg gtg tac Ile Thr Arg Ser Tyr Tyr Arg Gly Ala Ala Gly Ala Leu Leu Val Tyr 71 76 81 86	352
gac att aca agg cgt gaa acc ttc aac cac ctg acc tca tgg tta gag Asp Ile Thr Arg Arg Glu Thr Phe Asn His Leu Thr Ser Trp Leu Glu 87 92 97 102	400
gat gcc cgg cag cac tct agt tcc aac atg gtt atc atg ctc att ggg Asp Ala Arg Gln His Ser Ser Ser Asn Met Val Ile Met Leu Ile Gly 103 108 113 118	448
aat aag agt gac cta gag tcc cgc agg gat gtg aag aga gaa gaa gga Asn Lys Ser Asp Leu Glu Ser Arg Arg Asp Val Lys Arg Glu Glu Gly 119 124 129 134	496
gag gcc ttt gct agg gag cat gga ctt ata ttc atg gaa act tca gcc Glu Ala Phe Ala Arg Glu His Gly Leu Ile Phe Met Glu Thr Ser Ala 135 140 145 150	544
aaa aca gcc tgc aat gtt gaa gag gcc ttc att aac aca gcc aaa gaa Lys Thr Ala Cys Asn Val Glu Glu Ala Phe Ile Asn Thr Ala Lys Glu 151 156 161 166	592
ata tat agg aag atc cag cag ggt tta ttt gat gtc cac aat gag gca Ile Tyr Arg Lys Ile Gln Gln Gly Leu Phe Asp Val His Asn Glu Ala 167 172 177 182	640
aat ggc atc aag att ggg ccc caa cag tca att tca aca tca gtg gga Asn Gly Ile Lys Ile Gly Pro Gln Gln Ser Ile Ser Thr Ser Val Gly 183 188 193 198	688
ccc agt gcc tcc cag cgg aac tct cgt gac ata ggg tcc aac tct ggc Pro Ser Ala Ser Gln Arg Asn Ser Arg Asp Ile Gly Ser Asn Ser Gly 199 204 209 214	736
tgc tgc tga acatctg gcttgaactt tttttgtcct tcttgaata gcttcagatc Cys Cys * 215	792
aataggctta atgaaagagg tcttttcttga aaaaaaaaaa a	833

<210> 427
 <211> 1882
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (100)..(1371)

<400> 427

```

ttggaattct agggagacct aagctggcta gcgtttaaac ttaagcttgg taccgagctc      60

ggatccacta gtccagtgtg gtggaattcg ggggcgagc   atg gcc gct ccg cga      114
                                     Met Ala Ala Pro Arg
                                     1

gta ttc cca ctt tcc tgt gcg gtg cag cag tat gcc tgg ggg aag atg      162
Val Phe Pro Leu Ser Cys Ala Val Gln Gln Tyr Ala Trp Gly Lys Met
   6                11                16                21

ggc tcc aac agc gaa gtg gcg cgg ctg ttg gcc agc agt gat cca ctg      210
Gly Ser Asn Ser Glu Val Ala Arg Leu Leu Ala Ser Ser Asp Pro Leu
  22                27                32                37

gcc cag atc gca gag gac aag cct tat gca gag ttg tgg atg ggg act      258
Ala Gln Ile Ala Glu Asp Lys Pro Tyr Ala Glu Leu Trp Met Gly Thr
  38                43                48                53

cac ccc cga ggg gat gcc aag atc ctt gac aac cgc atc tca cag aag      306
His Pro Arg Gly Asp Ala Lys Ile Leu Asp Asn Arg Ile Ser Gln Lys
  54                59                64                69

acc cta agc cag tgg att gct gag aac cag gac agc ttg ggc tca aag      354
Thr Leu Ser Gln Trp Ile Ala Glu Asn Gln Asp Ser Leu Gly Ser Lys
  70                75                80                85

gtc aag gac acc ttt aat ggc aac ctg ccc ttc ctc ttc aaa gtg ctc      402
Val Lys Asp Thr Phe Asn Gly Asn Leu Pro Phe Leu Phe Lys Val Leu
  86                91                96                101

tca gtt gaa aca ccc ctg tcc atc cag gca cac cct aac aag gag ctg      450
Ser Val Glu Thr Pro Leu Ser Ile Gln Ala His Pro Asn Lys Glu Leu
 102                107                112                117

gca gag aag ctg cac ctc cag gct ccg cag cac tac ccc gat gcc aac      498
Ala Glu Lys Leu His Leu Gln Ala Pro Gln His Tyr Pro Asp Ala Asn
 118                123                128                133

cac aag cca gag atg gcc att gcc ctc acc ccc ttc cag ggc ttg tgt      546
His Lys Pro Glu Met Ala Ile Ala Leu Thr Pro Phe Gln Gly Leu Cys
 134                139                144                149

ggc ttc cgg cca gtt gag gag att gta acc ttt cta aag aag gtg cct      594
Gly Phe Arg Pro Val Glu Glu Ile Val Thr Phe Leu Lys Lys Val Pro
 150                155                160                165

gag ttt cag ttc ctg att gga gat gag gca gca aca cac ctg aag cag      642

```

Glu Phe Gln Phe Leu Ile Gly Asp Glu Ala Ala Thr His Leu Lys Gln	
166 171 176 181	
acc atg agc cat gac tcc cag gct gtg gcc tcc tct ctg cag agc tgt	690
Thr Met Ser His Asp Ser Gln Ala Val Ala Ser Ser Leu Gln Ser Cys	
182 187 192 197	
ttc tcc cac ctg atg aag agt gag aag aag gtg gtg gtg gaa cag ctc	738
Phe Ser His Leu Met Lys Ser Glu Lys Lys Val Val Val Glu Gln Leu	
198 203 208 213	
aac ctg ttg gtg aag cgg atc tcc cag caa gcg gct gcc gga aac aac	786
Asn Leu Leu Val Lys Arg Ile Ser Gln Gln Ala Ala Ala Gly Asn Asn	
214 219 224 229	
atg gag gac atc ttt ggg gag ctt ttg cta cag ctg cac cag cag tac	834
Met Glu Asp Ile Phe Gly Glu Leu Leu Leu Gln Leu His Gln Gln Tyr	
230 235 240 245	
cca ggt gat atc ggc tgc ttt gcc atc tac ttc ctg aac ctg ctt acc	882
Pro Gly Asp Ile Gly Cys Phe Ala Ile Tyr Phe Leu Asn Leu Leu Thr	
246 251 256 261	
ctg aag cct ggg gag gcc atg ttt ctg gag gcc aac gta ccc cat gcc	930
Leu Lys Pro Gly Glu Ala Met Phe Leu Glu Ala Asn Val Pro His Ala	
262 267 272 277	
tac ctg aaa gga gac tgc gtg gag tgc atg gcg tgt tca gac aac aca	978
Tyr Leu Lys Gly Asp Cys Val Glu Cys Met Ala Cys Ser Asp Asn Thr	
278 283 288 293	
gtt cgt gct ggc ctg aca ccc aag ttc att gat gtg cca acc ctg tgt	1026
Val Arg Ala Gly Leu Thr Pro Lys Phe Ile Asp Val Pro Thr Leu Cys	
294 299 304 309	
gaa atg ctc agc tat acc cct agc tcc agc aag gac agg ctc ttt ctc	1074
Glu Met Leu Ser Tyr Thr Pro Ser Ser Ser Lys Asp Arg Leu Phe Leu	
310 315 320 325	
cca aca cgg agt cag gaa gac ccc tac ctc tca atc tat gac ccc cct	1122
Pro Thr Arg Ser Gln Glu Asp Pro Tyr Leu Ser Ile Tyr Asp Pro Pro	
326 331 336 341	
gta cca gac ttc acc att atg aag acg gag gtc cct ggc tct gtc act	1170
Val Pro Asp Phe Thr Ile Met Lys Thr Glu Val Pro Gly Ser Val Thr	
342 347 352 357	
gaa tac aag gtc ttg gca ctg gac tct gcc agc atc ctc ctg atg gta	1218
Glu Tyr Lys Val Leu Ala Leu Asp Ser Ala Ser Ile Leu Leu Met Val	
358 363 368 373	
cag ggg aca gtg ata gcc agc aca ccc aca acc cag aca cca atc cct	1266
Gln Gly Thr Val Ile Ala Ser Thr Pro Thr Thr Gln Thr Pro Ile Pro	
374 379 384 389	
ctg caa cgt ggt ggc gtg ctc ttc att ggg gcc aat gag agt gtc tca	1314
Leu Gln Arg Gly Gly Val Leu Phe Ile Gly Ala Asn Glu Ser Val Ser	

390	395	400	405	
ctg aag ctt act gag ccg aag gac ctg ctg ata ttc cgt gcc tgc tgt				1362
Leu Lys Leu Thr Glu Pro Lys Asp Leu Leu Ile Phe Arg Ala Cys Cys				
406	411	416	421	
ctg ctg taa aggctgc agcctcccca gctctcctct gccagccacc ctaaattcca				1418
Leu Leu *				
422				
gccaacctca cctcctcggg cccagctcaa gcccccttcc ttgctctgga ccccttaggt				1478
ataccctgga agagctgggg tgggggagga gggagcgtga aggtagtgcac tcctgaacac				1538
accaggtgg aaccatcttt ggggaggaga ggcccgtgtg aggggtctga tactcccttt				1598
gtcttccctc tctactctc gctacacctg agccaggctc ttgccaaactc tgttccagcc				1658
tatggcttta ggctagctgt taaatatgtg acccagcatt agctcagcat ctgtcagagc				1718
aagagaccag gtaatttcta agaacagggt tctagcgatg ggactgccca tttcctcagc				1778
tgcagaggag gaaagggaaa gggtaggcct gtagactaac gctgtttaca cccttgttct				1838
gtcaaagcaa ttaaagatca cttgtgttga gaaaaaaaaa aaaa				1882

<210> 428
 <211> 2840
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (81)..(2459)

<400> 428		
gcacgagggtg tcgctggcct tagcagactc cacaggccac gctggctgcg aatggagccg		60
aggactcgcg cggaggcgag	atg cta cca gcc ggc gag atc ggc gcc tct	110
	Met Leu Pro Ala Gly Glu Ile Gly Ala Ser	
	1 5	
cct gca gcc ccg tgc tgc tct gaa agt ggt gac gaa agg aag aac ctc		158
Pro Ala Ala Pro Cys Cys Ser Glu Ser Gly Asp Glu Arg Lys Asn Leu		
11 16 21 26		
gag gag aaa agt gac ata aat gtt aca gtt ctt att gga agt aaa caa		206
Glu Glu Lys Ser Asp Ile Asn Val Thr Val Leu Ile Gly Ser Lys Gln		
27 32 37 42		
gtc agt gaa ggt aca gat aat ggt gat ctc cct tct tat gtg tct gca		254
Val Ser Glu Gly Thr Asp Asn Gly Asp Leu Pro Ser Tyr Val Ser Ala		
43 48 53 58		

ttc ata gaa aag gaa gtt gga aat gac ctt aaa tct tta aag aaa ctt	302
Phe Ile Glu Lys Glu Val Gly Asn Asp Leu Lys Ser Leu Lys Lys Leu	
59 64 69 74	
gat aaa ctc ata gaa cag agg aca gta agt aaa atg cag tta gaa gaa	350
Asp Lys Leu Ile Glu Gln Arg Thr Val Ser Lys Met Gln Leu Glu Glu	
75 80 85 90	
cag gta ctt aca att tca tca gaa att cct aaa aga att cga agt gcc	398
Gln Val Leu Thr Ile Ser Ser Glu Ile Pro Lys Arg Ile Arg Ser Ala	
91 96 101 106	
tta aaa aat gca gaa gaa tca aag caa ttt ctt aat cag ttt ctg gag	446
Leu Lys Asn Ala Glu Glu Ser Lys Gln Phe Leu Asn Gln Phe Leu Glu	
107 112 117 122	
cag gaa act cat ctc ttc agc gcc att aac agc cat ttg ctg act gcg	494
Gln Glu Thr His Leu Phe Ser Ala Ile Asn Ser His Leu Leu Thr Ala	
123 128 133 138	
caa cct tgg atg gac gat ctt gga acc atg att agc cag att gaa gag	542
Gln Pro Trp Met Asp Asp Leu Gly Thr Met Ile Ser Gln Ile Glu Glu	
139 144 149 154	
atc gaa cgt cat ctt gct tac ctt aaa tgg att tca caa att gaa gaa	590
Ile Glu Arg His Leu Ala Tyr Leu Lys Trp Ile Ser Gln Ile Glu Glu	
155 160 165 170	
cta agt gat aac att cag caa tat ctg atg acc aat aat gta ccg gag	638
Leu Ser Asp Asn Ile Gln Gln Tyr Leu Met Thr Asn Asn Val Pro Glu	
171 176 181 186	
gca gcc tcc act cta gtg tct atg gca gaa ctt gac att aaa ctt cag	686
Ala Ala Ser Thr Leu Val Ser Met Ala Glu Leu Asp Ile Lys Leu Gln	
187 192 197 202	
gaa tca tct tgt act cat ctt ctt ggt ttc atg aga gcc aca gtt aaa	734
Glu Ser Ser Cys Thr His Leu Leu Gly Phe Met Arg Ala Thr Val Lys	
203 208 213 218	
ttc tgg cat aaa att ctc aag gac aag ctt aca agt gat ttt gag gaa	782
Phe Trp His Lys Ile Leu Lys Asp Lys Leu Thr Ser Asp Phe Glu Glu	
219 224 229 234	
att tta gca cag ctt cat tgg cca ttc atc gca ccc cct caa tca caa	830
Ile Leu Ala Gln Leu His Trp Pro Phe Ile Ala Pro Pro Gln Ser Gln	
235 240 245 250	
act gtt ggc tta agt cga cct gcc agt gcc ccg gag ata tac agt tac	878
Thr Val Gly Leu Ser Arg Pro Ala Ser Ala Pro Glu Ile Tyr Ser Tyr	
251 256 261 266	
ctg gag aca ctg ttt tgt cag ctt ttg aaa cta caa acc tca gat gaa	926
Leu Glu Thr Leu Phe Cys Gln Leu Leu Lys Leu Gln Thr Ser Asp Glu	
267 272 277 282	
tta ctt act gag cca aag caa ctc cca gaa aaa tac tct ctt cct gcc	974

Leu Leu Thr Glu Pro Lys Gln Leu Pro Glu Lys Tyr Ser Leu Pro Ala	
283 288 293 298	
tcc cct tct gtc atc ctg ccc atc cag gtt atg ctg act cct ctt cag	1022
Ser Pro Ser Val Ile Leu Pro Ile Gln Val Met Leu Thr Pro Leu Gln	
299 304 309 314	
aag agg ttc agg tat cac ttc aga ggg aac cgg cag act aat gtg tta	1070
Lys Arg Phe Arg Tyr His Phe Arg Gly Asn Arg Gln Thr Asn Val Leu	
315 320 325 330	
agc aag cca gaa tgg tac ttg gct caa gta ctt atg tgg att gga aac	1118
Ser Lys Pro Glu Trp Tyr Leu Ala Gln Val Leu Met Trp Ile Gly Asn	
331 336 341 346	
cat act gaa ttt ctg gat gag aag att cag cca ata tta gac aaa gta	1166
His Thr Glu Phe Leu Asp Glu Lys Ile Gln Pro Ile Leu Asp Lys Val	
347 352 357 362	
ggc tct ttg gta aac gca agg ctt gaa ttt tct cgg ggc ctt atg atg	1214
Gly Ser Leu Val Asn Ala Arg Leu Glu Phe Ser Arg Gly Leu Met Met	
363 368 373 378	
ctg gtt ctt gag aag tta gcc act gat att cct tgt ctg cta tat gat	1262
Leu Val Leu Glu Lys Leu Ala Thr Asp Ile Pro Cys Leu Leu Tyr Asp	
379 384 389 394	
gac aat ctc ttc tgt cat ttg gtg gat gaa gta ctc ttg ttt gaa agg	1310
Asp Asn Leu Phe Cys His Leu Val Asp Glu Val Leu Leu Phe Glu Arg	
395 400 405 410	
gag cta cac agt gtt cat ggc tat cct ggc act ttt gct agt tgt atg	1358
Glu Leu His Ser Val His Gly Tyr Pro Gly Thr Phe Ala Ser Cys Met	
411 416 421 426	
cat att cta tca gag gaa acc tgt ttt cag aga tgg ttg acg gtg gag	1406
His Ile Leu Ser Glu Glu Thr Cys Phe Gln Arg Trp Leu Thr Val Glu	
427 432 437 442	
aga aaa ttt gct ctt caa aaa atg gac tca atg ctt tcc tca gaa gct	1454
Arg Lys Phe Ala Leu Gln Lys Met Asp Ser Met Leu Ser Ser Glu Ala	
443 448 453 458	
gcc tgg gta tcg caa tat aag gat atc act gac gtg gat gaa atg aaa	1502
Ala Trp Val Ser Gln Tyr Lys Asp Ile Thr Asp Val Asp Glu Met Lys	
459 464 469 474	
gtt cca gat tgt gca gaa act ttt atg act cta ctc ttg gtt ata act	1550
Val Pro Asp Cys Ala Glu Thr Phe Met Thr Leu Leu Leu Val Ile Thr	
475 480 485 490	
gac agg tat aaa aat ctt ccc aca gct tcc cga aag ctt cag ttc ctg	1598
Asp Arg Tyr Lys Asn Leu Pro Thr Ala Ser Arg Lys Leu Gln Phe Leu	
491 496 501 506	
gag tta cag aag gac tta gta gat gat ttt agg ata cga tta aca caa	1646
Glu Leu Gln Lys Asp Leu Val Asp Asp Phe Arg Ile Arg Leu Thr Gln	

507	512	517	522	
gtg atg aaa gaa gag	act aga gct tcc ctt	ggc ttt cga tac tgt	gca	1694
Val Met Lys Glu Glu	Thr Arg Ala Ser Leu	Gly Phe Arg Tyr Cys	Ala	
523	528	533	538	
att ctt aat gct gtg	aac tac atc tca aca	gta cta gca gat tgg	gct	1742
Ile Leu Asn Ala Val	Asn Tyr Ile Ser Thr	Val Leu Ala Asp Trp	Ala	
539	544	549	554	
gac aat gtt ttc ttt	cta caa ctt caa cag	gct gca ctg gag gtg	ttt	1790
Asp Asn Val Phe Phe	Leu Gln Leu Gln Gln	Ala Ala Leu Glu Val	Phe	
555	560	565	570	
gca gag aat aat act	ctg agt aaa ttg cag	cta gga cag cta gcc	tct	1838
Ala Glu Asn Asn Thr	Leu Ser Lys Leu Gln	Leu Gly Gln Leu Ala	Ser	
571	576	581	586	
atg gag agc tct gtc	ttt gat gac atg att	aac ctc tta gaa cgt	tta	1886
Met Glu Ser Ser Val	Phe Asp Asp Met Ile	Asn Leu Leu Glu Arg	Leu	
587	592	597	602	
aag cat gat atg ttg	acc cgt caa gta gac	cac gtt ttt aga gaa	gtt	1934
Lys His Asp Met Leu	Thr Arg Gln Val Asp	His Val Phe Arg Glu	Val	
603	608	613	618	
aaa gat gct gca aaa	ttg tat aaa aaa gaa	aga tgg ttg tcc ttg	cca	1982
Lys Asp Ala Ala Lys	Leu Tyr Lys Lys Glu	Arg Trp Leu Ser Leu	Pro	
619	624	629	634	
tct cag tca gag cag	gca gtg atg tcc ctg	tcc agt tcc gct tgc	ccg	2030
Ser Gln Ser Glu Gln	Ala Val Met Ser Leu	Ser Ser Ser Ala Cys	Pro	
635	640	645	650	
ttg ctg ctg acg tta	cga gac cat tta ctt	cag ttg gag cag cag	ctt	2078
Leu Leu Leu Thr Leu	Arg Asp His Leu Leu	Gln Leu Glu Gln Gln	Leu	
651	656	661	666	
tgt ttc tcc tta ttt	aaa att ttc tgg caa	atg ctt gta gag aag	ctg	2126
Cys Phe Ser Leu Phe	Lys Ile Phe Trp Gln	Met Leu Val Glu Lys	Leu	
667	672	677	682	
gat gta tac atc tac	caa gaa ata att ctt	gct aat cac ttc aat	gaa	2174
Asp Val Tyr Ile Tyr	Gln Glu Ile Ile Leu	Ala Asn His Phe Asn	Glu	
683	688	693	698	
gga gga gca gcc cag	ctg cag ttt gat atg	act cgg aat ctt ttc	cct	2222
Gly Gly Ala Ala Gln	Leu Gln Phe Asp Met	Thr Arg Asn Leu Phe	Pro	
699	704	709	714	
ttg ttt tct cac tat	tgc aag aga cca gaa	aat tat ttt aaa cat	ata	2270
Leu Phe Ser His Tyr	Cys Lys Arg Pro Glu	Asn Tyr Phe Lys His	Ile	
715	720	725	730	
aaa gaa gcc tgt att	gtt ttg aat ttg aac	gtc ggt tct gca cta	ctg	2318
Lys Glu Ala Cys Ile	Val Leu Asn Leu Asn	Val Gly Ser Ala Leu	Leu	
731	736	741	746	

ctg aaa gat gta ctg cag tca gct tca ggg cag ctt cct gcc aca gca 2366
 Leu Lys Asp Val Leu Gln Ser Ala Ser Gly Gln Leu Pro Ala Thr Ala
 747 752 757 762

gca tta aat gaa gtt gga att tac aaa ctg gct caa caa gat gtt gag 2414
 Ala Leu Asn Glu Val Gly Ile Tyr Lys Leu Ala Gln Gln Asp Val Glu
 763 768 773 778

att cta ctt aat ttg agg aca aat tgg cct aat act gga aaa taa tgt 2462
 Ile Leu Leu Asn Leu Arg Thr Asn Trp Pro Asn Thr Gly Lys *
 779 784 789

ctttcagaaa aaggtttctt tgggttttgt ttctaagaaa gaggaagcca attggatttc 2522

aagttatatg atgaaattct gaattaatga aactggaaaa ctttatagaa ttacttatta 2582

tcttggattt atggtgttat taaaatgctg accatatttc cttcatcctc ttgttcctaa 2642

ggaaacaaaa acagaaaacg aaacaatgaa aactcaattc tatttacaag tataaatgct 2702

gagtatgtct gttgaagaca agagcagaga tattaaatta taaccaactt tcaatttcct 2762

gtgctaatta agggaaattc tgttgtggat aatcaaacat agccaataaa tttttttaaa 2822

actccaaaaa aaaaaaaaa 2840

<210> 429
 <211> 3851
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (222) .. (2519)

<400> 429

gagagcggcg cctcactact gactatgctg cgaaaacact acataagggg ggggcgggggt 60

ggcgccaccc ctgattgcgg tgccacggac tgctcctgct gggcggagag gacagatttt 120

gcaaagcgga ggctgcgacg ggtcctgcag ggggacagtg aggaaagggc cgcctcgtct 180

ccgctcctgg gggaccgcag aaataagaat caaactccac a atg aca acc tat 233
 Met Thr Thr Tyr
 1

ttg gaa ttc att caa caa aat gaa gaa cga gat gga gtc cga ttt agt 281
 Leu Glu Phe Ile Gln Gln Asn Glu Glu Arg Asp Gly Val Arg Phe Ser
 5 10 15 20

tgg aat gtt tgg cca tca agt cga ctg gaa gct aca aga atg gtt gtt 329
 Trp Asn Val Trp Pro Ser Ser Arg Leu Glu Ala Thr Arg Met Val Val
 21 26 31 36

cct gtg gca gcc ctg ttt aca cca ctg aaa gag aga cct gac tta cca	377
Pro Val Ala Ala Leu Phe Thr Pro Leu Lys Glu Arg Pro Asp Leu Pro	
37 42 47 52	
cct att caa tat gaa cct gtt ctg tgt agt agg acc act tgc cgt gca	425
Pro Ile Gln Tyr Glu Pro Val Leu Cys Ser Arg Thr Thr Cys Arg Ala	
53 58 63 68	
gtt ttg aat cct tta tgt caa gtg gat tat cga gca aaa ctt tgg gct	473
Val Leu Asn Pro Leu Cys Gln Val Asp Tyr Arg Ala Lys Leu Trp Ala	
69 74 79 84	
tgc aac ttt tgt tac caa agg aat cag ttt cca cct agt tat gct ggt	521
Cys Asn Phe Cys Tyr Gln Arg Asn Gln Phe Pro Pro Ser Tyr Ala Gly	
85 90 95 100	
ata tct gaa ctg aat cag cct gct gaa ctt tta cct cag ttt tct agc	569
Ile Ser Glu Leu Asn Gln Pro Ala Glu Leu Leu Pro Gln Phe Ser Ser	
101 106 111 116	
att gaa tat gta gtt ctg cgt ggt cct cag atg cct ttg ata ttc ctc	617
Ile Glu Tyr Val Val Leu Arg Gly Pro Gln Met Pro Leu Ile Phe Leu	
117 122 127 132	
tat gtg gtt gat act tgc atg gaa gat gaa gat tta caa gcc ctg aaa	665
Tyr Val Val Asp Thr Cys Met Glu Asp Glu Asp Leu Gln Ala Leu Lys	
133 138 143 148	
gaa tcc atg cag atg tca tta agt ctt tta cca cct aca gct ttg gtt	713
Glu Ser Met Gln Met Ser Leu Ser Leu Leu Pro Pro Thr Ala Leu Val	
149 154 159 164	
gga ctt att act ttt ggg aga atg gtt cag gtt cat gaa ctt gga tgt	761
Gly Leu Ile Thr Phe Gly Arg Met Val Gln Val His Glu Leu Gly Cys	
165 170 175 180	
gaa ggc att tca aaa agc tat gtc ttc aga gga aca aaa gat atg tct	809
Glu Gly Ile Ser Lys Ser Tyr Val Phe Arg Gly Thr Lys Asp Met Ser	
181 186 191 196	
gcc aaa caa ctg cag gaa atg ctg ggg ctc tct aaa gta cca gtt act	857
Ala Lys Gln Leu Gln Glu Met Leu Gly Leu Ser Lys Val Pro Val Thr	
197 202 207 212	
caa gca aca cgt ggt cct cag gta cag cag cca cct cct tcc aac aga	905
Gln Ala Thr Arg Gly Pro Gln Val Gln Gln Pro Pro Pro Ser Asn Arg	
213 218 223 228	
ttc tta caa cca gta cag aaa ata gac atg aat ctc aca gat ctt ctg	953
Phe Leu Gln Pro Val Gln Lys Ile Asp Met Asn Leu Thr Asp Leu Leu	
229 234 239 244	
gga gaa ctc cag cga gac cct tgg cct gta cca cag gga aag aga cct	1001
Gly Glu Leu Gln Arg Asp Pro Trp Pro Val Pro Gln Gly Lys Arg Pro	
245 250 255 260	

ttg cgt tcc tct ggg gtg gca ctt tcc ata gct gta gga ctg ctg gag	1049
Leu Arg Ser Ser Gly Val Ala Leu Ser Ile Ala Val Gly Leu Leu Glu	
261 266 271 276	
tgt act ttt ccc aac act ggt gct cgt atc atg atg ttc att ggt ggt	1097
Cys Thr Phe Pro Asn Thr Gly Ala Arg Ile Met Met Phe Ile Gly Gly	
277 282 287 292	
cct gct act cag ggg cct gga atg gtg gtt gga gat gag ttg aag aca	1145
Pro Ala Thr Gln Gly Pro Gly Met Val Val Gly Asp Glu Leu Lys Thr	
293 298 303 308	
cct ata aga tgc tgg cat gac att gac aaa gac aat gcc aaa tat gtt	1193
Pro Ile Arg Ser Trp His Asp Ile Asp Lys Asp Asn Ala Lys Tyr Val	
309 314 319 324	
aaa aag gga act aag cat ttt gaa gca ttg gct aat cga gct gct aca	1241
Lys Lys Gly Thr Lys His Phe Glu Ala Leu Ala Asn Arg Ala Ala Thr	
325 330 335 340	
act ggc cat gtt att gat atc tat gcg tgt gca tta gat cag aca ggt	1289
Thr Gly His Val Ile Asp Ile Tyr Ala Cys Ala Leu Asp Gln Thr Gly	
341 346 351 356	
ctc ctg gag atg aaa tgc tgt ccc aac ctt act gga gga tac atg gta	1337
Leu Leu Glu Met Lys Cys Cys Pro Asn Leu Thr Gly Gly Tyr Met Val	
357 362 367 372	
atg ggt gat tct ttc aat act tcc tta ttc aaa caa act ttt caa aga	1385
Met Gly Asp Ser Phe Asn Thr Ser Leu Phe Lys Gln Thr Phe Gln Arg	
373 378 383 388	
gtc ttt acc aaa gac atg cat gga cag ttt aaa atg ggc ttt ggt ggt	1433
Val Phe Thr Lys Asp Met His Gly Gln Phe Lys Met Gly Phe Gly Gly	
389 394 399 404	
acg cta gaa ata aag acc tca agg gaa ata aag att tca gga gct att	1481
Thr Leu Glu Ile Lys Thr Ser Arg Glu Ile Lys Ile Ser Gly Ala Ile	
405 410 415 420	
gga ccc tgt gtg tca ctc aat tct aaa gga ccc tgt gtg tct gaa aat	1529
Gly Pro Cys Val Ser Leu Asn Ser Lys Gly Pro Cys Val Ser Glu Asn	
421 426 431 436	
gag ata gga aca ggt ggc aca tgt cag tgg aag ata tgt gga ctt agt	1577
Glu Ile Gly Thr Gly Gly Thr Cys Gln Trp Lys Ile Cys Gly Leu Ser	
437 442 447 452	
ccc act aca acc tta gcc ata tat ttt gag gtt gtc aat cag cat aat	1625
Pro Thr Thr Thr Leu Ala Ile Tyr Phe Glu Val Val Asn Gln His Asn	
453 458 463 468	
gct cca att cct caa gga ggg cgt ggt gca atc cag ttt gtg act cag	1673
Ala Pro Ile Pro Gln Gly Gly Arg Gly Ala Ile Gln Phe Val Thr Gln	
469 474 479 484	
tat cag cat tca agt ggg cag aga cgc atc cga gtg acc acc att gct	1721

Tyr Gln His Ser Ser Gly Gln Arg Arg Ile Arg Val Thr Thr Ile Ala	
485 490 495 500	
agg aac tgg gca gat gct caa act caa atc caa aac att gct gca tct	1769
Arg Asn Trp Ala Asp Ala Gln Thr Gln Ile Gln Asn Ile Ala Ala Ser	
501 506 511 516	
ttt gac cag gag gca gct gcc att ctt atg gcc cgg cta gca ata tat	1817
Phe Asp Gln Glu Ala Ala Ala Ile Leu Met Ala Arg Leu Ala Ile Tyr	
517 522 527 532	
aga gca gaa aca gaa gaa ggt cca gat gtg ctt agg tgg ctg gac aga	1865
Arg Ala Glu Thr Glu Glu Gly Pro Asp Val Leu Arg Trp Leu Asp Arg	
533 538 543 548	
cag ctc att cga ctg tgt cag aaa ttt gga gaa tat cat aaa gat gac	1913
Gln Leu Ile Arg Leu Cys Gln Lys Phe Gly Glu Tyr His Lys Asp Asp	
549 554 559 564	
cca agt tcc ttc aga ttt tca gaa act ttc tcc ctt tat cca cag ttt	1961
Pro Ser Ser Phe Arg Phe Ser Glu Thr Phe Ser Leu Tyr Pro Gln Phe	
565 570 575 580	
atg ttt cat tta aga aga tct tct ttc ctg caa gtt ttt aac aat agt	2009
Met Phe His Leu Arg Arg Ser Ser Phe Leu Gln Val Phe Asn Asn Ser	
581 586 591 596	
cct gat gag agt tca tat tat cgt cac cat ttt atg cgt caa gat ctg	2057
Pro Asp Glu Ser Ser Tyr Tyr Arg His His Phe Met Arg Gln Asp Leu	
597 602 607 612	
acc cag tct cta att atg att cag cct atc ctg tat gcg tat tct ttt	2105
Thr Gln Ser Leu Ile Met Ile Gln Pro Ile Leu Tyr Ala Tyr Ser Phe	
613 618 623 628	
agt gga cca cca gag ccg gtt ctt ctt gat agc agt agc att ctt gca	2153
Ser Gly Pro Pro Glu Pro Val Leu Leu Asp Ser Ser Ser Ile Leu Ala	
629 634 639 644	
gat cgt att ctt ctc atg gac aca ttc ttc cag att ttg att tat cat	2201
Asp Arg Ile Leu Leu Met Asp Thr Phe Phe Gln Ile Leu Ile Tyr His	
645 650 655 660	
ggt gag acc ata gca cag tgg cgg aag tca gga tac cag gat atg cct	2249
Gly Glu Thr Ile Ala Gln Trp Arg Lys Ser Gly Tyr Gln Asp Met Pro	
661 666 671 676	
gag tat gaa aat ttc cgc cac ctt ctg caa gcc cca gtg gat gat gca	2297
Glu Tyr Glu Asn Phe Arg His Leu Leu Gln Ala Pro Val Asp Asp Ala	
677 682 687 692	
cag gaa att ctt cac tcc aga ttt cca atg cca aga tac att gac act	2345
Gln Glu Ile Leu His Ser Arg Phe Pro Met Pro Arg Tyr Ile Asp Thr	
693 698 703 708	
gaa cat gga ggc agc cag gcc cgt ttc ctc ctt tca aaa gtc aac cct	2393
Glu His Gly Gly Ser Gln Ala Arg Phe Leu Leu Ser Lys Val Asn Pro	

709	714	719	724	
tca cag act cat aat aat atg tat gcc tgg ggg cag gag tct gga gca				2441
Ser Gln Thr His Asn Asn Met Tyr Ala Trp Gly Gln Glu Ser Gly Ala				
725	730	735	740	
cct att ctt aca gat gat gtt agt tta caa gtg ttt atg gat cac ttg				2489
Pro Ile Leu Thr Asp Asp Val Ser Leu Gln Val Phe Met Asp His Leu				
741	746	751	756	
aag aaa ctt gct gtg tcc agt gct gct tga a gtgctaataa tgttaaagac				2540
Lys Lys Leu Ala Val Ser Ser Ala Ala *				
757	762			
acttaagaag atgaaataat attcaaattt cattttttcc tttttccatt tatctgtgga				2600
aaccaacaga tattgctcta ttttttttgt attagtatgg tttgagacaa catatggaaa				2660
atgttcacat ttgtagatta agctggaatt ataatgagag caataagaac aaattttattt				2720
tgcttaccac agtggttatag ctggttctag aaatttgaag tctttataac ttaattatgt				2780
ttaataaaaa atagagtctg cctcgtacta cagatgtaac tcatttgtat attgcagaca				2840
gacccaaagt ggcactgaat tttcttgctc acctttttaa aacttggttc ttaattttag				2900
ccagaaagca aaaaaacaat agtaatgata aatgtgaaca tttttgctta ttcattgaat				2960
atttttctgt aattttcagc acttatgtat acactttttc tgtacttact aggttaaggc				3020
agattttattt ttatgatttg ttttaggaatt atttgatttt ataatggtaa ttttcatgat				3080
gataatgttt ttgggtattt ggaaagatag tttagagatg aaagggtttt ttgggtaaca				3140
atcccgagc tgacaaaaaa tgtgaaattt ccacaaaata tccaacttat gtgactaaac				3200
gcagtagttt ttttaaaagg ggagatagaa aataaatggt tttgttgag tgcattttag				3260
taagcctttg cagtaaaatg acggttgtaa ctactaaacc aaatttagtt ttcacagcat				3320
ggttttgttg tttttccctt gtttttcaga ggtaaatttt gcattatata cttcagtatt				3380
ttaacactat tttggcagtt tacacattac tttttgtttt tcttccctt ttgtgaaatg				3440
tattaagttg tgggttcttat tgaaacagta ttatataatg tttgcttaat tataatcatgt				3500
gatgctcagt tctattttga tttattcatt agtattcact tttaccttta aagtttactt				3560
gtagcaaata tgtttacatt gataaagcca gatatgtttt gacaatgaaa tttacatata				3620
aagtactgca aataaaaagg ggtgctatga tatatgctta ggaggacagt ttaaatgatt				3680
gtacttgcat gaacacaatc atatgatggt aaagcagaaa ctttaagaaaa aattgtttat				3740
gtgttatatt caattagctt aaataagttg ctttgttata ttttatttga attgaactac				3800
gctaggccta aatgccaata aaatatactt ttcactgtta aaaaaaaaa a				3851

<210> 430
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (92)..(646)

<400> 430

```

ctagatagcg atcaagctgg ctagcgttta aacttaagct tggtagcgag ctcggatcca      60
ctagtccagt gtggtggaat tcgcgctggc c   atg ctg gtc ttg gtg gtt tcg      112
                                   Met Leu Val Leu Val Val Ser
                                   1                               5

ccg tgg tct gcg gcc cgg gga gtg ctt cga aac tac tgg gag cga ctg      160
Pro Trp Ser Ala Ala Arg Gly Val Leu Arg Asn Tyr Trp Glu Arg Leu
  8                               13                               18                               23

cta cgg aag ctt ccg cag agc cgg ccg ggc ttt ccc agt cct ccg tgg      208
Leu Arg Lys Leu Pro Gln Ser Arg Pro Gly Phe Pro Ser Pro Pro Trp
 24                               29                               34                               39

gga cca gca tta gca gta cag ggc cca gcc atg ttt aca gag cca gca      256
Gly Pro Ala Leu Ala Val Gln Gly Pro Ala Met Phe Thr Glu Pro Ala
 40                               45                               50                               55

aat gat acc agt gga agt aaa gag aat tcc agc ctt ttg gac agt atc      304
Asn Asp Thr Ser Gly Ser Lys Glu Asn Ser Ser Leu Leu Asp Ser Ile
 56                               61                               66                               71

ttt tgg atg gca gct ccc aaa aat aga cgc acc att gaa gtt aac cgg      352
Phe Trp Met Ala Ala Pro Lys Asn Arg Arg Thr Ile Glu Val Asn Arg
 72                               77                               82                               87

tgt agg aga aga aat ccg cag aag ctt att aaa gtt aag aac aac ata      400
Cys Arg Arg Arg Asn Pro Gln Lys Leu Ile Lys Val Lys Asn Asn Ile
 88                               93                               98                               103

gac gtt tgt cct gaa tgt ggt cac ctg aaa cag aaa cat gtc ctt tgt      448
Asp Val Cys Pro Glu Cys Gly His Leu Lys Gln Lys His Val Leu Cys
104                               109                               114                               119

gcc tac tgc tat gaa aag gtg tgc aag gag act gca gaa atc aga cga      496
Ala Tyr Cys Tyr Glu Lys Val Cys Lys Glu Thr Ala Glu Ile Arg Arg
120                               125                               130                               135

cag ata ggg aag caa gaa ggg ggc cct ttt aag gct ccc acc ata gag      544
Gln Ile Gly Lys Gln Glu Gly Gly Pro Phe Lys Ala Pro Thr Ile Glu
136                               141                               146                               151

act gtg gtg ctg tac acg gga gag aca ccg tct gaa caa gat cag ggc      592

```

[illegible]

```
<220>
<221> CDS
<222> (135) .. (1007)
```

ctg tgt ttt ggg tct cag agg gcc aag gca gca aca gcc tgt ggt cgc 218
Leu Cys Phe Gly Ser Gln Arg Ala Lys Ala Ala Thr Ala Cys Gly Arg
13 18 23 28

gag tgg ccc tgg caa gtc agc atc cag cgc aac gga agc cac ttc tgc 314
Glu Trp Pro Trp Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys
45 50 55 60

ggg ggc agc ctc atc gcg gag cag tgg gtc ctg acg gct gcg cac tgc 362
Gly Gly Ser Leu Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys
61 66 71 76

ttc cgc aac acc tct gag acg tcc ctg tac cag gtc ctg ctg ggg gca	410
Phe Arg Asn Thr Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala	
77 82 87 92	
agg cag cta gtg cag ccg gga cca cac gct atg tat gcc cgg gtg agg	458
Arg Gln Leu Val Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg	
93 98 103 108	
cag gtg gag agc aac ccc ctg tac cag ggc acg gcc tcc agc gct gac	506
Gln Val Glu Ser Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp	
109 114 119 124	
gtg gcc ctg gtg gag ctg gag gca cca gtg ccc ttc acc aat tac atc	554
Val Ala Leu Val Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile	
125 130 135 140	
ctc ccc gtg tgc ctg cct gac ccc tcg gtg atc ttt gag acg ggc atg	602
Leu Pro Val Cys Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met	
141 146 151 156	
aac tgc tgg gtc act ggc tgg ggc agc ccc agt gag gaa gac ctc ctg	650
Asn Cys Trp Val Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu	
157 162 167 172	
ccc gaa ccg cgg atc ctg cag aaa ctc gct gtg ccc atc atc gac aca	698
Pro Glu Pro Arg Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr	
173 178 183 188	
ccc aag tgc acc ctg ctt tac agc aaa gac acc gag ttt ggc tac caa	746
Pro Lys Cys Thr Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln	
189 194 199 204	
ccc aaa acc atc aag aat gac atg ctg tgc gcc ggc ttc gag gag ggc	794
Pro Lys Thr Ile Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly	
205 210 215 220	
aag aag gat gcc tgc aag ggc gac tcg ggc ggc ccc ctg gtg tgc ctc	842
Lys Lys Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu	
221 226 231 236	
gtg ggt cag tcg tgg ctg cag gcg ggg gtg atc agc tgg ggt gag ggc	890
Val Gly Gln Ser Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly	
237 242 247 252	
tgt gcc cgc cag aac cgc cca ggt gtc tac atc cgt gtc acc gcc cac	938
Cys Ala Arg Gln Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His	
253 258 263 268	
cac aac tgg atc cat cgg atc atc ccc aaa ctg cag ttc cag cca gcg	986
His Asn Trp Ile His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala	
269 274 279 284	
agg ttg ggc ggc cag aag tga ga cccccggggc caggagcccc ttgagcagag	1039
Arg Leu Gly Gly Gln Lys *	
285 290	

ctctgcaccc agcctgcccc cccacacccat cctgctgggc ctcccagcgc tgctgttgca 1099
cctgtgagcc ccaccagact catttgtaaa tagcgctcct tcctcccctc tcaaataccc 1159
ttatttttatt tatgtttctc ccaataaaaa cccagcctgt gaaaaaaaaa aaa 1212

<210> 432
<211> 1399
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (313)..(1347)

<400> 432
tcggcactac cagcctgctt agttaaccct cactaaaggg aataagcttg cggccgccct 60
cccacagccc cacacactgg gagaccgccc accgcaaacc gcggagaccc ccgtctagat 120
ttaaagcgcg gctgcgcccc gctttctgacg tccattgaat cgcgcggggc gccggcgggc 180
agcgcgggggc tgcgcgggga tcgctgcgcc ctccgcccgt ggccctctgcg acgcgcgccg 240
ctcgcccgag ccaccgcgcg ccgcgcgggc tccccgcgcc gctgcgctcc tcgccccgcg 300
cctgccccca gg atg gtc cgc gcg agg cac cag ccg ggt ggg ctt tgc 348
Met Val Arg Ala Arg His Gln Pro Gly Gly Leu Cys
1 5 10
ctc ctg ctg ctg ctg ctc tgc cag ttc atg gag gac cgc agt gcc cag 396
Leu Leu Leu Leu Leu Leu Cys Gln Phe Met Glu Asp Arg Ser Ala Gln
13 18 23 28
gct ggg aac tgc tgg ctc cgt caa gcg aag aac ggc cgc tgc cag gtc 444
Ala Gly Asn Cys Trp Leu Arg Gln Ala Lys Asn Gly Arg Cys Gln Val
29 34 39 44
ctg tac aag acc gaa ctg agc aag gag gag tgc tgc agc acc ggc cgg 492
Leu Tyr Lys Thr Glu Leu Ser Lys Glu Glu Cys Cys Ser Thr Gly Arg
45 50 55 60
ctg agc acc tcg tgg acc gag gag gac gtg aat gac aac aca ctc ttc 540
Leu Ser Thr Ser Trp Thr Glu Glu Asp Val Asn Asp Asn Thr Leu Phe
61 66 71 76
aag tgg atg att ttc aac ggg ggc gcc ccc aac tgc atc ccc tgt aaa 588
Lys Trp Met Ile Phe Asn Gly Gly Ala Pro Asn Cys Ile Pro Cys Lys
77 82 87 92
gaa acg tgt gag aac gtg gac tgt gga cct ggg aaa aaa tgc cga atg 636
Glu Thr Cys Glu Asn Val Asp Cys Gly Pro Gly Lys Lys Cys Arg Met
93 98 103 108

aac aag aag aac aaa ccc cgc tgc gtc tgc gcc ccg gat tgt tcc aac	684
Asn Lys Lys Asn Lys Pro Arg Cys Val Cys Ala Pro Asp Cys Ser Asn	
109 114 119 124	
atc acc tgg aag ggt cca gtc tgc ggg ctg gat ggg aaa acc tac cgc	732
Ile Thr Trp Lys Gly Pro Val Cys Gly Leu Asp Gly Lys Thr Tyr Arg	
125 130 135 140	
aat gaa tgt gca ctc cta aag gca aga tgt aaa gag cag cca gaa ctg	780
Asn Glu Cys Ala Leu Leu Lys Ala Arg Cys Lys Glu Gln Pro Glu Leu	
141 146 151 156	
gaa gtc cag tac caa ggc aga tgt aaa aag act tgt cgg gat gtt ttc	828
Glu Val Gln Tyr Gln Gly Arg Cys Lys Lys Thr Cys Arg Asp Val Phe	
157 162 167 172	
tgt cca ggc agc tcc aca tgt gtg gtg gac cag acc aat aat gcc tac	876
Cys Pro Gly Ser Ser Thr Cys Val Val Asp Gln Thr Asn Asn Ala Tyr	
173 178 183 188	
tgt gtg acc tgt aat cgg att tgc cca gag cct gct tcc tct gag caa	924
Cys Val Thr Cys Asn Arg Ile Cys Pro Glu Pro Ala Ser Ser Glu Gln	
189 194 199 204	
tat ctc tgt ggg aat gat gga gtc acc tac tcc agt gcc tgc cac ctg	972
Tyr Leu Cys Gly Asn Asp Gly Val Thr Tyr Ser Ser Ala Cys His Leu	
205 210 215 220	
aga aag gct acc tgc ctg ctg ggc aga tct att gga tta gcc tat gag	1020
Arg Lys Ala Thr Cys Leu Leu Gly Arg Ser Ile Gly Leu Ala Tyr Glu	
221 226 231 236	
gga aag tgt atc aaa gca aag tcc tgt gaa gat atc cag tgc act ggt	1068
Gly Lys Cys Ile Lys Ala Lys Ser Cys Glu Asp Ile Gln Cys Thr Gly	
237 242 247 252	
ggg aaa aaa tgt tta tgg gat ttc aag gtt ggg aga ggc cgg tgt tcc	1116
Gly Lys Lys Cys Leu Trp Asp Phe Lys Val Gly Arg Gly Arg Cys Ser	
253 258 263 268	
ctc tgt gat gag ctg tgc cct gac agt aag tcg gat gag cct gtc tgt	1164
Leu Cys Asp Glu Leu Cys Pro Asp Ser Lys Ser Asp Glu Pro Val Cys	
269 274 279 284	
gcc agt gac aat gcc act tat gcc agc gag tgt gcc atg aag gaa gct	1212
Ala Ser Asp Asn Ala Thr Tyr Ala Ser Glu Cys Ala Met Lys Glu Ala	
285 290 295 300	
gcc tgc tcc tca ggt gtg cta ctg gaa gta aag cac tcc gga tct tgc	1260
Ala Cys Ser Ser Gly Val Leu Leu Glu Val Lys His Ser Gly Ser Cys	
301 306 311 316	
aac tcc att tcg gaa gac acc gag gaa gag gag gaa gat gaa gac cag	1308
Asn Ser Ile Ser Glu Asp Thr Glu Glu Glu Glu Glu Asp Glu Asp Gln	
317 322 327 332	
gac tac agc ttt cct ata tct tct att cta gag tgg taa actctctata	1357

Asp Tyr Ser Phe Pro Ile Ser Ser Ile Leu Glu Trp *
 333 338 343

agtgttcagt gttgacatag cctttgtgca aaaaaaaaaa aa 1399

<210> 433
 <211> 759
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (137)..(628)

<400> 433

atacaagcta cttgttcttt ttgcaggatc ccatcgattc gaattccgtt gctgtcgggc 60

cgcggtaggc tgccagccag gctgggaaag cggtggtagc tggttgggtt gctggggctc 120

ggttgttgta gtcgcg atg ttc ttc tcc gag gcc aga gcc agg tcg cgg 169
 Met Phe Phe Ser Glu Ala Arg Ala Arg Ser Arg
 1 5

acg tgg gaa gcc agt ccc tcg gaa cac agg aag tgg gtg gaa gta ttt 217
 Thr Trp Glu Ala Ser Pro Ser Glu His Arg Lys Trp Val Glu Val Phe
 12 17 22 27

aaa gca tgt gat gaa gat cac aaa gga tat ctc agc aga gag gac ttt 265
 Lys Ala Cys Asp Glu Asp His Lys Gly Tyr Leu Ser Arg Glu Asp Phe
 28 33 38 43

aaa act gct gtt gta atg ctg ttt ggg tac aag ccc tcc aag ata gaa 313
 Lys Thr Ala Val Val Met Leu Phe Gly Tyr Lys Pro Ser Lys Ile Glu
 44 49 54 59

gtg gat tct gtg atg tct tca ata aat cca aat act tct ggt ata tta 361
 Val Asp Ser Val Met Ser Ser Ile Asn Pro Asn Thr Ser Gly Ile Leu
 60 65 70 75

ctc gag ggg ttt tta aat att gtc agg aaa aag aag gaa gct caa cga 409
 Leu Glu Gly Phe Leu Asn Ile Val Arg Lys Lys Lys Glu Ala Gln Arg
 76 81 86 91

tat cgg aac gaa gta aga cac atc ttc aca gcc ttt gac acc tac tat 457
 Tyr Arg Asn Glu Val Arg His Ile Phe Thr Ala Phe Asp Thr Tyr Tyr
 92 97 102 107

cgt gga ttt tta act ttg gaa gat ttc aaa aaa gca ttt agg cag gtg 505
 Arg Gly Phe Leu Thr Leu Glu Asp Phe Lys Lys Ala Phe Arg Gln Val
 108 113 118 123

gct ccc aaa tta ccg gaa agg act gtt ctt gag gta ttc agg gaa gta 553
 Ala Pro Lys Leu Pro Glu Arg Thr Val Leu Glu Val Phe Arg Glu Val
 124 129 134 139

gat cga gat tca gat ggt cac gtc agc ttt aga gac ttt gaa tat gcc 601
 Asp Arg Asp Ser Asp Gly His Val Ser Phe Arg Asp Phe Glu Tyr Ala
 140 145 150 155

ctg aac tat gga cag aag gaa gcc taa ctatt gtgaactact tttggtaact 653
 Leu Asn Tyr Gly Gln Lys Glu Ala *
 156 161

ctggggagat caatagattg taatgtcagc agactctact ctactaatga tgtcatgcta 713

cagacttgatg attaaacatt taaaaatttt taaaaaaaaa aaaaaa 759

<210> 434
 <211> 2627
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (110) .. (1363)

<400> 434

gcttcgcccc agcgcggggcg gttccttgcg ctteagtcacc ccccggggtcc cctcctgctc 60

ccgggttttc tgccccgttc ccccggggtgg ctgtgggctc ccgagcccc atg tcg 115
 Met Ser
 1

gcc agc cgg ccc cag ggc ccc acg acc cca tgg tgt ctc cca aga agg 163
 Ala Ser Arg Pro Gln Gly Pro Thr Thr Pro Trp Cys Leu Pro Arg Arg
 3 8 13 18

tac atg aag cac aag cgc gac gat ggg ccc gag aag cag gag gac gag 211
 Tyr Met Lys His Lys Arg Asp Asp Gly Pro Glu Lys Gln Glu Asp Glu
 19 24 29 34

gcg gtg gac gtg acg ccg gtg atg acc tgc gtg ttt gtg gtg atg tgc 259
 Ala Val Asp Val Thr Pro Val Met Thr Cys Val Phe Val Val Met Cys
 35 40 45 50

tgc tcc atg ctg gtg ctg ctc tac tat ttc tac gac ctc ctc gtg tac 307
 Cys Ser Met Leu Val Leu Leu Tyr Tyr Phe Tyr Asp Leu Leu Val Tyr
 51 56 61 66

gtg gtc atc ggg atc ttc tgc ctg gcc tcc gcc acc ggc ctc tac agc 355
 Val Val Ile Gly Ile Phe Cys Leu Ala Ser Ala Thr Gly Leu Tyr Ser
 67 72 77 82

tgc ctg gcg ccc tgt gtg cgg cgg ctg cct tcg gca agt gca ggt gag 403
 Cys Leu Ala Pro Cys Val Arg Arg Leu Pro Ser Ala Ser Ala Gly Glu
 83 88 93 98

tct gcc ctg ctg gcc ccg acg atc ccc aac aac agc ctg ccc tac ttc 451

Ser	Ala	Leu	Leu	Ala	Pro	Thr	Ile	Pro	Asn	Asn	Ser	Leu	Pro	Tyr	Phe		
99					104				109						114		
cac	aag	cgc	ccg	cag	gcc	cgt	atg	ctg	ctc	ctg	gcg	ctc	ttc	tgc	gtg	499	
His	Lys	Arg	Pro	Gln	Ala	Arg	Met	Leu	Leu	Leu	Ala	Leu	Phe	Cys	Val		
115					120				125						130		
gcc	gtc	agc	gtg	gtg	tgg	ggc	gtc	ttc	cgc	aac	gag	gac	cag	tgg	gcc	547	
Ala	Val	Ser	Val	Val	Trp	Gly	Val	Phe	Arg	Asn	Glu	Asp	Gln	Trp	Ala		
131					136				141						146		
tgg	gtc	ctc	cag	gat	gcc	ctg	ggc	atc	gcc	ttc	tgc	ctc	tac	atg	ctg	595	
Trp	Val	Leu	Gln	Asp	Ala	Leu	Gly	Ile	Ala	Phe	Cys	Leu	Tyr	Met	Leu		
147					152				157						162		
aag	acc	atc	cgt	ctg	ccc	acc	ttc	aag	gcc	tgc	acg	ctg	ctg	ctg	ctg	643	
Lys	Thr	Ile	Arg	Leu	Pro	Thr	Phe	Lys	Ala	Cys	Thr	Leu	Leu	Leu	Leu		
163					168				173						178		
gtg	ctg	ttc	ctc	tac	gac	atc	ttc	ttc	gtg	ttc	atc	acg	ccc	ttc	ctg	691	
Val	Leu	Phe	Leu	Tyr	Asp	Ile	Phe	Phe	Val	Phe	Ile	Thr	Pro	Phe	Leu		
179					184				189						194		
acc	aag	agt	ggg	agc	agc	atc	atg	gtg	gag	gtg	gcc	act	ggg	ccc	tcg	739	
Thr	Lys	Ser	Gly	Ser	Ser	Ile	Met	Val	Glu	Val	Ala	Thr	Gly	Pro	Ser		
195					200				205						210		
gac	tca	gcc	acc	cgt	gag	aag	ctg	ccc	atg	gtc	ctg	aag	gtg	ccc	agg	787	
Asp	Ser	Ala	Thr	Arg	Glu	Lys	Leu	Pro	Met	Val	Leu	Lys	Val	Pro	Arg		
211					216				221						226		
ctg	aac	tcc	tca	cct	ctg	gcc	ctg	tgt	gac	cgg	ccc	ttc	tcc	ctc	ctg	835	
Leu	Asn	Ser	Ser	Pro	Leu	Ala	Leu	Cys	Asp	Arg	Pro	Phe	Ser	Leu	Leu		
227					232				237						242		
ggg	ttc	gga	gac	att	ttg	gtg	cca	ggg	ctg	ctg	gtg	gcc	tac	tgc	cac	883	
Gly	Phe	Gly	Asp	Ile	Leu	Val	Pro	Gly	Leu	Leu	Val	Ala	Tyr	Cys	His		
243					248				253						258		
agg	ttt	gac	atc	cag	gta	cag	tcc	tcc	agg	gta	tac	ttc	gtg	gcc	tgc	931	
Arg	Phe	Asp	Ile	Gln	Val	Gln	Ser	Ser	Arg	Val	Tyr	Phe	Val	Ala	Cys		
259					264				269						274		
acc	atc	gcc	tat	ggc	gtt	ggc	ctc	ctt	gtg	aca	ttc	gtg	gca	ctg	gcc	979	
Thr	Ile	Ala	Tyr	Gly	Val	Gly	Leu	Leu	Val	Thr	Phe	Val	Ala	Leu	Ala		
275					280				285						290		
ctg	atg	cag	cgt	ggc	cag	ccc	gct	ctc	ctc	tac	ctg	gtg	ccc	tgc	acg	1027	
Leu	Met	Gln	Arg	Gly	Gln	Pro	Ala	Leu	Leu	Tyr	Leu	Val	Pro	Cys	Thr		
291					296				301						306		
ctg	gtg	acg	agc	tgc	gct	gtg	gcg	ctc	tgg	cgc	cgg	gag	ctg	ggc	gtg	1075	
Leu	Val	Thr	Ser	Cys	Ala	Val	Ala	Leu	Trp	Arg	Arg	Glu	Leu	Gly	Val		
307					312				317						322		
ttc	tgg	acg	ggc	agc	ggc	ttt	gcg	aaa	gtc	cta	cct	cca	tct	ccg	tgg	1123	
Phe	Trp	Thr	Gly	Ser	Gly	Phe	Ala	Lys	Val	Leu	Pro	Pro	Ser	Pro	Trp		

323	328	333	338	
gcc cca gca cca gcc gac ggc ccg cag cct ccc aaa gac tct gcc acg				1171
Ala Pro Ala Pro Ala Asp Gly Pro Gln Pro Pro Lys Asp Ser Ala Thr				
339	344	349	354	
cca ctc tcc ccg cag ccg ccc agc gaa gaa cca gcc aca tcc ccc tgg				1219
Pro Leu Ser Pro Gln Pro Pro Ser Glu Glu Pro Ala Thr Ser Pro Trp				
355	360	365	370	
cct gct gag cag tcc cca aaa tca cgc acg tcc gag gag atg ggg gct				1267
Pro Ala Glu Gln Ser Pro Lys Ser Arg Thr Ser Glu Glu Met Gly Ala				
371	376	381	386	
gga gcc ccc atg cgg gag cct ggg agc cca gct gaa tcc gag ggc cgg				1315
Gly Ala Pro Met Arg Glu Pro Gly Ser Pro Ala Glu Ser Glu Gly Arg				
387	392	397	402	
gac cag gcc cag ccg tcc ccg gta acc cag cct ggc gcc tcg gcc tag				1363
Asp Gln Ala Gln Pro Ser Pro Val Thr Gln Pro Gly Ala Ser Ala *				
403	408	413	418	
gggaggggtg agacgctcgc tgccgtgccc gccacaccaa gatgttgggg ctgcctggcg				1423
cccactggag acagacagac agacgcctgt cccccgggac cgaggcctgt gccgtcccca				1483
cccgcccaaa catggtgctc atccttgccg agaccctgc agtcctgccc cgcgcccagc				1543
ccagctgccc cggtgcacg cctgctgctc ccagctcgcc cggtgcccac aagctctctg				1603
cggttccatc ctccccaccg gggtccgtcc tcgcaggccc tgcccggcct ctctgcagac				1663
cctcaagcgt cgtctgcatg agtgagcagg cgtgggtgga ctctggccgc ggccacactt				1723
ggtgctcacc agctgcttcg gccttcaggt gacctccctc cccacggcat cctgctctcc				1783
gggtggaaga gcagctttct gtctcccaga aggcctcgct tttccctctt gagcagatcg				1843
gagccctgg gaggtttgga agctgcctcc aagcctagga cacggaccgg tggccggggc				1903
ggcctctggc cctgacgct ggctgagaca ggccctgggg gcgggggtttt ggggcgtgaa				1963
caaggctggc agtaagtgga caagctgctc ccctggctaa ggccctgccc tgccctcagc				2023
cagaggtgcc tggccatgcc tgcacactcc tccccatttt aataaatggc cgcaacttct				2083
agaagtcttg ctggtgccac ctggtggggg ggacgtctct cagactgccc ttctgacaag				2143
caggggtggg cgccaggcag gctgggtcag gccctcaggg gtccctggag ccctgggagg				2203
gagggactgg gtcgtgggag gtccctggtag ctcccggcac ccaacctcgc ttcccgtgtg				2263
ggcccccgtgt tgcttttctg ctgagagggg cttgggcctc ggttctccct gtggcagcgg				2323
cattggtgcc tgggttctta accctctgga ccagcagct aggagcttct ggaacccacg				2383
aggacatctg ccactggcat ggtctactca ctgatggggg cctcctgact ccagggcaga				2443

gacgtccgtg cgggaaactga ccgaggcgtg gccccaggcc ccggcatcct cccctcgctg 2503
cacgtgggtca cttccgaagc agcgctccct gtggccgcag agacagagcc cgcaccctgg 2563
ctgtctgtgg tgccctgggccc ccagctcccc cccgccaccc gccctgttga gtgcgggctc 2623
caga 2627

<210> 435
<211> 1864
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (164)..(1420)

<400> 435
taagcttgcg gccgcgcgac atttcttttt tttttttttt ttgccggagt cgagcgggtg 60
ctgctagcgg aggcgccata ttggagggga caaaactcgc gcgacagcga gtgacacaaa 120
taaacccttg gaccccttg ttccctcagc tctaagggcc gcg atg ttg tac cta 175
Met Leu Tyr Leu
1
gaa gac tat ctg gaa atg att gag cag ctt cct atg gat ctg cgg gac 223
Glu Asp Tyr Leu Glu Met Ile Glu Gln Leu Pro Met Asp Leu Arg Asp
5 10 15 20
cgc ttc acg gaa atg cgc gag atg gac ctg cag gtg cag aat gca atg 271
Arg Phe Thr Glu Met Arg Glu Met Asp Leu Gln Val Gln Asn Ala Met
21 26 31 36
gat caa cta gaa caa aga gtc agt gaa ttc ttt atg aat gca aag aaa 319
Asp Gln Leu Glu Gln Arg Val Ser Glu Phe Phe Met Asn Ala Lys Lys
37 42 47 52
aat aaa cct gag tgg agg gaa gag caa atg gca tcc atc aaa aaa gac 367
Asn Lys Pro Glu Trp Arg Glu Glu Gln Met Ala Ser Ile Lys Lys Asp
53 58 63 68
tac tat aaa gct ttg gaa gat gca gat gag aag gtt cag ttg gca aac 415
Tyr Tyr Lys Ala Leu Glu Asp Ala Asp Glu Lys Val Gln Leu Ala Asn
69 74 79 84
cag ata tat gac ttg gta gat cga cac ttg aga aag ctg gat cag gaa 463
Gln Ile Tyr Asp Leu Val Asp Arg His Leu Arg Lys Leu Asp Gln Glu
85 90 95 100
ctg gct aag ttt aaa atg gag ctg gaa gct gat aat gct gga att aca 511
Leu Ala Lys Phe Lys Met Glu Leu Glu Ala Asp Asn Ala Gly Ile Thr
101 106 111 116

gaa ata tta gag agg cga tct ttg gaa tta gac act cct tca cag cca	559
Glu Ile Leu Glu Arg Arg Ser Leu Glu Leu Asp Thr Pro Ser Gln Pro	
117 122 127 132	
gtg aac aat cac cat gct cat tca cat act cca gtg gaa aaa agg aaa	607
Val Asn Asn His His Ala His Ser His Thr Pro Val Glu Lys Arg Lys	
133 138 143 148	
tat aat cca act tct cac cat acg aca aca gat cat att cct gaa aag	655
Tyr Asn Pro Thr Ser His His Thr Thr Thr Asp His Ile Pro Glu Lys	
149 154 159 164	
aaa ttt aaa tct gaa gct ctt cta tcc acc ctt acg tca gat gcc tct	703
Lys Phe Lys Ser Glu Ala Leu Leu Ser Thr Leu Thr Ser Asp Ala Ser	
165 170 175 180	
aag gaa aat aca cta ggt tgt cga aat aat aat tcc aca gcc tct tct	751
Lys Glu Asn Thr Leu Gly Cys Arg Asn Asn Asn Ser Thr Ala Ser Ser	
181 186 191 196	
aac aat gcc tac aat gtg aat tcc tcc caa cct ctg gga tcc tat aac	799
Asn Asn Ala Tyr Asn Val Asn Ser Ser Gln Pro Leu Gly Ser Tyr Asn	
197 202 207 212	
att ggc tcg tta tct tca gga act ggt gca ggg gca att acc atg gca	847
Ile Gly Ser Leu Ser Ser Gly Thr Gly Ala Gly Ala Ile Thr Met Ala	
213 218 223 228	
gct gct caa gca gtt cag gct aca gct cag atg aag gag gga cga aga	895
Ala Ala Gln Ala Val Gln Ala Thr Ala Gln Met Lys Glu Gly Arg Arg	
229 234 239 244	
aca tca agt tta aaa gcc agt tat gaa gca ttt aag aat aat gac ttt	943
Thr Ser Ser Leu Lys Ala Ser Tyr Glu Ala Phe Lys Asn Asn Asp Phe	
245 250 255 260	
cag ttg gga aaa gaa ttt tca atg gcc agg gaa aca gtt ggc tat tca	991
Gln Leu Gly Lys Glu Phe Ser Met Ala Arg Glu Thr Val Gly Tyr Ser	
261 266 271 276	
tca tct tcg gca ctt atg aca aca tta aca cag aat gcc agt tca tca	1039
Ser Ser Ser Ala Leu Met Thr Thr Leu Thr Gln Asn Ala Ser Ser Ser	
277 282 287 292	
gca gcc gac tca cgg agt ggt cga aag agc aaa aac aac aac aag tct	1087
Ala Ala Asp Ser Arg Ser Gly Arg Lys Ser Lys Asn Asn Asn Lys Ser	
293 298 303 308	
tca agc cag cag tca tca tct tcc tcc tcc tct tct tcc tta tca tcg	1135
Ser Ser Gln Gln Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Leu Ser Ser	
309 314 319 324	
tgt tct tca tca tca act gtt gta caa gaa atc tct caa caa aca act	1183
Cys Ser Ser Ser Ser Thr Val Val Gln Glu Ile Ser Gln Gln Thr Thr	
325 330 335 340	

gta gtg cca gaa tct gat tca aat agt cag gtt gat tgg act tac gac	1231
Val Val Pro Glu Ser Asp Ser Asn Ser Gln Val Asp Trp Thr Tyr Asp	
341 346 351 356	
cca aat gaa cct cga tac tgc att tgt aat cag gta tct tat ggt gag	1279
Pro Asn Glu Pro Arg Tyr Cys Ile Cys Asn Gln Val Ser Tyr Gly Glu	
357 362 367 372	
atg gtg gga tgt gat aac caa gat tgc cct ata gaa tgg ttc cat tat	1327
Met Val Gly Cys Asp Asn Gln Asp Cys Pro Ile Glu Trp Phe His Tyr	
373 378 383 388	
ggc tgc gtt gga ttg aca gag gca cca aaa ggc aaa tgg tac tgt cca	1375
Gly Cys Val Gly Leu Thr Glu Ala Pro Lys Gly Lys Trp Tyr Cys Pro	
389 394 399 404	
cag tgc act gct gca atg aag aga aga ggc agc aga cac aaa taa agg	1423
Gln Cys Thr Ala Ala Met Lys Arg Arg Gly Ser Arg His Lys *	
405 410 415	
tggtcctttt gtttgatgaa gaaataaact tcagctgaag attttatata ggactttaaa	1483
aagaagagaa gagaaagaag aaacaatgca tttccaggca accacttaaa ggattttacat	1543
agacaatcct ataagatctt gaacttgaat tttatgggtt gtatttttaat aatgtaagta	1603
aattatttat gcactcctgg tgtgctatga atattattcc agttagcctt ggattatttc	1663
agtggccaac atatgcagac atttgtactc ctcaaccatt ttctcaaagt aatgggcatt	1723
ctatgattta gacttcaagg aattccaatg atgaagattt taaggaaagt attttatatt	1783
caacaggtat attctgctgc atgtactgta ctccagagct gttatgtaac actgtatata	1843
aatggttgca aaaaaaaaaa a	1864

<210> 436
 <211> 3289
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (201)..(2558)

<400> 436	
attgataggc tgatgtatat aactatctat tcgatgatga agatacccca ccaaacccaa	60
aaaaagagat ctctcgagga tccgaattcg cggccgcgtc gacgtccggg ttcgcttgcc	120
tcgtcagcgt ccgcgttttt cccggccccc cccaaccccc ccggacagga ccccttgag	180
cttgccctc agctgccacc atg agc gac caa gat cac tcc atg gat gaa	230
Met Ser Asp Gln Asp His Ser Met Asp Glu	

atg aca gct gtg gtg aaa att gaa aaa gga gtt ggt ggc aat aat ggg	278
Met Thr Ala Val Val Lys Ile Glu Lys Gly Val Gly Gly Asn Asn Gly	
11 16 21 26	
ggc aat ggt aat ggt ggt ggt gcc ttt tca cag gct cga agt agc agc	326
Gly Asn Gly Asn Gly Gly Gly Ala Phe Ser Gln Ala Arg Ser Ser Ser	
27 32 37 42	
aca ggc agt agc agc agc act gga gga gga ggg cag gag tcc cag cca	374
Thr Gly Ser Ser Ser Ser Thr Gly Gly Gly Gly Gln Glu Ser Gln Pro	
43 48 53 58	
tcc cct ttg gct ctg ctg gca gca act tgc agc aga att gag tca ccc	422
Ser Pro Leu Ala Leu Leu Ala Ala Thr Cys Ser Arg Ile Glu Ser Pro	
59 64 69 74	
aat gag aac agc aac aac tcc cag ggc ccg agt cag tca ggg gga aca	470
Asn Glu Asn Ser Asn Asn Ser Gln Gly Pro Ser Gln Ser Gly Gly Thr	
75 80 85 90	
ggg gag ctt gac ctc aca gcc aca caa ctt tca cag ggt gcc aat ggc	518
Gly Glu Leu Asp Leu Thr Ala Thr Gln Leu Ser Gln Gly Ala Asn Gly	
91 96 101 106	
tgg cag atc atc tct tcc tcc tct ggg gct acc cct acc tca aag gaa	566
Trp Gln Ile Ile Ser Ser Ser Ser Gly Ala Thr Pro Thr Ser Lys Glu	
107 112 117 122	
cag agt ggc agc agt acc aat ggc agc aat ggc agt gag tct tcc aag	614
Gln Ser Gly Ser Ser Thr Asn Gly Ser Asn Gly Ser Glu Ser Ser Lys	
123 128 133 138	
aat cgc aca gtc tct ggt ggg cag tat gtt gtg gct gcc gct ccc aac	662
Asn Arg Thr Val Ser Gly Gly Gln Tyr Val Val Ala Ala Ala Pro Asn	
139 144 149 154	
tta cag aac cag caa gtt ctg aca gga cta cct gga gtg atg cct aat	710
Leu Gln Asn Gln Gln Val Leu Thr Gly Leu Pro Gly Val Met Pro Asn	
155 160 165 170	
att cag tat caa gta atc cca cag ttc cag acc gtt gat ggg caa cag	758
Ile Gln Tyr Gln Val Ile Pro Gln Phe Gln Thr Val Asp Gly Gln Gln	
171 176 181 186	
ctg cag ttt gct gcc act ggg gcc caa gtg cag cag gat ggt tct ggt	806
Leu Gln Phe Ala Ala Thr Gly Ala Gln Val Gln Gln Asp Gly Ser Gly	
187 192 197 202	
caa ata cag atc ata cca ggt gca aac caa cag att atc aca aat cga	854
Gln Ile Gln Ile Ile Pro Gly Ala Asn Gln Gln Ile Ile Thr Asn Arg	
203 208 213 218	
gga agt gga ggc aac atc att gct gct atg cca aac cta ctc cag cag	902
Gly Ser Gly Gly Asn Ile Ile Ala Ala Met Pro Asn Leu Leu Gln Gln	
219 224 229 234	

gct gtc ccc ctc caa ggc ctg gct aat aat gta ctc tca gga cag act	950
Ala Val Pro Leu Gln Gly Leu Ala Asn Asn Val Leu Ser Gly Gln Thr	
235 240 245 250	
cag tat gtg acc aat gta cca gtg gcc ctg aat ggg aac atc acc ttg	998
Gln Tyr Val Thr Asn Val Pro Val Ala Leu Asn Gly Asn Ile Thr Leu	
251 256 261 266	
cta cct gtc aac agc gtt tct gca gct acc ttg act ccc agc tct cag	1046
Leu Pro Val Asn Ser Val Ser Ala Ala Thr Leu Thr Pro Ser Ser Gln	
267 272 277 282	
gca gtc acg atc agc agc tct ggg tcc cag gag agt ggc tca cag cct	1094
Ala Val Thr Ile Ser Ser Ser Gly Ser Gln Glu Ser Gly Ser Gln Pro	
283 288 293 298	
gtc acc tca ggg act acc atc agt tct gcc agc ttg gta tca tca caa	1142
Val Thr Ser Gly Thr Thr Ile Ser Ser Ala Ser Leu Val Ser Ser Gln	
299 304 309 314	
gcc agt tcc agc tcc ttt ttc acc aat gcc aat agc tac tca act act	1190
Ala Ser Ser Ser Ser Phe Phe Thr Asn Ala Asn Ser Tyr Ser Thr Thr	
315 320 325 330	
act acc acc agc aac atg gga att atg aac ttt act acc agt gga tca	1238
Thr Thr Thr Ser Asn Met Gly Ile Met Asn Phe Thr Thr Ser Gly Ser	
331 336 341 346	
tca ggg acc aac tct caa ggc cag aca ccc cag agg gtc agt ggg cta	1286
Ser Gly Thr Asn Ser Gln Gly Gln Thr Pro Gln Arg Val Ser Gly Leu	
347 352 357 362	
cag ggg tct gat gct ctg aac atc cag caa aac cag aca tct gga ggc	1334
Gln Gly Ser Asp Ala Leu Asn Ile Gln Gln Asn Gln Thr Ser Gly Gly	
363 368 373 378	
tca ttg caa gca ggc cag cag aaa gaa gga gag caa aac cag cag aca	1382
Ser Leu Gln Ala Gly Gln Gln Lys Glu Gly Glu Gln Asn Gln Gln Thr	
379 384 389 394	
cag cag caa caa att ctt atc cag cct cag cta gtt caa ggg gga cag	1430
Gln Gln Gln Gln Ile Leu Ile Gln Pro Gln Leu Val Gln Gly Gly Gln	
395 400 405 410	
gcc ctc cag gcc ctc caa gca gca cca ttg tca ggg cag acc ttt aca	1478
Ala Leu Gln Ala Leu Gln Ala Ala Pro Leu Ser Gly Gln Thr Phe Thr	
411 416 421 426	
act caa gcc atc tcc cag gaa acc ctc cag aac ctc cag ctt cag gct	1526
Thr Gln Ala Ile Ser Gln Glu Thr Leu Gln Asn Leu Gln Leu Gln Ala	
427 432 437 442	
gtt cca aac tct ggt ccc atc atc atc cgg aca cca aca gtg ggg ccc	1574
Val Pro Asn Ser Gly Pro Ile Ile Ile Arg Thr Pro Thr Val Gly Pro	
443 448 453 458	

aat gga cag gtc agt tgg cag act cta cag ctg cag aac ctc caa gtt	1622
Asn Gly Gln Val Ser Trp Gln Thr Leu Gln Leu Gln Asn Leu Gln Val	
459 464 469 474	
cag aac cca caa gcc caa aca atc acc tta gcc cca atg cag ggt gtt	1670
Gln Asn Pro Gln Ala Gln Thr Ile Thr Leu Ala Pro Met Gln Gly Val	
475 480 485 490	
tcc ttg ggg cag acc agc agc agc aac acc act ctc aca ccc att gcc	1718
Ser Leu Gly Gln Thr Ser Ser Ser Asn Thr Thr Leu Thr Pro Ile Ala	
491 496 501 506	
tca gct gct tcc att cct gct ggc aca gtc act gtg aat gct gct caa	1766
Ser Ala Ala Ser Ile Pro Ala Gly Thr Val Thr Val Asn Ala Ala Gln	
507 512 517 522	
ctc tcc tcc atg cca ggc ctc cag acc att aac ctc agt gca ttg ggt	1814
Leu Ser Ser Met Pro Gly Leu Gln Thr Ile Asn Leu Ser Ala Leu Gly	
523 528 533 538	
act tca gga atc cag gtg cac cca att caa ggc ctg ccg ttg gct ata	1862
Thr Ser Gly Ile Gln Val His Pro Ile Gln Gly Leu Pro Leu Ala Ile	
539 544 549 554	
gca aat gcc cca ggt gat cat gga gct cag ctt ggt ctc cat ggg gct	1910
Ala Asn Ala Pro Gly Asp His Gly Ala Gln Leu Gly Leu His Gly Ala	
555 560 565 570	
ggg ggt gat gga ata cat gat gac aca gca ggt gga gag gaa gga gaa	1958
Gly Gly Asp Gly Ile His Asp Asp Thr Ala Gly Gly Glu Glu Gly Glu	
571 576 581 586	
aac agc cca gat gcc caa ccc caa gcc ggt cgg agg acc cgg cgg gaa	2006
Asn Ser Pro Asp Ala Gln Pro Gln Ala Gly Arg Arg Thr Arg Arg Glu	
587 592 597 602	
gca tgc acc tgc ccc tac tgt aaa gac agt gaa gga agg ggc tcg ggg	2054
Ala Cys Thr Cys Pro Tyr Cys Lys Asp Ser Glu Gly Arg Gly Ser Gly	
603 608 613 618	
gat cct ggc aaa aag aaa cag cat att tgc cac atc caa ggc tgt ggg	2102
Asp Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly Cys Gly	
619 624 629 634	
aaa gtg tat ggc aag acc tct cac ctg cgg gca cac ttg cgc tgg cat	2150
Lys Val Tyr Gly Lys Thr Ser His Leu Arg Ala His Leu Arg Trp His	
635 640 645 650	
aca ggc gag agg cca ttt atg tgt acc tgg tca tac tgt ggg aaa cgc	2198
Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg	
651 656 661 666	
ttc aca cgt tcg gat gag cta cag agg cac aaa cgt aca cac aca ggt	2246
Phe Thr Arg Ser Asp Glu Leu Gln Arg His Lys Arg Thr His Thr Gly	
667 672 677 682	
gag aag aaa ttt gcc tgc cct gag tgt cct aag cgc ttc atg agg agt	2294

Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met Arg Ser	
683 688 693 698	
gac cac ctg tca aaa cat atc aag acc cac cag aat aag aag gga ggc	2342
Asp His Leu Ser Lys His Ile Lys Thr His Gln Asn Lys Lys Gly Gly	
699 704 709 714	
cca ggt gta gct ctg agt gtg ggc act ttg ccc ctg gac agt ggg gca	2390
Pro Gly Val Ala Leu Ser Val Gly Thr Leu Pro Leu Asp Ser Gly Ala	
715 720 725 730	
ggt tca gaa ggc agt ggc act gcc act cct tca gcc ctt att acc acc	2438
Gly Ser Glu Gly Ser Gly Thr Ala Thr Pro Ser Ala Leu Ile Thr Thr	
731 736 741 746	
aat atg gta gcc atg gag gcc atc tgt cca gag ggc att gcc cgt ctt	2486
Asn Met Val Ala Met Glu Ala Ile Cys Pro Glu Gly Ile Ala Arg Leu	
747 752 757 762	
gcc aac agt ggc atc aac gtc atg cag gtg gca gat ctg cag tcc att	2534
Ala Asn Ser Gly Ile Asn Val Met Gln Val Ala Asp Leu Gln Ser Ile	
763 768 773 778	
aat atc agt ggc aat ggc ttc tga gatcagggcac ccggggccag agacatatgg	2588
Asn Ile Ser Gly Asn Gly Phe *	
779 784	
gccatacccc ttaaccccg gatgcaaggt agcatgggtc caagagacat ggaagagaga	2648
gccatgaagc attaaaaatgc atggtgttga gaagaatcag gagagggata caagagagga	2708
gatgggggtcc cggcacccat ctgtatcatc agtgcctctt tgaaggtggg aaacattagt	2768
gaaaattctg ttggtgccac gctttgatga gcatttgttt gaccccagtt tcttcttaca	2828
cttcttacct cagcctacct ttcttgcatt tctcttctca gctcttccat gatggattcc	2888
cccccttttc cttaaagccat catgccttga taaatatata tgatcattga aatacttttt	2948
aacaaaaaac agattctata ttattatata tatatatata tatatatata gatatataga	3008
gatgcattca caggggttgg ctgggaggag gaagaccatt ctgtgaccaa aataccttgg	3068
tcattttttt tatattgcct tatttcccta tggttgagcc ttgttgtgac acatcaagct	3128
tttctgtaga tgttgtcttg gcttcccacc agcttaagcg ttcatatgct ctgcttttag	3188
ttcatatata catacataat gtttttctt tottaatttt gtctttttgt ttgggatcag	3248
cttcttgcac tcttcccta actcaactcg gcgcaagctt a	3289

<210> 437
 <211> 1650
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (45)..(857)

<400> 437

atttggccct cgaggaagga attcggcacg aggggcccggg cgcc atg gca ccg tgg 56
Met Ala Pro Trp
1

ggc aag cgg ctg gct ggc gtg cgc ggg gtg ctg ctt gac atc tcg ggc 104
Gly Lys Arg Leu Ala Gly Val Arg Gly Val Leu Leu Asp Ile Ser Gly
5 10 15 20

gtg ctg tac gac agc ggc gcg ggc ggc ggc acg gcc atc gcc ggc tcg 152
Val Leu Tyr Asp Ser Gly Ala Gly Gly Gly Thr Ala Ile Ala Gly Ser
21 26 31 36

gtg gag gcg gtg gcc aga ctg aag cgt tcc cgg ctg aag gtg agg ttc 200
Val Glu Ala Val Ala Arg Leu Lys Arg Ser Arg Leu Lys Val Arg Phe
37 42 47 52

tgc acc aac gag tcg cag aag tcc cgg gca gag ctg gtg ggg cag ctt 248
Cys Thr Asn Glu Ser Gln Lys Ser Arg Ala Glu Leu Val Gly Gln Leu
53 58 63 68

cag agg ctg gga ttt gac atc tct gag cag gag gtg acc gcc ccg gca 296
Gln Arg Leu Gly Phe Asp Ile Ser Glu Gln Glu Val Thr Ala Pro Ala
69 74 79 84

cca gct gcc tgc cag atc ctg aag gag cga ggc ctg cga cca tac ctg 344
Pro Ala Ala Cys Gln Ile Leu Lys Glu Arg Gly Leu Arg Pro Tyr Leu
85 90 95 100

ctc atc cat gac gga gtc cgc tca gaa ttt gat cag atc gac aca tcc 392
Leu Ile His Asp Gly Val Arg Ser Glu Phe Asp Gln Ile Asp Thr Ser
101 106 111 116

aac cca aac tgt gtg gta att gca gac gca gga gaa agc ttt tct tat 440
Asn Pro Asn Cys Val Val Ile Ala Asp Ala Gly Glu Ser Phe Ser Tyr
117 122 127 132

caa aac atg aat aac gcc ttc cag gtg ctc atg gag ctg gaa aaa cct 488
Gln Asn Met Asn Asn Ala Phe Gln Val Leu Met Glu Leu Glu Lys Pro
133 138 143 148

gtg ctc ata tca ctg gga aaa ggg cgt tac tac aag gag acc tct ggc 536
Val Leu Ile Ser Leu Gly Lys Gly Arg Tyr Tyr Lys Glu Thr Ser Gly
149 154 159 164

ctg atg ctg gac gtt ggt ccc tac atg aag gcg ctt gag tat gcc tgt 584
Leu Met Leu Asp Val Gly Pro Tyr Met Lys Ala Leu Glu Tyr Ala Cys
165 170 175 180

ggc atc aaa gcc gag gtg ggg ggg aag cct tct cct gag ttt ttc aag 632
Gly Ile Lys Ala Glu Val Gly Gly Lys Pro Ser Pro Glu Phe Phe Lys

181	186	191	196	
tct gcc ctg caa gcg ata gga gtg gaa gcc cac cag gcc gtc atg att				680
Ser Ala Leu Gln Ala Ile Gly Val Glu Ala His Gln Ala Val Met Ile				
197	202	207	212	
ggg gac gat atc gtg ggc gac gtc ggc ggt gcc cag cgg tgt gga atg				728
Gly Asp Asp Ile Val Gly Asp Val Gly Gly Ala Gln Arg Cys Gly Met				
213	218	223	228	
aga gcg ctg cag gtg cgc acc ggg aag ttc agg ccc agt gac gag cac				776
Arg Ala Leu Gln Val Arg Thr Gly Lys Phe Arg Pro Ser Asp Glu His				
229	234	239	244	
cat ccg gaa gtg aag gct gat ggg tac gtg gac aac ctc gca gag gca				824
His Pro Glu Val Lys Ala Asp Gly Tyr Val Asp Asn Leu Ala Glu Ala				
245	250	255	260	
gtg gac ctg ctg ctg cag cac gcc gac aag tga tggcctcc tgggagagcc				875
Val Asp Leu Leu Leu Gln His Ala Asp Lys *				
261	266	271		
ccgcctcctc caccctgcc tctcctccac cctgcctcc cctccacccc tgcctcctc				935
ccaccgccc aggagagccc cacctcctcc acccctgqct ctccctcacc cctgcctccc				995
ctccacctgc cccagtgcc agaccaacca aggcctgac agccctgcct tctgacctct				1055
gccctgcatg ggcaggcatt tgttccctac ctgggtggcc tgctcccctg cctgggacct				1115
gacttcagct cctgtagtg aagtccagga ggggtgggaca ggccgtgtcag gcctctggga				1175
atctcccaaa tcccagaact caccactcac catgggcctt taaatgcagt aaactccacc				1235
taaccagatt caggggcact atgccactg cctcctcttc agactctttg catttcagt				1295
aagagcctgg aagaaaccca ggggcctcct atgcacagat cttgcagccc agaaccaagt				1355
cagcctccct gcgactgccc aggcacactg ccaccacccc caccctcgaa acaatgccag				1415
cccgtgctt tttctatcct cccagtcacc tttgcagaca aagaccaggg gcagctccc				1475
agggcactgt gaaggctccc atgccacaca gtgagaactg tagcctctgc gtccaaggca				1535
cacagggtag tttctggacc cactgctgga cagaattgaa ggtgtcatgc ccggtgtgtg				1595
caggaggaaa ctaacagttc agtaaaactct gccttgacca gcaaaaaaaaa aaaaa				1650

<210> 438
 <211> 603
 <212> DNA
 <213> Homo sapiens
 <220>

<221> CDS
<222> (251)..(469)

<400> 438

ttcgggctcga	cccacgcgtc	cgcagctact	cggaaggctg	aggcattaga	attattgaac	60
ccgggaggtg	gaggttgtag	tgagctgaga	ttgtgccact	gcactctagc	ctgggtgaca	120
gagtgaact	ccctctcaaa	aaataaaaat	aaaatataaa	taaataaaac	aattggggcc	180
tcactatttt	atatttttgt	ctcaaaaaac	aactctctct	tgtggtgtgt	gcttgattct	240
gcttcttgtc	atg tct tct cac aag tct ttt aag agt aag cga ttc ctg	289				
	Met Ser Ser His Lys Ser Phe Lys Ser Lys Arg Phe Leu					
	1 5 10					
gcc aag aaa caa aag cca aat cgt ccc att ctc cag tgg atc tgg ttg	337					
Ala Lys Lys Gln Lys Pro Asn Arg Pro Ile Leu Gln Trp Ile Trp Leu						
14 19 24 29						
aaa act ggt aat aaa atc agg cac aac tgg aaa gga gac att gca gaa	385					
Lys Thr Gly Asn Lys Ile Arg His Asn Trp Lys Gly Asp Ile Ala Glu						
30 35 40 45						
cag cca agc tgg gtc tat aag gaa ctg cac gtg agc tgg cac aca tat	433					
Gln Pro Ser Trp Val Tyr Lys Glu Leu His Val Ser Trp His Thr Tyr						
46 51 56 61						
tca cgc tgt atc aag gtc acg gcc atc tta cta tag caag ctgaaaacgt	483					
Ser Arg Cys Ile Lys Val Thr Ala Ile Leu Leu *						
62 67 72						
caccactgtc tgaacagttg gacgtgtttt attgggaata tattttttct ctttgcttat	543					
atgccctgcg atagtaggct gggttcagta ataaatatgt gagacctttt gtttcaggaa	603					

<210> 439
<211> 1816
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (178)..(729)

<400> 439

ttgcgttccg	gaattcccgg	gtcgaccac	gcgtccggtt	gggaagggcg	ctcctgggcg	60
gcttgccggg	tgaacctgca	gggagcctgg	ggagagcggt	caggggtcag	agcgtccgag	120
gcggaatccc	cggggaaacg	cgcagatgta	agctggtgga	gccgccagct	ggagacg	177
atg gtg gac cac ttg gcc aac acg gag atc aac agc cag cgc atc gcg	225					
Met Val Asp His Leu Ala Asn Thr Glu Ile Asn Ser Gln Arg Ile Ala						
1 5 10 15						

gca gtg gag agc tgc ttc ggg gcc tcg ggg cag ccg ctg gcg ctg cca	273
Ala Val Glu Ser Cys Phe Gly Ala Ser Gly Gln Pro Leu Ala Leu Pro	
17 22 27 32	
ggc cga gtg ctg ctg ggc gag ggc gtg ctg acc aaa gag tgc cgc aag	321
Gly Arg Val Leu Leu Gly Glu Gly Val Leu Thr Lys Glu Cys Arg Lys	
33 38 43 48	
aag gcc aag ccg cgc atc ttc ttc ctc ttt aac gac atc ctg gtg tat	369
Lys Ala Lys Pro Arg Ile Phe Phe Leu Phe Asn Asp Ile Leu Val Tyr	
49 54 59 64	
ggc agc atc gtg ctc aac aag cgc aag tac cgc agc cag cac atc atc	417
Gly Ser Ile Val Leu Asn Lys Arg Lys Tyr Arg Ser Gln His Ile Ile	
65 70 75 80	
ccc ctg gag gag gtc aca ctg gag ctg ttg ccg gag acg ctg cag gcc	465
Pro Leu Glu Glu Val Thr Leu Glu Leu Leu Pro Glu Thr Leu Gln Ala	
81 86 91 96	
aag aac cgc tgg atg atc aag acg gcc aag aag tcc ttt gtg gtg tcg	513
Lys Asn Arg Trp Met Ile Lys Thr Ala Lys Lys Ser Phe Val Val Ser	
97 102 107 112	
gcc gcc tcc gct acg gag cgc cag gaa tgg att agc cac atc gag gag	561
Ala Ala Ser Ala Thr Glu Arg Gln Glu Trp Ile Ser His Ile Glu Glu	
113 118 123 128	
tgc gtg cgg cgg caa ctg agg gcc acg ggc cgc ccg ccc agc acg gag	609
Cys Val Arg Arg Gln Leu Arg Ala Thr Gly Arg Pro Pro Ser Thr Glu	
129 134 139 144	
cac gcg gca ccc tgg atc ccc gac aag gcc acg gac atc tgc atg cgc	657
His Ala Ala Pro Trp Ile Pro Asp Lys Ala Thr Asp Ile Cys Met Arg	
145 150 155 160	
tgc acg cag acg cgc ttc tct gcc ctc acg agg cgc cac cac tgc cgc	705
Cys Thr Gln Thr Arg Phe Ser Ala Leu Thr Arg Arg His His Cys Arg	
161 166 171 176	
aag tgc gtt cgt ggt ctg cgc tga gtgctgcgc cagcgccttcc tgctccgcg	759
Lys Cys Val Arg Gly Leu Arg *	
177 182	
cctgtccccc aagcccgtag gcgtctgcag cctctgttac cgcgaactgg ccgcccagca	819
gcggcaggag gaggcggagg agcagggcgc ggggtcccca gggcagccag cccacctggc	879
ccggcccatc tgcggacgtc cagtggagat gacgatgact ccgacgagga caaggagggc	939
agcagggacg gcgactggcc cagcagcgtg gagttctacg cctcgggggt ggctgtgtct	999
gccttcaca gctgaccccc ggctgcaga acatctgtcc ccaagccagc tccactgccc	1059
aggcccccaa gagggcagct ccagaagctg ccaggggtc cgggaccca tcccatggtg	1119

```

gcagggtgcag cgggtggggag tggctctttc tggactccca gtgccttttt gctggacact 1179
gtgtccttat ggcttcactg caggtaatgc ctttccttc aggaagcccc agaacaccca 1239
caggctcttg taacaaacgc caccttacac tctgcaggct gcagcggcag ctccagatgg 1299
cctcctgagc tggacgaccc caggctctcca gacatctagg gaccagagca ggtttgggaa 1359
cacagagggga agacaggatg ggagtgtagc cacagaaccc acctgcaccc tgacaggcac 1419
accccactga agagcctgag tcccaggagg cctcctggaa gcccaggact gcccacccac 1479
caegctgggtg cccaccgcct ggccagccaa gccctgccga tcagacatgt gggctccccg 1539
aagcccagcc agagactgcc gtgctgtggg tgccaccagg cccagggact gcagcctgag 1599
ctccccgagg cccagggcag cggggtgagg actctgtcct gtgtcacctc tctccagggtg 1659
tccagctgtc tcatgccttt ttgtcctgtc ctcagctctc cgtgtggtca gcgaaaccat 1719
tgttttctgt taggactcag ttgcaagaac agaaaccctg cccccactta ataataaaaa 1779
agaaagttaa ttgatgggtg gttgcaaaaa aaaaaaa 1816

```

```

<210> 440
<211> 833
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (258)..(467)

```

```

<220>
<221> misc_feature
<222> (1)...(833)
<223> n = a,t,c or g

```

```

<400> 440
cgtgccagct ctactgaac atgaaagcag tcgnaacca gaaaagtaag aaagttcaac 60
gcaccttgnn ccgcctgagt cgacgcccgc gtcctgcgt attgctcctt tnccacagtg 120
gactctgtgg tcgccacatc cttctcctgc atgtggcaag ccaccgggac atgggctgct 180
gaccgctctc gctggccttc gtgggtgcct ccactagcc taccagcaga cctcggcctt 240
cgcccggcag ccccgcg atg agc tgg agc gcg tgc gtg tca gct gca cca 290
Met Ser Trp Ser Ala Cys Val Ser Ala Ala Pro
1 5
tca tct tcc tgg cca gca tct tcc agc tgg cca tgt gga cca cgg cgc 338
Ser Ser Ser Trp Pro Ala Ser Ser Ser Trp Pro Cys Gly Pro Arg Arg
12 17 22 27

```

tgc tgc acc agg cgg aga cgc tgc agc cct cgg tgt ggt ttg gcg gcc	386
Cys Cys Thr Arg Arg Arg Arg Cys Ser Pro Arg Cys Gly Leu Ala Ala	
28 33 38 43	
ggg agc atg tgc tca tgt tgc cca agc tgg cgc tgt acc cct gtg cca	434
Gly Ser Met Cys Ser Cys Ser Pro Ser Trp Arg Cys Thr Pro Val Pro	
44 49 54 59	
gcc tgc tgg cct tgc cct cca cct gcc tgc tga gcaggttc agtgtgggca	485
Ala Cys Trp Pro Ser Pro Pro Pro Ala Cys *	
60 65 70	
tcttcacact catgcagatc gccgtgccct gcgccttct gttgctgcgc ctgctcgtgg	545
gcctggccct ggccaccctg cgggtcctgc ggggcctgc ccggcccgaa cccccccgc	605
cagccccac gggccaggac gaccacagt ccagctcct ccctgcccc tgctagcagc	665
cacagagccc actccagcc gtcctcacca gagatggacc agggaggaca ggatgctggg	725
caggggaagc caagtcacgg gcaggccgca gtggttcttg cgtggcctgg ttttattttc	785
attgtgaaat atcatgctct tatttcagtc ctcaaaaaaa aaaaaaaa	833

<210> 441
 <211> 1241
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (350) .. (553)

<220>
 <221> misc_feature
 <222> (1) ... (1241)
 <223> n = a,t,c or g

<400> 441	
atgactggaa agtgcagaaa gccccgaagc tgatgctggt agtggaaatct caggcactga	60
gtgtggcgag tctcaactgg ccaactccac ggagcctggg gaggcttcag caagagccaa	120
gtgagagcag gtcagaggcc gggcccagcg ccagcgaggc atctggggag ccgtgccctt	180
gttagcgctg aaaatggaag cccctccatt caggcctgga cagatgatgg gcagogaatg	240
tgctcacatg ctgagctgtg gggctggact aggtaccaa atcagggtag aacactgaga	300
cgtctgtggg cgggtgtgtg cacatccaca cttgtacact cacattcac	355
	atg cac
	Met His
	1

ata tgt gca cac gca tgc aat tca tac aca tgc aca gtt gtg ctc aca	403
Ile Cys Ala His Ala Cys Asn Ser Tyr Thr Cys Thr Val Val Leu Thr	
3 8 13 18	
gcc tcg cac gcc ctt gca cac tcg cac tta tac aca tgc atg gtc atg	451
Ala Ser His Ala Leu Ala His Ser His Leu Tyr Thr Cys Met Val Met	
19 24 29 34	
ctc aca gcc tcg cac acg ccc tcg cac act cat cca cac aca gct gtg	499
Leu Thr Ala Ser His Thr Pro Ser His Thr His Pro His Thr Ala Val	
35 40 45 50	
cac aag gaa cac aga gca gat gtt ctc aga ggg act ctg aca cct ttg	547
His Lys Glu His Arg Ala Asp Val Leu Arg Gly Thr Leu Thr Pro Leu	
51 56 61 66	
aga tga gggtttttta atcactggaa ggctctcttg ggtctaacag gttcagagaa	603
Arg *	
67	
tgtaacacct ggttttcaaa acatttttca aagaaataga gaattcccat acacagggcat	663
acgtgacgtt atgaggccgg tggaggcctc gtcggtgtt gccctgtatg gttgagctgt	723
ggtttaaggt gaactctgga gtgtgggctg cangtgaggg ctccgtccct gggagctggt	783
gggaggagct ggaggctggc gccgccctgc tcaaagctgc ctgcttgggc tcgtctgagg	843
cggttccgag ctgcaggtgt ctccaccaac ctgctgtgct acacagcggg gtcctgggca	903
gcctcaccac tgcgtgtctt gggttcctct tctgtaaaac agaggtgcc tccgaccctt	963
tggacaaaca gggaagagcc gtaacacgca ggatgtgaat ggaaccttaa gcttgtgcct	1023
gaagggtcga gctactggtg gccgtgatgc ctgaccgacg cgaggctcgt cggaaggtag	1083
ggcacgatgg cagactgagc cctggtgtct atgaagcacc gagcaatgcg aggagggcag	1143
cagggaggaa cgcggcacgc gagtgggtgca gacacggaga gaacacaacg atcggaagtc	1203
gctgagggat gtatgggacg gtgagacttc actcagt	1241

<210> 442
 <211> 1990
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (636)..(1202)

<400> 442
 cctcgtagac cactagtcca gtgtgggtgga atgactacca tgataaaaga attttcaagg 60

aactgaaatc	cagtgacaaa	aatgaaatcg	atcaaggctg	tagttgcaca	cctgagacat	120
tcctcgagaa	ggcagaggag	aaaggtgtga	aaaacagtga	accagagaag	gatggccagg	180
gacaacaaag	attggagctc	ggaagttgaa	tgacagatat	tctggagaaa	cacaccagag	240
atgacaaaag	ggtttgtcaa	acacagccca	actcaactgg	agtcttgaga	aggtgaccag	300
accaggatgg	aggcccaggg	aactcaccag	aagtccocat	gcatcagaac	aaggtcgaag	360
catcctgacg	gagtctcgct	ctttcgcaag	gctggagtg	aatggcatga	tctcggtca	420
ctgcagcctc	cgctcctgg	gttcaagtga	ttctttctgc	tcagcctccc	gagtagctgg	480
gactacagaa	atgctggtaa	tttcagtcac	ttgctgatga	cttctgatgt	cccagcaaat	540
gttggcattg	ttgactgctg	agaagatact	tctgaggacc	cacgtctaag	gtggacttgg	600
ttcgactct	tctggttagt	ccctgaacag	gagtg	atg cct cca ggc agg tgg		653

cat gct gcc tat cca gct cag gcc cag tct tcg agg gag cga ggg cgg 701
His Ala Ala Tyr Pro Ala Gln Ala Gln Ser Ser Arg Glu Arg Gly Arg
7 12 17 22

ctt cag aca gta aag aag gaa gaa gag gat gaa agc tat act cca gtg 749
Leu Gln Thr Val Lys Lys Glu Glu Glu Asp Glu Ser Tyr Thr Pro Val
23 28 33 38

cag gct gcc agg cca cag act ctc aac cgc cct ggc cag gag ctg ttc 797
Gln Ala Ala Arg Pro Gln Thr Leu Asn Arg Pro Gly Gln Glu Leu Phe
39 44 49 54

cgc cag ctc ttc aga cag ctt cgc tac cat gag tct tca ggg ccc cta 845
Arg Gln Leu Phe Arg Gln Leu Arg Tyr His Glu Ser Ser Gly Pro Leu
55 60 65 70

gaa act ctg agc cgg ctc cgg gaa ctc tgt cgc tgg tgg ctg agg cct 893
Glu Thr Leu Ser Arg Leu Arg Glu Leu Cys Arg Trp Trp Leu Arg Pro
71 76 81 86

gac gtt ctc tcc aag gca cag atc cta gag ctg ctg gtg ctg gaa cag 941
Asp Val Leu Ser Lys Ala Gln Ile Leu Glu Leu Leu Val Leu Glu Gln
87 92 97 102

ttc	ctg	agc	atc	ctg	cct	ggg	gag	ctc	cgg	gtt	tgg	gtg	cag	ctt	cat	989
Phe	Leu	Ser	Ile	Leu	Pro	Gly	Glu	Leu	Arg	Val	Trp	Val	Gln	Leu	His	
103					108					113					118	

aac cct gag agt ggc gag gag gct gtg gcc ttg ctg gag gag ctg cag 1037
Asn Pro Glu Ser Gly Glu Glu Ala Val Ala Leu Leu Glu Glu Leu Gln
119 124 129 134

agg gac ctt gat ggg aca tcc tgg agg gac ccg ggc cct gcc cag agc 1085
Arg Asp Leu Asp Gly Thr Ser Trp Arg Asp Pro Gly Pro Ala Gln Ser
135 140 145 150

cca gat gtg cat tgg atg ggt aca gga gcc tgc gat ctg cac aga tat	1133
Pro Asp Val His Trp Met Gly Thr Gly Ala Cys Asp Leu His Arg Tyr	
151 156 161 166	
ggt ccc ttg ctt cac ctc tca gga gca gct ctg ctc tgg ggg acc acc	1181
Gly Pro Leu Leu His Leu Ser Gly Ala Ala Leu Leu Trp Gly Thr Thr	
167 172 177 182	
tgg agc ctc cct atg aaa tag aa gcacgtgact tcotggctgg gcaatccgat	1234
Trp Ser Leu Pro Met Lys *	
183 188	
actcctgctg cccagatgcc tgcccttttc ccgagagagg ggtgcccggg agaccaggta	1294
acaccaacca ggtccctgac agcccagctc caggagacca tgactttcaa ggatgtggag	1354
gtgaccttct cccaggacga gtgggggtgg ctggactctg ctcagaggaa cctgtacagg	1414
gatgtgatgc tggagaatta taggaacatg gcttccctgg tgggaccatt caccaaact	1474
gctctgatct cctggttgga agcaaggag ccatggggcc tgaacatgca ggcagctcag	1534
cctaagggga atccagttgc tgctcctaca ggagatgacc tccagggtaa aacaaacaaa	1594
ttcatcttaa atcaggaacc tttggaagaa gcagaaacct tagctgtgtc atcaggatgt	1654
cctgcgacaa gtgtttctga ggggaattgat cgatcgatcc tcagagaatc ttttcaacag	1714
aatcagagca gggacaagat gagggacctc agggagggac agatggagcc cccaagtct	1774
gaactcatag gctggggagg aggagaaact tctaggtggg ttcgaggggg tgcgagccca	1834
cctccagccc tcagccctct tttccgcata acttggtcag ggcacaagga cttgaaggac	1894
ttgaaagtca gggggttgag aggactggag ggcctcgag tcaatgtctg ggaaacagag	1954
gctaaccagg cagcctccac ccctggaccc ccagcc	1990

<210> 443
 <211> 2146
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (690)..(1214)

<220>
 <221> misc_feature
 <222> (1)...(2146)
 <223> n = a,t,c or g

<400> 443

cggaattccc nnacgacgat ttcgtgtgcg agaaggggcg taactgattt ggaaaccaga	60
ggaaaggcgc tgttttcacc gaattagaat cgcgggaaaa tagagaagag tttgtttgaa	120
ggtctcgcga gatcgagtga gtacggctcg ccaagttgga gcgctctcgc gatagacaca	180
gcaactattc agctgcgagg ggacgggaga ggtggtgagc actctcgcga gatttgaagg	240
agcggcggag gccagagggg ggagaggacc ggaagtccct catctcaagc atccaatgct	300
gaaagcggcc tgattttctc taccggaagc ccttttccag aggctgggaa cacggcccac	360
ctagcaggaa gtcccacctc cttgagctcc gccacccttc ccgaagtttt tctgtcacct	420
gtgttaggct ccgtcccctt tccgcgtttt atccccgtac cagaaaagga tacatttagt	480
gcctcccacc cagctccact aaacgggttg gatatctcat tctttgagtt ggtgttcctt	540
ccccggcgcc cccatgtagc tgggaagtgg gacctggggg tggttggacc cctgggatcc	600
taaaggaggg gcagggaggg cgcagaactc cgcttctgct ccttgctacc aggacgcgcg	660
gcctcctcag cctctttcct cccgctgcc atg cac cct gca gcc ttc ccg ctt	713
Met His Pro Ala Ala Phe Pro Leu	
1 5	
cct gtg gtt gtg gcc gct gtg ctg tgg gga gcg gcc ccg acc cgg ggg	761
Pro Val Val Val Ala Ala Val Leu Trp Gly Ala Ala Pro Thr Arg Gly	
9 14 19 24	
ctc att cga gcg acc tcg gac cac aat gcc agc atg gac ttt gca gac	809
Leu Ile Arg Ala Thr Ser Asp His Asn Ala Ser Met Asp Phe Ala Asp	
25 30 35 40	
ctt cca gct ctg ttt ggg gct acc ttg agc cag gag ggc ctc cag ggg	857
Leu Pro Ala Leu Phe Gly Ala Thr Leu Ser Gln Glu Gly Leu Gln Gly	
41 46 51 56	
ttc ctt gtg gag gct cac cca gac aat gcc tgc agc ccc att gcc cca	905
Phe Leu Val Glu Ala His Pro Asp Asn Ala Cys Ser Pro Ile Ala Pro	
57 62 67 72	
cca ccc cca gcc ccg gtc aat ggg tca gtc ttt att gcg ctg ctt cga	953
Pro Pro Pro Ala Pro Val Asn Gly Ser Val Phe Ile Ala Leu Leu Arg	
73 78 83 88	
aga ttc gac tgc aac ttt gac ctc aag gtc cta aat gcc cag aag gct	1001
Arg Phe Asp Cys Asn Phe Asp Leu Lys Val Leu Asn Ala Gln Lys Ala	
89 94 99 104	
gga tat ggt gcc gct gta gta cac aat gtg aat tgc aat gaa ctt ctg	1049
Gly Tyr Gly Ala Ala Val Val His Asn Val Asn Cys Asn Glu Leu Leu	
105 110 115 120	
aac atg gtg tgg aat agt ggt aag gct ggg gga atc tat aca gct ggg	1097
Asn Met Val Trp Asn Ser Gly Lys Ala Gly Gly Ile Tyr Thr Ala Gly	
121 126 131 136	

ctt tca gta gga ccc aaa gat ggt ggg aag gct gaa ggc ctc agg aaa	1145
Leu Ser Val Gly Pro Lys Asp Gly Gly Lys Ala Glu Gly Leu Arg Lys	
137 142 147 152	
aga agc caa tcc ttt agg tgg ggt ggg gcc aaa gtg caa gat gcc agg	1193
Arg Ser Gln Ser Phe Arg Trp Gly Gly Ala Lys Val Gln Asp Ala Arg	
153 158 163 168	
gtt ccc aga gga ttt gag tag aa ggttgtgagt cccagagta acaccttgat	1246
Val Pro Arg Gly Phe Glu *	
169 174	
ccctgcagag gaaatccagc agcagatctg gatcccgctct gtattttattg gggagagaag	1306
ctccgagtag ctgcgtgccc tctttgtcta cgagaagggg gctcgggtgc ttctggttcc	1366
agacaatacc ttccccttgg gctattacct catccctttc acagggattg tgggactgct	1426
ggttttggcc atgggagcag taatgatagc tcgttgtatc cagcaccgga aacggctcca	1486
gcggaatcga cttaccaaag agcaactgaa acagattcct acacatgact atcagaaggg	1546
agaccagtat gatgtctgtg ccatttgctt ggatgaatat gaggatgggg acaagctgcg	1606
ggtactcccc tgtgtcatg cctaccacag ccgctgcgtg gacccctggc tctactcagac	1666
ccggaagacc tgccccattt gcaagcagcc tgttcatcgg ggtcctgggg acgaagacca	1726
agaggaagaa actcaagggc aagaggaggg tgatgaaggg gagccaaggg accaccctgc	1786
ctcagaaagg accccacttt tgggttctag cccactcctt cccacctcct ttggttcctt	1846
agccccagct ccccttgttt ttcttgggcc ttcaacagat cccccactgt cccctccctc	1906
ttcccctggt atcctggtct aataaccccc cacacatata cctctggtga cctatttgca	1966
cagaccgtcg tcttccctcc agtcttctga gggatagggg acattccatc ccaagcttct	2026
cccttaccga cactatcct tttgaggggc tttgggggtg ggctggggca agcagagggg	2086
ctgggtcttc acttcttggg ctaataaaat tgtttctttg tggactaaaa aaaaaaaaaa	2146

<210> 444
 <211> 787
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (30) .. (659)

<400> 444	
taagcttgcg gccgcaccca cttcagata atg aca aag caa ggg aag gag aca	53

Met Thr Lys Gln Gly Lys Glu Thr
1 5

aac aaa gag aag gaa caa ttt agg gga caa gaa gag aaa ggg gag aac	101
Asn Lys Glu Lys Glu Gln Phe Arg Gly Gln Glu Glu Lys Gly Glu Asn	
9 14 19 24	
aag gac agc acc ttg aca agg acc ccg ctc gag ccg ctg gag aaa aac	149
Lys Asp Ser Thr Leu Thr Arg Thr Pro Leu Glu Pro Leu Glu Lys Asn	
25 30 35 40	
aag caa atc cta gtg ctg ggc ctg gat gga gca gga aaa acc agt gtc	197
Lys Gln Ile Leu Val Leu Gly Leu Asp Gly Ala Gly Lys Thr Ser Val	
41 46 51 56	
ctg cac tct cta gct tca aac aga gtc cag cac agt gtg gca ccc acc	245
Leu His Ser Leu Ala Ser Asn Arg Val Gln His Ser Val Ala Pro Thr	
57 62 67 72	
caa ggt ttc cat gca gtt tgc atc aac act gaa gac agc cag atg gag	293
Gln Gly Phe His Ala Val Cys Ile Asn Thr Glu Asp Ser Gln Met Glu	
73 78 83 88	
ttc ctg gag att ggt ggc agt aaa cct ttt cgg tcc tac tgg gaa atg	341
Phe Leu Glu Ile Gly Gly Ser Lys Pro Phe Arg Ser Tyr Trp Glu Met	
89 94 99 104	
tac cta tcc aag gga ttg ctg ctg atc ttt gtg gtg gat tca gca gat	389
Tyr Leu Ser Lys Gly Leu Leu Leu Ile Phe Val Val Asp Ser Ala Asp	
105 110 115 120	
cac agc cga tta cct gaa gcc aag aaa tac ctt cat cag cta att gca	437
His Ser Arg Leu Pro Glu Ala Lys Lys Tyr Leu His Gln Leu Ile Ala	
121 126 131 136	
gca aac cca gta ctt cct ctg gtt gtg ttt gca aac aaa cag gat ctt	485
Ala Asn Pro Val Leu Pro Leu Val Val Phe Ala Asn Lys Gln Asp Leu	
137 142 147 152	
gaa gca gcc tat cac att aca gat atc cat gaa gct ttg gca tta tct	533
Glu Ala Ala Tyr His Ile Thr Asp Ile His Glu Ala Leu Ala Leu Ser	
153 158 163 168	
gaa gtg gga aat gac agg aag atg ttc ttg ttt gga acc tac ctg act	581
Glu Val Gly Asn Asp Arg Lys Met Phe Leu Phe Gly Thr Tyr Leu Thr	
169 174 179 184	
aag aat ggc tca gag ata ccc tcc acc atg caa gat gcc aaa gac ttg	629
Lys Asn Gly Ser Glu Ile Pro Ser Thr Met Gln Asp Ala Lys Asp Leu	
185 190 195 200	
att gca cag ctg gct gca gat gtg cag tga c caggactcag cccactgtgc	680
Ile Ala Gln Leu Ala Ala Asp Val Gln *	
201 206	
ggctcacgac tgagatgtca tcagtgttga atggcaggct tgaagccaaa gggtttccacc	740

tcaaataaaa attaagccat ttcctattaa aaaaaaaaaa aaaaaaa

787

<210> 445
<211> 1635
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (327)..(986)

<220>
<221> misc_feature
<222> (1)...(1635)
<223> n = a,t,c or g

<400> 445
ccccccccca tagaatacat tgcataccnc gagagcagga antccctca caacacatgt 60
catgacaaaa gacacacata caagctccaa aggcttttgt caggtaattc ttcctccagg 120
accccatctg gccctccct catccctccc cttggacttt gcccttctta ctggccaggc 180
agggggggcca gagtccaggc ttgactcatt cccaccttgt cctgggctga gatcccaggt 240
ttgtaacaga aaacaccact aaagccccag cacaggagag aaccacccag cccagaagtt 300
ccaggaagg aactctccgg tccacc atg gag tac ctc tca gct ctg aac ccc 353
Met Glu Tyr Leu Ser Ala Leu Asn Pro
1 5
agt gac tta ctc agg tca gta tct aat ata agc tcg gag ttt gga cgg 401
Ser Asp Leu Leu Arg Ser Val Ser Asn Ile Ser Ser Glu Phe Gly Arg
10 15 20 25
agg gtc tgg acc tca gct cca cca ccc cag cga cct ttc cgt gtc tgt 449
Arg Val Trp Thr Ser Ala Pro Pro Pro Gln Arg Pro Phe Arg Val Cys
26 31 36 41
gat cac aag cgg acc atc cgg aaa ggc ctg aca gct gcc acc cgc cag 497
Asp His Lys Arg Thr Ile Arg Lys Gly Leu Thr Ala Ala Thr Arg Gln
42 47 52 57
gag ctg cta gcc aaa gca ttg gag acc cta ctg ctg aat gga gtg cta 545
Glu Leu Leu Ala Lys Ala Leu Glu Thr Leu Leu Leu Asn Gly Val Leu
58 63 68 73
acc ctg gtg cta gag gag gat gga act gca gtg gac agt gag gac ttc 593
Thr Leu Val Leu Glu Glu Asp Gly Thr Ala Val Asp Ser Glu Asp Phe
74 79 84 89
ttc cag ctg ctg gag gat gac acg tgc ctg atg gtg ttg cag tct ggt 641
Phe Gln Leu Leu Glu Asp Asp Thr Cys Leu Met Val Leu Gln Ser Gly
90 95 100 105

cag agc tgg agc cct aca agg agt gga gtg ctg tca tat ggc ctg gga	689
Gln Ser Trp Ser Pro Thr Arg Ser Gly Val Leu Ser Tyr Gly Leu Gly	
106 111 116 121	
cgg gag agg ccc aag cac agc aag gac atc gcc cga ttc acc ttt gac	737
Arg Glu Arg Pro Lys His Ser Lys Asp Ile Ala Arg Phe Thr Phe Asp	
122 127 132 137	
gtg tac aag caa aac cct cga gac ctc ttt ggc agc ctg aat gtc aaa	785
Val Tyr Lys Gln Asn Pro Arg Asp Leu Phe Gly Ser Leu Asn Val Lys	
138 143 148 153	
gcc aca ttc tac ggg ctc tac tct atg agt tgt gac ttt caa gga ctt	833
Ala Thr Phe Tyr Gly Leu Tyr Ser Met Ser Cys Asp Phe Gln Gly Leu	
154 159 164 169	
ggc cca aag aaa gta ctc agg gag ctc ctt cgt tgg acc tcc aca ctg	881
Gly Pro Lys Lys Val Leu Arg Glu Leu Leu Arg Trp Thr Ser Thr Leu	
170 175 180 185	
ctg caa ggc ctg ggc cat atg ttg ctg gga att tcc tcc acc ctt cgt	929
Leu Gln Gly Leu Gly His Met Leu Leu Gly Ile Ser Ser Thr Leu Arg	
186 191 196 201	
cat gca gtg gag ggg gct gag cag tgg cag cag aag ggc cgc ctc cat	977
His Ala Val Glu Gly Ala Glu Gln Trp Gln Gln Lys Gly Arg Leu His	
202 207 212 217	
tcc tac taa ggggctc tgagcttctg cccccagaat cattccaacc gacccactgc	1033
Ser Tyr *	
218	
aaagactatg acagcatcaa atttcaggac ctgcagacag tacaggctag ataaccacc	1093
caatttcccc actgtcctct gatccccctcg tgacagaacc tttcagcata acgcctcaca	1153
tcccaagtct atacccttac ctgaagaatg ctgttctttc ctagccacct ttctagcctc	1213
ccacttgccc tgaaaggcca agatcaagat gtcccccagg catcttgatc ccagcctgac	1273
tgctgtctaca tctaatacccc taccaatgcc tctgtccct aaactoccca gcatactgat	1333
gacagccctc tctgacttta ccttgagatc tgtcttcata cccttcccct caaactaaca	1393
aaaacatttc caataaaaaat atcaaataatt taccacttaa gactttctgac tccaatttaa	1453
accaggaaag ggatgggggtg gataccocat tttgccctcc cccatcaaca cccagtccca	1513
gatccaaagc ctcagtcttc aagtatggag ttcaatgcnc gcctccgctt ggccaccgca	1573
ccctgctgct gttcccaagc ttctcgccgc tttaggaagg tagtcaaggc cacatttccg	1633
ac	1635

<210> 446
 <211> 1471
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (904) .. (1293)

<400> 446

caaagagacc cgggggacct ccacgtcttc ccagaggacc cgatccgctg atctgtggcg	60
ccctggcttg cggggagcaa gccaaaggcca agactttggc ctctccaata aaacctagtg	120
gctcttttgc ggcccatagc ctcaaagaca aaagatattt tggctaggcg agcttggtcc	180
tcccgctcagc acaggaagca ttcacgtctg gtcacactc tagcttcaga ctcaaaagtg	240
aacgattggc tggctgtgag ccgcaggacc ctgcggggag accaggggtgg tctctacact	300
gttgggtagc tagctggagg caaggcgctt gtataagaaa cagtccaagg accctgtcct	360
gggcaggcag aattccgcgg acaggctgtt gtttcgcata agcagcacgg gctgcggaga	420
cagaaacctc cctgagtagt acggtgtatt atatgagaac atccacttag catagcaacg	480
tctacggaca acccctgtag ctcttcttct ggattgtttt ctgtttcaaa ccatgttttc	540
ttatttcta cgagtttatg tgcttggaag cgagcgtggc cgtgaaaaac cgtaccgc	600
taaattcacc tgggtcccca aagactgagc cggtggcct cgttatttat gtgagcggct	660
atgtaaata ggattcggag attgctctat tgattggaga gagctggagg aggcgggtctc	720
tcttcacagag cgctagttgg gagcggagct tgctgtcat tggctgccag agccaatgga	780
aaggggctgc cgcgcggccg taaagagttt gtagaggcag ttccgggtgcg gtacgttgca	840
ttccggtacc ggacgccgag agcggtttgt ctccgtctct ggagttgtag gcgagaggtg	900
atc atg tcc ggt cgc ggg aaa cag ggc ggc aaa gtg cga gca aag gcc	948
Met Ser Gly Arg Gly Lys Gln Gly Gly Lys Val Arg Ala Lys Ala	
1 5 10	
aaa tcc cgc tcc tcc cgc gcg ggc ctg cag ttc ccg gtg ggc cga gtg	996
Lys Ser Arg Ser Ser Arg Ala Gly Leu Gln Phe Pro Val Gly Arg Val	
16 21 26 31	
cac aga ctg ctg cgc aaa ggg aac tac gcg gag cga gtg ggc gcc ggg	1044
His Arg Leu Leu Arg Lys Gly Asn Tyr Ala Glu Arg Val Gly Ala Gly	
32 37 42 47	
gcg ccg gtg tac ctg gcg gcg gtg ttg gag tac ctt acg gcg gag atc	1092
Ala Pro Val Tyr Leu Ala Ala Val Leu Glu Tyr Leu Thr Ala Glu Ile	
48 53 58 63	

ctg gag ctg gct ggc aac gcc gcg cgt gac aac aag aag acc agg ata	1140
Leu Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Thr Arg Ile	
64 69 74 79	
att ccc cgc cac ctg cag ctc gcc atc cgc aac gac gag gag tta aac	1188
Ile Pro Arg His Leu Gln Leu Ala Ile Arg Asn Asp Glu Glu Leu Asn	
80 85 90 95	
aag ctg ctg ggc aaa gtg acc atc gct cag ggc ggc gtc ctg ccc aac	1236
Lys Leu Leu Gly Lys Val Thr Ile Ala Gln Gly Gly Val Leu Pro Asn	
96 101 106 111	
atc cag gcc gtg ctg ctg ccc aag aag acg gag agt cag aag acg aag	1284
Ile Gln Ala Val Leu Leu Pro Lys Lys Thr Glu Ser Gln Lys Thr Lys	
112 117 122 127	
agc aaa tga ccctgac gccgccctca gggagctggc tccgccagca aaggcccttt	1340
Ser Lys *	
128	
tcattggtcgt cccgcaatgc ttttgaatgt gctggatgtc atggagggcc ggtgacatct	1400
agcggggagg tgggcggcga ggggtcccgcc gggagccaat aaagttggtg aaaatcgta	1460
aaaaaaaaa a	1471

<210> 447
 <211> 1662
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (152)..(1438)

<400> 447	
ttttgattgt aagctggtac gcctgcaggt accggtccgg tattcccggtg tcgacgattt	60
cgtcagggcg caggcgcgcg ggtcccgga gcccgtaga cgcccgctgc tgggcgcggtg	120
tagccgtctg aggtgccgga gctgcgggag g atg gag cgg ctg aag gtg gaa	172
Met Glu Pro Leu Lys Val Glu	
1 5	
aag ttc gca acc gcc aac agg gga aac ggg ctg cgc gcc gtg acc ccg	220
Lys Phe Ala Thr Ala Asn Arg Gly Asn Gly Leu Arg Ala Val Thr Pro	
8 13 18 23	
ctg cgc ccc gga gag cta ctc ttc cgc tgg gat ccc ttg gcg tac acg	268
Leu Arg Pro Gly Glu Leu Leu Phe Arg Ser Asp Pro Leu Ala Tyr Thr	
24 29 34 39	
gtg tgc aag ggg agt cgt gcc gtc gtc tgc gac cgc tgc ctt ctc ggg	316
Val Cys Lys Gly Ser Arg Gly Val Val Cys Asp Arg Cys Leu Leu Gly	

40	45	50	55	
aag gaa aag ctg atg cga tgc tct cag tgc cgc gtc gcc aaa tac tgt				364
Lys Glu Lys Leu Met Arg Cys Ser Gln Cys Arg Val Ala Lys Tyr Cys				
56	61	66	71	
agt gct aag tgt cag aaa aaa gct tgg cca gac cac aag cgg gaa tgc				412
Ser Ala Lys Cys Gln Lys Lys Ala Trp Pro Asp His Lys Arg Glu Cys				
72	77	82	87	
aaa tgc ctt aaa agc tgc aaa ccc aga tat cct cca gac tcc gtt cga				460
Lys Cys Leu Lys Ser Cys Lys Pro Arg Tyr Pro Pro Asp Ser Val Arg				
88	93	98	103	
ctt ctt ggc aga gtt gtc ttc aaa ctt atg gat gga gca cct tca gaa				508
Leu Leu Gly Arg Val Val Phe Lys Leu Met Asp Gly Ala Pro Ser Glu				
104	109	114	119	
tca gag aag ctt tac tca ttt tat gat ctg gag tca aat att aac aaa				556
Ser Glu Lys Leu Tyr Ser Phe Tyr Asp Leu Glu Ser Asn Ile Asn Lys				
120	125	130	135	
ctg act gaa gat aag aaa gag ggc ctc agg caa ctc gta atg aca ttt				604
Leu Thr Glu Asp Lys Lys Glu Gly Leu Arg Gln Leu Val Met Thr Phe				
136	141	146	151	
caa cat ttc atg aga gaa gaa ata cag gat gcc tct cag ctg cca cct				652
Gln His Phe Met Arg Glu Glu Ile Gln Asp Ala Ser Gln Leu Pro Pro				
152	157	162	167	
gcc ttt gac ctt ttt gaa gcc ttt gca aaa gtg atc tgc aac tct ttc				700
Ala Phe Asp Leu Phe Glu Ala Phe Ala Lys Val Ile Cys Asn Ser Phe				
168	173	178	183	
acc atc tgt aat gcg gag atg cag gaa gtt ggt gtt ggc cta tat ccc				748
Thr Ile Cys Asn Ala Glu Met Gln Glu Val Gly Val Gly Leu Tyr Pro				
184	189	194	199	
agt atc tct ttg ctc aat cac agc tgt gac ccc aac tgt tgc att gtg				796
Ser Ile Ser Leu Leu Asn His Ser Cys Asp Pro Asn Cys Ser Ile Val				
200	205	210	215	
ttc aat ggg ccc cac ctc tta ctg cga gca gtc cga gac atc gag gtg				844
Phe Asn Gly Pro His Leu Leu Leu Arg Ala Val Arg Asp Ile Glu Val				
216	221	226	231	
gga gag gag ctc acc atc tgc tac ctg gat atg ctg atg acc agt gag				892
Gly Glu Glu Leu Thr Ile Cys Tyr Leu Asp Met Leu Met Thr Ser Glu				
232	237	242	247	
gag cgc cgg aag cag ctg agg gac cag tac tgc ttt gaa tgt gac tgt				940
Glu Arg Arg Lys Gln Leu Arg Asp Gln Tyr Cys Phe Glu Cys Asp Cys				
248	253	258	263	
ttc cgt tgc caa acc cag gac aag gat gct gat atg cta act ggt gat				988
Phe Arg Cys Gln Thr Gln Asp Lys Asp Ala Asp Met Leu Thr Gly Asp				
264	269	274	279	

gag caa gta tgg aag gaa gtt caa gaa tcc ctg aaa aaa att gaa gaa	1036
Glu Gln Val Trp Lys Glu Val Gln Glu Ser Leu Lys Lys Ile Glu Glu	
280 285 290 295	
ctg aag gca cac tgg aag tgg gag cag gtt ctg gcc atg tgc cag gcg	1084
Leu Lys Ala His Trp Lys Trp Glu Gln Val Leu Ala Met Cys Gln Ala	
296 301 306 311	
atc ata agc agc aat tct gaa cgg ctt ccc gat atc aac atc tac cag	1132
Ile Ile Ser Ser Asn Ser Glu Arg Leu Pro Asp Ile Asn Ile Tyr Gln	
312 317 322 327	
ctg aag gtg ctc gac tgc gcc atg gat gcc tgc atc aac ctc ggc ctg	1180
Leu Lys Val Leu Asp Cys Ala Met Asp Ala Cys Ile Asn Leu Gly Leu	
328 333 338 343	
ttg gag gaa gcc ttg ttc tat ggt act cgg acc atg gag cca tac agg	1228
Leu Glu Glu Ala Leu Phe Tyr Gly Thr Arg Thr Met Glu Pro Tyr Arg	
344 349 354 359	
att ttt ttc cca gga agc cat ccc gtc aga ggg gtt caa gtg atg aaa	1276
Ile Phe Phe Pro Gly Ser His Pro Val Arg Gly Val Gln Val Met Lys	
360 365 370 375	
gtt ggc aaa ctg cag cta cat caa ggc atg ttt ccc caa gca atg aag	1324
Val Gly Lys Leu Gln Leu His Gln Gly Met Phe Pro Gln Ala Met Lys	
376 381 386 391	
aat ctg aga ctg gct ttt gat att atg aga gtg aca cat ggc aga gaa	1372
Asn Leu Arg Leu Ala Phe Asp Ile Met Arg Val Thr His Gly Arg Glu	
392 397 402 407	
cac agc ctg att gaa gat ttg att cta ctt tta gaa gaa tgc gac gcc	1420
His Ser Leu Ile Glu Asp Leu Ile Leu Leu Glu Glu Cys Asp Ala	
408 413 418 423	
aac atc aga gca tcc taa gggaac gcagtcagag ggaaatacgg cgtgtgtctt	1474
Asn Ile Arg Ala Ser *	
424 429	
tggtgaatgc cttattgagg tcacacactc tatgctttgt tagctgtgtg aacctctcct	1534
attggaaatt ctgttccgtg tttgtgtagg taaataaagg cagacatggt ttgcaaacca	1594
caagaatcat tagttgtaga gaagcacgat tataataaat tcaaaacatt tggttgaaaa	1654
aaaaaaaa	1662

<210> 448
 <211> 2464
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (20) .. (2320)

<400> 448

agaattcggc acgaggaaa atg gcg gac gga gga gca gcg agt caa gat gag	52
Met Ala Asp Gly Gly Ala Ala Ser Gln Asp Glu	
1 5	
agt tca gcc gcg gcg gca gca gca gca gac tca aga atg aac aat ccg	100
Ser Ser Ala Ala Ala Ala Ala Ala Asp Ser Arg Met Asn Asn Pro	
12 17 22 27	
tca gaa acc agt aaa cca tct atg gag agt gga gat ggc aac aca ggc	148
Ser Glu Thr Ser Lys Pro Ser Met Glu Ser Gly Asp Gly Asn Thr Gly	
28 33 38 43	
aca caa acc aat ggt ctg gac ttt cag aag cag cct gtg cct gta gga	196
Thr Gln Thr Asn Gly Leu Asp Phe Gln Lys Gln Pro Val Pro Val Gly	
44 49 54 59	
gga gca atc tca aca gcc cag gcg cag gct ttc ctt gga cat ctc cat	244
Gly Ala Ile Ser Thr Ala Gln Ala Gln Ala Phe Leu Gly His Leu His	
60 65 70 75	
cag gtc caa ctc gct gga aca agt tta cag gct gct gct cag tct tta	292
Gln Val Gln Leu Ala Gly Thr Ser Leu Gln Ala Ala Ala Gln Ser Leu	
76 81 86 91	
aat gta cag tct aaa tct aat gaa gaa tcg ggg gat tcg cag cag cca	340
Asn Val Gln Ser Lys Ser Asn Glu Glu Ser Gly Asp Ser Gln Gln Pro	
92 97 102 107	
agc cag cct tcc cag cag cct tca gtg cag gca gcc att ccc cag acc	388
Ser Gln Pro Ser Gln Gln Pro Ser Val Gln Ala Ala Ile Pro Gln Thr	
108 113 118 123	
cag ctt atg cta gct gga gga cag ata act ggg ctt act ttg acg cct	436
Gln Leu Met Leu Ala Gly Gly Gln Ile Thr Gly Leu Thr Leu Thr Pro	
124 129 134 139	
gcc cag caa cag tta cta ctc cag cag gca cag gca cag gca cag ctg	484
Ala Gln Gln Gln Leu Leu Leu Gln Gln Ala Gln Ala Gln Ala Gln Leu	
140 145 150 155	
ctg gct gct gca gtg cag cag cac tcc gcc agc cag cag cac agt gct	532
Leu Ala Ala Ala Val Gln Gln His Ser Ala Ser Gln Gln His Ser Ala	
156 161 166 171	
gct gga gcc acc atc tcc gcc tct gct gcc acg ccc atg acg cag atc	580
Ala Gly Ala Thr Ile Ser Ala Ser Ala Ala Thr Pro Met Thr Gln Ile	
172 177 182 187	
ccc ctg tct cag ccc ata cag atc gca cag gat ctt caa caa ctg caa	628
Pro Leu Ser Gln Pro Ile Gln Ile Ala Gln Asp Leu Gln Gln Leu Gln	
188 193 198 203	

cag ctt caa cag cag aat ctc aac ctg caa cag ttt gtg ttg gtg cat	676
Gln Leu Gln Gln Gln Asn Leu Asn Leu Gln Gln Phe Val Leu Val His	
204 209 214 219	
cca acc acc aat ttg cag cca gcg cag ttt atc atc tca cag acg ccc	724
Pro Thr Thr Asn Leu Gln Pro Ala Gln Phe Ile Ile Ser Gln Thr Pro	
220 225 230 235	
cag ggc cag cag ggt ctc ctg caa gcg caa aat ctt caa acg caa cta	772
Gln Gly Gln Gln Gly Leu Leu Gln Ala Gln Asn Leu Gln Thr Gln Leu	
236 241 246 251	
cct cag caa agc caa gcc aac ctc cta cag tcg cag cca agc atc acc	820
Pro Gln Gln Ser Gln Ala Asn Leu Leu Gln Ser Gln Pro Ser Ile Thr	
252 257 262 267	
ctc acc tcc cag cca gca acc cca aca cgc aca ata gca gca acc cca	868
Leu Thr Ser Gln Pro Ala Thr Pro Thr Arg Thr Ile Ala Ala Thr Pro	
268 273 278 283	
att cag aca ctt cca cag agc cag tca aca cca aag cga att gat act	916
Ile Gln Thr Leu Pro Gln Ser Gln Ser Thr Pro Lys Arg Ile Asp Thr	
284 289 294 299	
ccc agc ttg gag gag ccc agt gac ctt gag gag ctt gag cag ttt gcc	964
Pro Ser Leu Glu Glu Pro Ser Asp Leu Glu Glu Leu Glu Gln Phe Ala	
300 305 310 315	
aag acc ttc aaa caa aga cga atc aaa ctt gga ttc act cag ggt gat	1012
Lys Thr Phe Lys Gln Arg Arg Ile Lys Leu Gly Phe Thr Gln Gly Asp	
316 321 326 331	
gtt ggg ctc gct atg ggg aaa cta tat gga aat gac ttc agc caa act	1060
Val Gly Leu Ala Met Gly Lys Leu Tyr Gly Asn Asp Phe Ser Gln Thr	
332 337 342 347	
acc atc tct cga ttt gaa gcc ttg aac ctc agc ttt aag aac atg tgc	1108
Thr Ile Ser Arg Phe Glu Ala Leu Asn Leu Ser Phe Lys Asn Met Cys	
348 353 358 363	
aag ttg aag cca ctt tta gag aag tgg cta aat gat gca gag aac ctc	1156
Lys Leu Lys Pro Leu Leu Glu Lys Trp Leu Asn Asp Ala Glu Asn Leu	
364 369 374 379	
tca tct gat tcg tcc ctc tcc agc cca agt gcc ctg aat tct cca gga	1204
Ser Ser Asp Ser Ser Leu Ser Ser Pro Ser Ala Leu Asn Ser Pro Gly	
380 385 390 395	
att gag ggc ttg agc cgt agg agg aag aaa cgc acc agc ata gag acc	1252
Ile Glu Gly Leu Ser Arg Arg Arg Lys Lys Arg Thr Ser Ile Glu Thr	
396 401 406 411	
aac atc cgt gtg gcc tta gag aag agt ttc ttg gag aat caa aag cct	1300
Asn Ile Arg Val Ala Leu Glu Lys Ser Phe Leu Glu Asn Gln Lys Pro	
412 417 422 427	
acc tcg gaa gag atc act atg att gct gat cag ctc aat atg gaa aaa	1348

Thr Ser Glu Glu Ile Thr Met Ile Ala Asp Gln Leu Asn Met Glu Lys	
428 433 438 443	
gag gtg att cgt gtt tgg ttc tgt aac cgc cgc cag aaa gaa aaa aga	1396
Glu Val Ile Arg Val Trp Phe Cys Asn Arg Arg Gln Lys Glu Lys Arg	
444 449 454 459	
atc aac cca cca agc agt ggt ggg acc agc agc tca cct att aaa gca	1444
Ile Asn Pro Pro Ser Ser Gly Gly Thr Ser Ser Ser Pro Ile Lys Ala	
460 465 470 475	
att ttc ccc agc cca act tca ctg gtg gcg acc aca cca agc ctt gtg	1492
Ile Phe Pro Ser Pro Thr Ser Leu Val Ala Thr Thr Pro Ser Leu Val	
476 481 486 491	
act agc agt gca gca act acc ctc aca gtc agc cct gtc ctc cct ctg	1540
Thr Ser Ser Ala Ala Thr Thr Leu Thr Val Ser Pro Val Leu Pro Leu	
492 497 502 507	
acc agt gct gct gtg acg aat ctt tca gtt aca ggc act tca gac acc	1588
Thr Ser Ala Ala Val Thr Asn Leu Ser Val Thr Gly Thr Ser Asp Thr	
508 513 518 523	
acc tcc aac aac aca gca acc gtg att tcc aca gcg cct cca gct tcc	1636
Thr Ser Asn Asn Thr Ala Thr Val Ile Ser Thr Ala Pro Pro Ala Ser	
524 529 534 539	
tca gca gtc acg tcc ccc tct ctg agt ccc tcc cct tct gcc tca gcc	1684
Ser Ala Val Thr Ser Pro Ser Leu Ser Pro Ser Pro Ser Ala Ser Ala	
540 545 550 555	
tcc acc tcc gag gca tcc agt gcc agt gag acc agc aca aca cag acc	1732
Ser Thr Ser Glu Ala Ser Ser Ala Ser Glu Thr Ser Thr Thr Gln Thr	
556 561 566 571	
acc tcc act cct ttg tcc tcc cct ctt ggg acc agc cag gtg atg gtg	1780
Thr Ser Thr Pro Leu Ser Ser Pro Leu Gly Thr Ser Gln Val Met Val	
572 577 582 587	
aca gca tca ggt ttg caa aca gca gca gct gct gcc ctt caa gga gct	1828
Thr Ala Ser Gly Leu Gln Thr Ala Ala Ala Ala Ala Leu Gln Gly Ala	
588 593 598 603	
gca cag ttg cca gca aat gcc agt ctt gct gcc atg gca gct gct gca	1876
Ala Gln Leu Pro Ala Asn Ala Ser Leu Ala Ala Met Ala Ala Ala Ala	
604 609 614 619	
gga cta aac cca agc ctg atg gca ccc tca cag ttt gcg gct gga ggt	1924
Gly Leu Asn Pro Ser Leu Met Ala Pro Ser Gln Phe Ala Ala Gly Gly	
620 625 630 635	
gcc tta ctc agt ctg aat cca ggg acc ctg agc ggt gct ctc agc cca	1972
Ala Leu Leu Ser Leu Asn Pro Gly Thr Leu Ser Gly Ala Leu Ser Pro	
636 641 646 651	
gct cta atg agc aac agt aca ctg gca act att caa gct ctt gct tct	2020
Ala Leu Met Ser Asn Ser Thr Leu Ala Thr Ile Gln Ala Leu Ala Ser	

652	657	662	667	
ggg ggc tct ctt cca ata aca tca ctt gat gca act ggg aac ctg gta				2068
Gly Gly Ser Leu Pro Ile Thr Ser Leu Asp Ala Thr Gly Asn Leu Val				
668	673	678	683	
ttt gcc aat gcg gga gga gcc ccc aac atc gtg act gcc cct ctg ttc				2116
Phe Ala Asn Ala Gly Gly Ala Pro Asn Ile Val Thr Ala Pro Leu Phe				
684	689	694	699	
ctg aac cct cag aac ctc tct ctg ctc acc agc aac cct gtt agc ttg				2164
Leu Asn Pro Gln Asn Leu Ser Leu Leu Thr Ser Asn Pro Val Ser Leu				
700	705	710	715	
gtc tct gcc gcc gca gca tct gca ggg aac tct gca cct gta gcc agc				2212
Val Ser Ala Ala Ala Ala Ser Ala Gly Asn Ser Ala Pro Val Ala Ser				
716	721	726	731	
ctt cac gcc acc tcc acc tct gct gag tcc atc cag aac tct ctc ttc				2260
Leu His Ala Thr Ser Thr Ser Ala Glu Ser Ile Gln Asn Ser Leu Phe				
732	737	742	747	
aca gtg gcc tct gcc agc ggg gct gcg tcc acc acc acc acc gcc tcc				2308
Thr Val Ala Ser Ala Ser Gly Ala Ala Ser Thr Thr Thr Thr Ala Ser				
748	753	758	763	
aag gca cag tga gct gggcagagct gggctgccag aagccttttt cactctgcag				2363
Lys Ala Gln *				
764				
tgtgattgga ctgccagcca ggtaataaaa ctgaaaaatg tgattggcctt cctctcgccg				2423
tggtgtgagg gcaaaggaga gaagggagaa aaaaaaaaaa a				2464

<210> 449
 <211> 3382
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (341)..(3238)

<400> 449	
atttgccct cgaggccaag aattcggcac gagcggcacg agtgcctttt atgacataga	60
catttttgaa gcgtgctggc cattttatttc ctatgatgtt tcttgattgg agttacatga	120
tatttctca tgattaggtt atgctttttg gccagaatat ctgaggagg atgctgtgtc	180
cctctcgggg ttttaacttt tctttctca cacctagatc aagtactttg tgggtgcagaa	240
cccgctctct tggccggtct ccttgagct cctgcctctc tccttgtaacc cttaaaccga	300

agccctagtg cacctgctcc acagatgggt tggcactgat	atg cag atg att aat	355
	Met Gln Met Ile Asn	
	1	
ttc aca act ggt gaa ttc cag ctc acc gaa gct tgc cct tac ctg ggt		403
Phe Thr Thr Gly Glu Phe Gln Leu Thr Glu Ala Cys Pro Tyr Leu Gly		
6 11 16 21		
acg cat tct gag gaa tcc agg ttt ggc atc ctc cac tta cat ctg cag		451
Thr His Ser Glu Glu Ser Arg Phe Gly Ile Leu His Leu His Leu Gln		
22 27 32 37		
cct ttg gaa atg aaa agg gtt ggc gta gtt ttc aca cct gct gac tat		499
Pro Leu Glu Met Lys Arg Val Gly Val Val Phe Thr Pro Ala Asp Tyr		
38 43 48 53		
gga aaa gtt acc tca ctc ata cta atc cgg aat aac ttg act gtt att		547
Gly Lys Val Thr Ser Leu Ile Leu Ile Arg Asn Asn Leu Thr Val Ile		
54 59 64 69		
gac atg att ggc gtg gaa gga ttt gga gca aga gag tta tta aaa gtg		595
Asp Met Ile Gly Val Glu Gly Phe Gly Ala Arg Glu Leu Leu Lys Val		
70 75 80 85		
ggt gga aga ctt cct ggt gca gga ggc tca ctc cga ttt aag gtg ccc		643
Gly Gly Arg Leu Pro Gly Ala Gly Gly Ser Leu Arg Phe Lys Val Pro		
86 91 96 101		
gag tcc acg ctg atg gac tgc cgt aga caa ctg aaa gac agt aag caa		691
Glu Ser Thr Leu Met Asp Cys Arg Arg Gln Leu Lys Asp Ser Lys Gln		
102 107 112 117		
att tta tct att aca aag aac ttt aaa gtt gag aat att gga cct ctt		739
Ile Leu Ser Ile Thr Lys Asn Phe Lys Val Glu Asn Ile Gly Pro Leu		
118 123 128 133		
cct ata act gtt tgc tct ctg aaa att aat ggg tat aac tgc caa ggt		787
Pro Ile Thr Val Ser Ser Leu Lys Ile Asn Gly Tyr Asn Cys Gln Gly		
134 139 144 149		
tat gga ttc gag gtg ctg gat tgt cat cag ttt tcc ctg gac cca aac		835
Tyr Gly Phe Glu Val Leu Asp Cys His Gln Phe Ser Leu Asp Pro Asn		
150 155 160 165		
aca tcc cgc gat atc agc att gtg ttc act cca gac ttt acc tcc tcc		883
Thr Ser Arg Asp Ile Ser Ile Val Phe Thr Pro Asp Phe Thr Ser Ser		
166 171 176 181		
tgg gta att cgg gac cta agt ctt gta acc gca ggc gac cta gaa ttt		931
Trp Val Ile Arg Asp Leu Ser Leu Val Thr Ala Ala Asp Leu Glu Phe		
182 187 192 197		
cgc ttc act ctc aat gtg act ctc cct cat cac ctg ttg ccc ttg tgt		979
Arg Phe Thr Leu Asn Val Thr Leu Pro His His Leu Leu Pro Leu Cys		
198 203 208 213		
gca gac gtg gtt cca gga ccc agc tgg gag gag tca ttt tgg agg ctc		1027

Ala Asp Val Val Pro Gly Pro Ser Trp Glu Glu Ser Phe Trp Arg Leu	
214 219 224 229	
aac gtc ttc ttt gtc agt ttg tcc ctg ttg ggt gtg att tta ata gcc	1075
Thr Val Phe Phe Val Ser Leu Ser Leu Leu Gly Val Ile Leu Ile Ala	
230 235 240 245	
ttc caa caa gca cag tac att ctc atg gaa ttc atg aaa aca aga cag	1123
Phe Gln Gln Ala Gln Tyr Ile Leu Met Glu Phe Met Lys Thr Arg Gln	
246 251 256 261	
agg caa aat gct agc tcc tct tca cag caa aac aat ggt cct atg gat	1171
Arg Gln Asn Ala Ser Ser Ser Ser Gln Gln Asn Asn Gly Pro Met Asp	
262 267 272 277	
gta atc agc ccc cat tct tac aaa agc aat tgc aag aac ttt ctc gat	1219
Val Ile Ser Pro His Ser Tyr Lys Ser Asn Cys Lys Asn Phe Leu Asp	
278 283 288 293	
aca tat ggc ccc tct gat aaa ggc agg ggg aag aac tgc ctt cca gtg	1267
Thr Tyr Gly Pro Ser Asp Lys Gly Arg Gly Lys Asn Cys Leu Pro Val	
294 299 304 309	
aac act ccc caa agc agg atc cag aat gct gca aag agg agc cca gcc	1315
Asn Thr Pro Gln Ser Arg Ile Gln Asn Ala Ala Lys Arg Ser Pro Ala	
310 315 320 325	
acc tat ggt cat tct cag aag aag cac aaa tgc tca gtg tat tac agt	1363
Thr Tyr Gly His Ser Gln Lys Lys His Lys Cys Ser Val Tyr Tyr Ser	
326 331 336 341	
aaa cac aaa acc agc aca gct gcg gcc agc agc acc agc acg act act	1411
Lys His Lys Thr Ser Thr Ala Ala Ala Ser Ser Thr Ser Thr Thr Thr	
342 347 352 357	
gag gaa aaa cag act tca ccc ctg ggc agc tca ctg cct gct gct aaa	1459
Glu Glu Lys Gln Thr Ser Pro Leu Gly Ser Ser Leu Pro Ala Ala Lys	
358 363 368 373	
gag gac att tgc act gat gcc atg cgt gag aac tgg atc agc ctc aga	1507
Glu Asp Ile Cys Thr Asp Ala Met Arg Glu Asn Trp Ile Ser Leu Arg	
374 379 384 389	
tat gca agt ggc ata aat gtc aac ctg cag aag aat tta acc ctt ccc	1555
Tyr Ala Ser Gly Ile Asn Val Asn Leu Gln Lys Asn Leu Thr Leu Pro	
390 395 400 405	
aaa aac tta ctg aat aaa gaa gaa aac aca ctg aaa aac aca att gtt	1603
Lys Asn Leu Leu Asn Lys Glu Glu Asn Thr Leu Lys Asn Thr Ile Val	
406 411 416 421	
ttc agt aat cct tct tca gaa tgt agt atg aag gag gga ata cag aca	1651
Phe Ser Asn Pro Ser Ser Glu Cys Ser Met Lys Glu Gly Ile Gln Thr	
422 427 432 437	
tgt atg ttt cct aag gaa act gac att aaa act tca gag aac aca gcc	1699
Cys Met Phe Pro Lys Glu Thr Asp Ile Lys Thr Ser Glu Asn Thr Ala	

438	443	448	453	
gag ttc aag gaa cgg	gag ctc tgt cca ctg	aag acc tcc aag aaa cta		1747
Glu Phe Lys Glu Arg	Glu Leu Cys Pro Leu	Lys Thr Ser Lys Lys Leu		
454	459	464	469	
cct gaa aac cat tta	cca aga aac tca cct	cag tac cac cag cca gac		1795
Pro Glu Asn His Leu	Pro Arg Asn Ser Pro	Gln Tyr His Gln Pro Asp		
470	475	480	485	
ttg cca gaa att tcc	agg aaa aat aat ggg	aat aac cag caa gta cct		1843
Leu Pro Glu Ile Ser	Arg Lys Asn Asn Gly	Asn Asn Gln Gln Val Pro		
486	491	496	501	
gtc aag aat gaa gta	gat cat tgt gaa aat	ttg aag aag gtg gac aca		1891
Val Lys Asn Glu Val	Asp His Cys Glu Asn	Leu Lys Lys Val Asp Thr		
502	507	512	517	
aag cct tct tca gaa	aag aag att cac aaa	aca tct aga gaa gac atg		1939
Lys Pro Ser Ser Glu	Lys Lys Ile His Lys	Thr Ser Arg Glu Asp Met		
518	523	528	533	
ttt tct gag aaa cag	gac ata cct ttc gta	gag caa gaa gat cct tat		1987
Phe Ser Glu Lys Gln	Asp Ile Pro Phe Val	Glu Gln Glu Asp Pro Tyr		
534	539	544	549	
agg aag aaa aag ctt	cag gag aaa aga gaa	gga aat tta caa aat tta		2035
Arg Lys Lys Lys Leu	Gln Glu Lys Arg Glu	Gly Asn Leu Gln Asn Leu		
550	555	560	565	
aat tgg agt aaa agt	cga aca tgt aga aag	aac aag aaa agg ggt gtt		2083
Asn Trp Ser Lys Ser	Arg Thr Cys Arg Lys	Asn Lys Lys Arg Gly Val		
566	571	576	581	
gct cca gtc tca agg	cct cct gaa cag agt	gat cta aag ctt gtg tgc		2131
Ala Pro Val Ser Arg	Pro Pro Glu Gln Ser	Asp Leu Lys Leu Val Cys		
582	587	592	597	
agt gac ttt gag agg	tct gag ctg agc agt	gac atc aat gta aga agc		2179
Ser Asp Phe Glu Arg	Ser Glu Leu Ser Ser	Asp Ile Asn Val Arg Ser		
598	603	608	613	
tgg tgt ata cag gaa	agc act agg gag gtt	tgt aaa gca gat gcc gaa		2227
Trp Cys Ile Gln Glu	Ser Thr Arg Glu Val	Cys Lys Ala Asp Ala Glu		
614	619	624	629	
att gca agc agt tta	cct gct gcc cag aga	gag gca gaa ggt tac tac		2275
Ile Ala Ser Ser Leu	Pro Ala Ala Gln Arg	Glu Ala Glu Gly Tyr Tyr		
630	635	640	645	
cag aag cct gag aag	aaa tgt gtg gac aag	ttc tgc tcc gat tcc agc		2323
Gln Lys Pro Glu Lys	Lys Cys Val Asp Lys	Phe Cys Ser Asp Ser Ser		
646	651	656	661	
tct gac tgt ggg agc	tcc tct ggc agc gtg	cgt gcc agc cgg ggc agc		2371
Ser Asp Cys Gly Ser	Ser Ser Gly Ser Val	Arg Ala Ser Arg Gly Ser		
662	667	672	677	

tgg ggg agc tgg agc agc acc agc agc tcc gac ggg gat aag aag ccc	2419
Trp Gly Ser Trp Ser Ser Thr Ser Ser Ser Asp Gly Asp Lys Lys Pro	
678 683 688 693	
atg gtg gac gcc cag cac ttc ctg ccg gcc gga gac agt gtt tca caa	2467
Met Val Asp Ala Gln His Phe Leu Pro Ala Gly Asp Ser Val Ser Gln	
694 699 704 709	
aat gat ttt cct tct gaa gct ccc atc tcc ttg aat ctt tct cat aac	2515
Asn Asp Phe Pro Ser Glu Ala Pro Ile Ser Leu Asn Leu Ser His Asn	
710 715 720 725	
atc tgc aat ccc atg acc gtg aat agt ctc cca caa tac gca gag cct	2563
Ile Cys Asn Pro Met Thr Val Asn Ser Leu Pro Gln Tyr Ala Glu Pro	
726 731 736 741	
tcc tgt ccc agc ctt cct gcc ggg ccc aca ggt gtt gaa gaa gat aaa	2611
Ser Cys Pro Ser Leu Pro Ala Gly Pro Thr Gly Val Glu Glu Asp Lys	
742 747 752 757	
ggg ctt tac tca cct gga gac ctg tgg ccc act ccg cca gtg tgt gtg	2659
Gly Leu Tyr Ser Pro Gly Asp Leu Trp Pro Thr Pro Pro Val Cys Val	
758 763 768 773	
aca agc agc tta aac tgc acc ctg gag aac ggc gtg cct tgt gtg att	2707
Thr Ser Ser Leu Asn Cys Thr Leu Glu Asn Gly Val Pro Cys Val Ile	
774 779 784 789	
cag gag tgc gcc ccg gtt cat aat agt ttc att gat tgg agt gca aca	2755
Gln Glu Ser Ala Pro Val His Asn Ser Phe Ile Asp Trp Ser Ala Thr	
790 795 800 805	
tgc gaa ggc cag ttt tcc agc gca tac tgt cca ttg gaa ttg aac gat	2803
Cys Glu Gly Gln Phe Ser Ser Ala Tyr Cys Pro Leu Glu Leu Asn Asp	
806 811 816 821	
tac aat gcc ttt cca gaa gaa aac atg aac tat gcc aat ggc ttc ccc	2851
Tyr Asn Ala Phe Pro Glu Glu Asn Met Asn Tyr Ala Asn Gly Phe Pro	
822 827 832 837	
tgt cct gca gat gtt cag aca gac ttt att gat cac aac tct cag tct	2899
Cys Pro Ala Asp Val Gln Thr Asp Phe Ile Asp His Asn Ser Gln Ser	
838 843 848 853	
acc tgg aac acc cca ccc aac atg cct gct gcc tgg gga cat gcc agt	2947
Thr Trp Asn Thr Pro Pro Asn Met Pro Ala Ala Trp Gly His Ala Ser	
854 859 864 869	
ttc atc agc tct ccg ccc tac ctc aca agc acc cga agc ttg tct cca	2995
Phe Ile Ser Ser Pro Pro Tyr Leu Thr Ser Thr Arg Ser Leu Ser Pro	
870 875 880 885	
atg tct gga ctt ttt ggt tcc atc tgg gcc ccg caa agc gat gtg tat	3043
Met Ser Gly Leu Phe Gly Ser Ile Trp Ala Pro Gln Ser Asp Val Tyr	
886 891 896 901	

gaa aat tgc tgc ccc atc aac ccc acc acg gaa cat tcg acc cac atg 3091
 Glu Asn Cys Cys Pro Ile Asn Pro Thr Thr Glu His Ser Thr His Met
 902 907 912 917

gaa aac caa gcg gtc gtg tgc aag gaa tac tac ccg ggg ttc aac ccg 3139
 Glu Asn Gln Ala Val Val Cys Lys Glu Tyr Tyr Pro Gly Phe Asn Pro
 918 923 928 933

ttt cgc gcc tat atg aac ctg gac ata tgg act acc aca gcg aat agg 3187
 Phe Arg Ala Tyr Met Asn Leu Asp Ile Trp Thr Thr Thr Ala Asn Arg
 934 939 944 949

aat gca aat ttc cca ctg tct aga gac tcg agt tac tgt ggg aat gtg 3235
 Asn Ala Asn Phe Pro Leu Ser Arg Asp Ser Ser Tyr Cys Gly Asn Val
 950 955 960 965

tga aaat aattggattt ttaaacaatg tgaataaaga ggcttgtgtt ttgattacta 3292
 *
 966

gtgtaaactg gttattgaga tagattatga cattggtgga tattttggca ctttttatatg 3352

aaaataaatt ttttaatgaa aaaaaaaaaa 3382

<210> 450
 <211> 1609
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (77)..(1378)

<400> 450
 gtcggtacga ctactatag ggaatttggc cctcgagcaa gaattcggac gagggcggct 60

ggccggtgag cgcggc atg ggg cga gtg cag ctc ttc gag atc agc ctg 109
 Met Gly Arg Val Gln Leu Phe Glu Ile Ser Leu
 1 5

agc cac ggc cgc gtc gtc tac agc ccc ggg gag ccg ttg gct ggg acc 157
 Ser His Gly Arg Val Val Tyr Ser Pro Gly Glu Pro Leu Ala Gly Thr
 12 17 22 27

gtg cgc gtg cgc ctg ggg gca ccg ctg ccg ttc cga gcc atc cgg gtg 205
 Val Arg Val Arg Leu Gly Ala Pro Leu Pro Phe Arg Ala Ile Arg Val
 28 33 38 43

acc tgc ata ggt tcc tgc ggg gtc tcc aac aag gct aat gac aca gcg 253
 Thr Cys Ile Gly Ser Cys Gly Val Ser Asn Lys Ala Asn Asp Thr Ala
 44 49 54 59

tgg gta gtg gag gag ggt tac ttc aac agt tcc ctg tcg ctg gca gac 301
 Trp Val Val Glu Glu Gly Tyr Phe Asn Ser Ser Leu Ser Leu Ala Asp

60	65	70	75	
aag ggg agc ctg ccc gct gga gag cac agc ttc ccc ttc cag ttc ctg				349
Lys Gly Ser Leu Pro Ala Gly Glu His Ser Phe Pro Phe Gln Phe Leu				
76	81	86	91	
ctt cct gcc act gca ccc acg tcc ttt gag ggt cct ttc ggg aag atc				397
Leu Pro Ala Thr Ala Pro Thr Ser Phe Glu Gly Pro Phe Gly Lys Ile				
92	97	102	107	
gtg cac cag gtg agg gcc gcc atc cac acg cca cgg ttt tcc aag gat				445
Val His Gln Val Arg Ala Ala Ile His Thr Pro Arg Phe Ser Lys Asp				
108	113	118	123	
cac aag tgc agc ctc gtg ttc tat atc ttg agc ccc ttg aac ctg aac				493
His Lys Cys Ser Leu Val Phe Tyr Ile Leu Ser Pro Leu Asn Leu Asn				
124	129	134	139	
agc atc cca gac att gag caa ccc aac gtg gcc tct gcc acc aag aag				541
Ser Ile Pro Asp Ile Glu Gln Pro Asn Val Ala Ser Ala Thr Lys Lys				
140	145	150	155	
ttc tcc tac aag ctg gtg aag acg ggc agc gtg gtc ctc aca gcc agc				589
Phe Ser Tyr Lys Leu Val Lys Thr Gly Ser Val Val Leu Thr Ala Ser				
156	161	166	171	
act gat ctc cgc ggc tat gtg gtg ggg cag gca ctg cag ctg cat gcc				637
Thr Asp Leu Arg Gly Tyr Val Val Gly Gln Ala Leu Gln Leu His Ala				
172	177	182	187	
gac gtt gag aac cag tca ggc aag gac acc agc cct gtg gtg gcc agt				685
Asp Val Glu Asn Gln Ser Gly Lys Asp Thr Ser Pro Val Val Ala Ser				
188	193	198	203	
ctg ctg cag aaa gtg tcc tat aag gcc aag cgc tgg atc cac gac gta				733
Leu Leu Gln Lys Val Ser Tyr Lys Ala Lys Arg Trp Ile His Asp Val				
204	209	214	219	
cgg acc att gcg gag gtg gag ggt gcg ggc gtc aag gcc tgg cgg cgg				781
Arg Thr Ile Ala Glu Val Glu Gly Ala Gly Val Lys Ala Trp Arg Arg				
220	225	230	235	
gcg cag tgg cac gag cag atc ctg gtg cct gcc ttg ccc cag tcg gcc				829
Ala Gln Trp His Glu Gln Ile Leu Val Pro Ala Leu Pro Gln Ser Ala				
236	241	246	251	
ctg ccg ggc tgc agc ctc atc cac atc gac tac tac tta cag gtc tct				877
Leu Pro Gly Cys Ser Leu Ile His Ile Asp Tyr Tyr Leu Gln Val Ser				
252	257	262	267	
ctg aag gcg ccg gaa gct act gtg acc ctc ccg gtc ttc att ggc aat				925
Leu Lys Ala Pro Glu Ala Thr Val Thr Leu Pro Val Phe Ile Gly Asn				
268	273	278	283	
att gct gtg aac cat gcc cca gtg agc ccc cgg cca ggc ctg ggg ctg				973
Ile Ala Val Asn His Ala Pro Val Ser Pro Arg Pro Gly Leu Gly Leu				
284	289	294	299	

cct cct ggg gcc cca ccc ctg gtg gtg cct tcc gca cca ccc cag gag	1021
Pro Pro Gly Ala Pro Pro Leu Val Val Pro Ser Ala Pro Pro Gln Glu	
300 305 310 315	
gag gct gag gct gag gct gcg gct ggc ggc ccc cac ttc ttg gac ccc	1069
Glu Ala Glu Ala Glu Ala Ala Ala Gly Gly Pro His Phe Leu Asp Pro	
316 321 326 331	
gtc ttc ctc tcc acc aag agc cat tcg cag cgg cag ccc ctg ctg gcc	1117
Val Phe Leu Ser Thr Lys Ser His Ser Gln Arg Gln Pro Leu Leu Ala	
332 337 342 347	
acc ttg agt tct gtg cct ggt gcg ccg gag ccc tgc cct cag gat ggc	1165
Thr Leu Ser Ser Val Pro Gly Ala Pro Glu Pro Cys Pro Gln Asp Gly	
348 353 358 363	
agc cct gcc tca cac ccg ctg cac cct ccc ttg tgc att tca aca ggt	1213
Ser Pro Ala Ser His Pro Leu His Pro Pro Leu Cys Ile Ser Thr Gly	
364 369 374 379	
gcc act gtc ccc tac ttt gca gag ggc tcc ggg ggg cca gtg ccc act	1261
Ala Thr Val Pro Tyr Phe Ala Glu Gly Ser Gly Gly Pro Val Pro Thr	
380 385 390 395	
acc agc acc ttg att ctt cct cca gag tac agt tct tgg ggc tac ccc	1309
Thr Ser Thr Leu Ile Leu Pro Pro Glu Tyr Ser Ser Trp Gly Tyr Pro	
396 401 406 411	
tat gag gcc cca ccg tct tat gag cag agc tgc ggc ggc gtg gaa ccc	1357
Tyr Glu Ala Pro Pro Ser Tyr Glu Gln Ser Cys Gly Gly Val Glu Pro	
412 417 422 427	
agc ctg acc cct gag agc tga cc ccgtgctgcc ttctccaggc aggcctggcc	1410
Ser Leu Thr Pro Glu Ser *	
428 433	
tctgccctgg gactggggcg cccagggcct cgtgccttct ctcttggcct agcctggccc	1470
actcaggacc tgcccagcct ctgccagctc ctctggcatc cgccctcttc tccctggggc	1530
tggggtgggg gtggcagggg gctgggacct ggagagacaa ctctgtaaa taaaacactt	1590
tatttgtaaa aaaaaaaaaa	1609

<210> 451
 <211> 3856
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (105)..(1481)

<400> 451

acccgcgtcc ggcgccccgg ggagctcgga gcgcgtgcac gcttttcata cggagaaggc 60

cagtgccag cttgaagggt ctgtcacctt ttgcagtggg ccac atg aga aaa aag 116
Met Arg Lys Lys
1

tgg aaa atg gga ggc atg aaa tac ata ttt tcg ttg ttg ttc ttt ctt 164
Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe Phe Leu
5 10 15 20

ttg cta gaa gga ggc aaa aca gag caa gta aaa cat tca gag aca tat 212
Leu Leu Glu Gly Gly Lys Thr Glu Gln Val Lys His Ser Glu Thr Tyr
21 26 31 36

tgc atg ttt caa gac aag aag tac aga gtg ggt gag aga tgg cat cct 260
Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp His Pro
37 42 47 52

tac ctg gaa cct tat ggg ttg gtt tac tgc gtg aac tgc atc tgc tca 308
Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile Cys Ser
53 58 63 68

cag aat ggg aat gtg ctt tgc agc cga gtc aga tgt cca aat gtt cat 356
Gln Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Asn Val His
69 74 79 84

tgc ctt tct cct gtg cat att cct cat ctg tgc tgc cct cgc tgc cca 404
Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg Cys Pro
85 90 95 100

gaa gac tcc tta ccc cca gtg aac aat aag gtg acc agc aag tct tgc 452
Glu Asp Ser Leu Pro Pro Val Asn Asn Lys Val Thr Ser Lys Ser Cys
101 106 111 116

gag tac aat ggg aca act tac caa cat gga gag ctg ttc gta gct gaa 500
Glu Tyr Asn Gly Thr Thr Tyr Gln His Gly Glu Leu Phe Val Ala Glu
117 122 127 132

ggg ctc ttt cag aat cgg caa ccc aat caa tgc acc cag tgc agc tgt 548
Gly Leu Phe Gln Asn Arg Gln Pro Asn Gln Cys Thr Gln Cys Ser Cys
133 138 143 148

tcg gag gga aac gtg tat tgt ggt ctc aag act tgc ccc aaa tta acc 596
Ser Glu Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys Pro Lys Leu Thr
149 154 159 164

tgt gcc ttc cca gtc tct gtt cca gat tcc tgc tgc cgg gta tgc aga 644
Cys Ala Phe Pro Val Ser Val Pro Asp Ser Cys Cys Arg Val Cys Arg
165 170 175 180

gga gat gga gaa ctg tca tgg gaa cat tct gat ggt gat atc ttc cgg 692
Gly Asp Gly Glu Leu Ser Trp Glu His Ser Asp Gly Asp Ile Phe Arg
181 186 191 196

caa cct gcc aac aga gaa gca aga cat tct tac cac cgc tct cac tat 740
Gln Pro Ala Asn Arg Glu Ala Arg His Ser Tyr His Arg Ser His Tyr

197	202	207	212	
gat cct cca cca agc cga cag gct gga ggt ctg tcc cgc ttt cct ggg				788
Asp Pro Pro Pro Ser Arg Gln Ala Gly Gly Leu Ser Arg Phe Pro Gly				
213	218	223	228	
gcc aga agt cac cgg gga gct ctt atg gat tcc cag caa gca tca gga				836
Ala Arg Ser His Arg Gly Ala Leu Met Asp Ser Gln Gln Ala Ser Gly				
229	234	239	244	
acc att gtg caa att gtc atc aat aac aaa cac aag cat gga caa gtg				884
Thr Ile Val Gln Ile Val Ile Asn Asn Lys His Lys His Gly Gln Val				
245	250	255	260	
tgt gtt tcc aat gga aag acc tat tct cat ggc gag tcc tgg cac cca				932
Cys Val Ser Asn Gly Lys Thr Tyr Ser His Gly Glu Ser Trp His Pro				
261	266	271	276	
aac ctc cgg gca ttt ggc att gtg gag tgt gtg cta tgt act tgt aat				980
Asn Leu Arg Ala Phe Gly Ile Val Glu Cys Val Leu Cys Thr Cys Asn				
277	282	287	292	
gtc acc aag caa gag tgt aag aaa atc cac tgc ccc aat cga tac ccc				1028
Val Thr Lys Gln Glu Cys Lys Lys Ile His Cys Pro Asn Arg Tyr Pro				
293	298	303	308	
tgc aag tat cct caa aaa ata gac gga aaa tgc tgc aag gtg tgt cca				1076
Cys Lys Tyr Pro Gln Lys Ile Asp Gly Lys Cys Cys Lys Val Cys Pro				
309	314	319	324	
ggg aaa aaa aca aaa gaa gaa ctt cca ggc caa agc ttt gac aat aaa				1124
Gly Lys Lys Thr Lys Glu Glu Leu Pro Gly Gln Ser Phe Asp Asn Lys				
325	330	335	340	
ggc tac ttc tgc ggg gaa gaa acg atg cct gtg tat gag tct gta ttc				1172
Gly Tyr Phe Cys Gly Glu Glu Thr Met Pro Val Tyr Glu Ser Val Phe				
341	346	351	356	
atg gag gat ggg gag aca acc aga aaa ata gca ctg gag act gag aga				1220
Met Glu Asp Gly Glu Thr Thr Arg Lys Ile Ala Leu Glu Thr Glu Arg				
357	362	367	372	
cca cct cag gta gag gtc cac gtt tgg act att cga aag ggc att ctc				1268
Pro Pro Gln Val Glu Val His Val Trp Thr Ile Arg Lys Gly Ile Leu				
373	378	383	388	
cag cac ttc cat att gag aag atc tcc aag agg atg ttt gag gag ctt				1316
Gln His Phe His Ile Glu Lys Ile Ser Lys Arg Met Phe Glu Glu Leu				
389	394	399	404	
cct cac ttc aag ctg gtg acc aga aca acc ctg agc cag tgg aag atc				1364
Pro His Phe Lys Leu Val Thr Arg Thr Thr Leu Ser Gln Trp Lys Ile				
405	410	415	420	
ttc acc gaa gga gaa gct cag atc agc cag atg tgt tca agt cgt gta				1412
Phe Thr Glu Gly Glu Ala Gln Ile Ser Gln Met Cys Ser Ser Arg Val				
421	426	431	436	

aaccccatat	gtctcattcc	atgactatag	gtgagagaat	tctttcctaa	gagggtttga	3013
taccaatagg	ggaaaatgta	aaatgttcag	tctttatgac	aacctggcat	aaaggagtca	3073
attcttatga	aagagacaca	agggccttat	ggccagggtt	tcttgggaca	agactctcac	3133
cagcacatca	cacacgttct	cottggaaga	gagaagcagt	acatcccggg	tgagagggtca	3193
caaagcatta	gtttgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtgtgtgtgt	3253
ggtaaagggg	ggaagggtgt	atgcggctgc	tccctccgtc	ccagagggtg	cagtgattcc	3313
ataatgtgga	gactagtaac	tagatcctaa	ggcaaagagg	tgtttctcct	tctggatgat	3373
tcaccccaaa	gccttcccac	ccagggtgtc	tctgaaagct	tagccttaag	agaacacgca	3433
gagagtttcc	ctagatatac	tcttgcctcc	aggtgctggg	acacaccttt	gcaaaatgct	3493
gtgggaagca	ggagctgggg	agctgtgtta	agtcaaagta	gaaaccctcc	agtgtttggt	3553
gttggtgtaga	gaataggaca	tagggtaaag	aggccaagct	gcctgtagtt	agtagagaag	3613
aatggatgtg	gttcttcttg	tgtatttatt	tgtatcataa	acacttggaa	caacaaagac	3673
cataagcatc	atttagcagt	tgtagccatt	ttctagttaa	ctcatgtaaa	caagtaagag	3733
taacataaca	gtattaccct	ttcactgttc	tcacaggaca	tgtacctaat	tatgggtactt	3793
atttatgtag	tcactgtatt	tctggatttt	taaattaata	aaaaagttaa	ttttgaaaaa	3853
tca						3856

<210> 452
 <211> 1546
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (404)..(1189)

<400> 452		
cgctcctata	gggaatttgg	ccctcgaggc
gcagcgggtt	cactctgatt	tgcttctcca
gggtcaggaa	catggaggcg	gtgctgggga
aaccacaaag	gaaaaaggca	gaacgttcct
tgcttctcct	cggggcaagg	tcgcagcatc
ctttctgctg	gctcagccgg	gaggcccaga
	gtgttctgca	gaggctgcgt
	attgaaggct	
		60
		120
		180
		240
		300
		360

Gln	Leu	Ala	Arg	Trp	Arg	Leu	Phe	Gln	Cys	Leu	Thr	Gly	His	Phe	Trp	
213					218					223					228	
tcc	aag	gtc	tgt	gac	gtg	ctc	cag	ttc	cac	ttt	gcg	ttt	ttg	ttt	ctg	1135
Ser	Lys	Val	Cys	Asp	Val	Leu	Gln	Phe	His	Phe	Ala	Phe	Leu	Phe	Leu	
229					234					239					244	
acg	cat	ttc	aac	act	cac	cca	aga	ttc	cat	ccc	tct	ggc	ggg	aag	acg	1183
Thr	His	Phe	Asn	Thr	His	Pro	Arg	Phe	His	Pro	Ser	Gly	Gly	Lys	Thr	
245					250					255					260	
cgt	tga	acccagggaa	gaacctgctg	aaaaccgatg	acccccagca	ttgaaatgga										1239
Arg	*															
261																
ctctgagatg	gcagcgtggt	gccagtgtca	gacatcctgt	gtgtgatgat	atgcactgat											1299
cacacaagac	tgccctttcc	tgagaagctg	cgggcttcgg	tgtggagggg	tggagtgtctg											1359
tgatctcgac	aacttacttt	caaagacata	aagcacagat	ctccgcacag	gggatgtgtg											1419
tgttcctgat	gtaatttgca	taacttttct	gtagtgtgaa	atgtttccaa	ataaatattg											1479
gcaaggggag	tggaaatgac	accaagaagc	ccctcatgct	catggttgga	cagagaaaaa											1539
aaaaaaa																1546

<210> 453
 <211> 1470
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (184)..(1014)

<400>	453															
gcacgagggga	cggctcagcg	acgccacggc	cagcagcgct	cgcgtcctcc	ccagcaacag											60
ttactcaaag	ctaatacagat	agcgaaagaa	gcaggagagc	aagtcaagaa	atacggtgaa											120
ggagtccttc	ccaaagtgtg	ctaggtcctt	ccgcgccggg	gcctggtctt	cgtcgtcaac											180
acc	atg	gac	agc	tcc	cgg	gaa	ccg	act	ctg	ggg	cgc	ttg	gac	gcc	gct	228
	Met	Asp	Ser	Ser	Arg	Glu	Pro	Thr	Leu	Gly	Arg	Leu	Asp	Ala	Ala	
	1						5								10	
ggc	ttc	tgg	cag	gtc	tgg	cag	cgc	ttt	gat	gcg	gat	gaa	aaa	ggt	tac	276
Gly	Phe	Trp	Gln	Val	Trp	Gln	Arg	Phe	Asp	Ala	Asp	Glu	Lys	Gly	Tyr	
	16					21				26					31	
ata	gaa	gag	aag	gaa	ctc	gat	gct	ttc	ttt	ctc	cac	atg	ttg	atg	aaa	324
Ile	Glu	Glu	Lys	Glu	Leu	Asp	Ala	Phe	Phe	Leu	His	Met	Leu	Met	Lys	
	32					37				42					47	

ctg ggt act gat gac acg gtc atg aaa gca aat ttg cac aag gtg aaa	372
Leu Gly Thr Asp Asp Thr Val Met Lys Ala Asn Leu His Lys Val Lys	
48 53 58 63	
cag cag ttt atg act acc caa gat gcc tct aaa gat ggt cgc att cgg	420
Gln Gln Phe Met Thr Thr Gln Asp Ala Ser Lys Asp Gly Arg Ile Arg	
64 69 74 79	
atg aaa gag ctt gct ggt atg ttc tta tct gag gat gaa aac ttt ctt	468
Met Lys Glu Leu Ala Gly Met Phe Leu Ser Glu Asp Glu Asn Phe Leu	
80 85 90 95	
ctg ctc ttt cgc cgg gaa aac cca ctg gac agc agc gtg gag ttt atg	516
Leu Leu Phe Arg Arg Glu Asn Pro Leu Asp Ser Ser Val Glu Phe Met	
96 101 106 111	
cag att tgg cgc aaa tat gac gct gac agc agt ggc ttt ata tca gct	564
Gln Ile Trp Arg Lys Tyr Asp Ala Asp Ser Ser Gly Phe Ile Ser Ala	
112 117 122 127	
gct gag ctc cgc aac ttc ctc cga gac ctc ttt ctt cac cac aaa aag	612
Ala Glu Leu Arg Asn Phe Leu Arg Asp Leu Phe Leu His His Lys Lys	
128 133 138 143	
gcc att tct gag gct aaa ctg gaa gaa tac act ggc acc atg atg aag	660
Ala Ile Ser Glu Ala Lys Leu Glu Glu Tyr Thr Gly Thr Met Met Lys	
144 149 154 159	
att ttt gac aga aat aaa gat ggt cgg ttg gat cta aat gac tta gca	708
Ile Phe Asp Arg Asn Lys Asp Gly Arg Leu Asp Leu Asn Asp Leu Ala	
160 165 170 175	
agg att ctg gct ctt cag gaa aac ttc ctt ctc caa ttt aaa atg gat	756
Arg Ile Leu Ala Leu Gln Glu Asn Phe Leu Leu Gln Phe Lys Met Asp	
176 181 186 191	
gct tgt tct act gaa gaa agg aaa agg gac ttt gag aaa atc ttt gcc	804
Ala Cys Ser Thr Glu Glu Arg Lys Arg Asp Phe Glu Lys Ile Phe Ala	
192 197 202 207	
tac tat gat gtt agt aaa aca gga gcc ctg gaa ggc cca gaa gtg gat	852
Tyr Tyr Asp Val Ser Lys Thr Gly Ala Leu Glu Gly Pro Glu Val Asp	
208 213 218 223	
ggg ttt gtc aaa gac atg atg gag ctt gtc cag ccc agc atc agc ggg	900
Gly Phe Val Lys Asp Met Met Glu Leu Val Gln Pro Ser Ile Ser Gly	
224 229 234 239	
gtg gac ctt gat aag ttc cgc gag att ctc ctg cgt cac tgc gac gtg	948
Val Asp Leu Asp Lys Phe Arg Glu Ile Leu Leu Arg His Cys Asp Val	
240 245 250 255	
aac aag gat gga aaa att cag aag tct gag ctg gct ttg tgt ctt ggg	996
Asn Lys Asp Gly Lys Ile Gln Lys Ser Glu Leu Ala Leu Cys Leu Gly	
256 261 266 271	

ctg aaa atc aac cca taa tcccag actgctttgc cttttgctct tactatgttt 1050
 Leu Lys Ile Asn Pro *
 272 277

ctgtgatctt gctggtagaa ttgtatctgt gcattgatgt tgggaacaca gtgggcaaac 1110
 tcacaaatgg tgtgctattc ttgggcaaga agagggacgc tagggccttc cttccaccgg 1170
 cgtgatctat cctgtctca ctgaaagccc ctgtgtagtg tctgtgttgt tttcccttga 1230
 ccctgggctt tcctatcctc ccaaagactc agctccctg ttagatggct ctgcctgtcc 1290
 ttccccagtc accagggcgg gggggacagg ggcagctgag tgcattcatt ttgtgctttt 1350
 cttatgggct ttctgcttag tctgaaaggt gtgtggcatt catggcaatc ctgtaacttc 1410
 aacatagatt ttttttgtgt gtgtggaaat aaatctgcaa ttggaaacaa aaaaaaaaaa 1470

<210> 454
 <211> 2539
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (97) .. (1755)

<400> 454
 tagggaatgt ggccctcgag gccagaatt cggcacgaga acacgtggag tccacgtagg 60

ctgtgttcgg tccgagatgc cttctagaca tgcagg atg tca agg agg cag ctg 114
 Met Ser Arg Arg Gln Leu
 1

gag aga tgg gtc tgg agc tca cag caa gtc cag gct aga ggt aga aac 162
 Glu Arg Trp Val Trp Ser Ser Gln Gln Val Gln Ala Arg Gly Arg Asn
 7 12 17 22

gtg aga gcc cca cgg ctg ggg aag att gcc atg gga ttg gag atg agc 210
 Val Arg Ala Pro Arg Leu Gly Lys Ile Ala Met Gly Leu Glu Met Ser
 23 28 33 38

tcc aag gac agc cct ggc agt ctg gat gga aga gct tgg gaa gat gct 258
 Ser Lys Asp Ser Pro Gly Ser Leu Asp Gly Arg Ala Trp Glu Asp Ala
 39 44 49 54

cag aaa cca caa agt gcc tgg tgc ggt ggg agg aaa acc aga gtg tat 306
 Gln Lys Pro Gln Ser Ala Trp Cys Gly Gly Arg Lys Thr Arg Val Tyr
 55 60 65 70

gct aca agc agc cgg cgg gcg ccg ccg agt gag ggg acg cgg cgc ggt 354
 Ala Thr Ser Ser Arg Arg Ala Pro Pro Ser Glu Gly Thr Arg Arg Gly
 71 76 81 86

ggg gcg gcg cgg ccc gag gag gcg gcg gag gag ggg ccg ccc gcg gcc	402
Gly Ala Ala Arg Pro Glu Glu Ala Ala Glu Glu Gly Pro Pro Ala Ala	
87 92 97 102	
ccc ggc tca ctc cgg cac tcc ggg ccg ctc ggc ccc cat gcc tgc ccg	450
Pro Gly Ser Leu Arg His Ser Gly Pro Leu Gly Pro His Ala Cys Pro	
103 108 113 118	
acc gcg ctg ccg gag ccc cag gtg acc agc gcc atg tcc agc cag gtg	498
Thr Ala Leu Pro Glu Pro Gln Val Thr Ser Ala Met Ser Ser Gln Val	
119 124 129 134	
gtg ggc att gag cct ctc tac atc aag gca gag ccg gcc agc cct gac	546
Val Gly Ile Glu Pro Leu Tyr Ile Lys Ala Glu Pro Ala Ser Pro Asp	
135 140 145 150	
agt cca aag ggt tcc tcg gag aca gag acc gag cct cct gtg gcc ctg	594
Ser Pro Lys Gly Ser Ser Glu Thr Glu Thr Glu Pro Pro Val Ala Leu	
151 156 161 166	
gcc cct ggt cca gct ccc act cgc tgc ctc cca ggc cac aag gaa gag	642
Ala Pro Gly Pro Ala Pro Thr Arg Cys Leu Pro Gly His Lys Glu Glu	
167 172 177 182	
gag gat ggg gag ggg gct ggg cct ggc gag cag ggc ggt ggg aag ctg	690
Glu Asp Gly Glu Gly Ala Gly Pro Gly Glu Gln Gly Gly Gly Lys Leu	
183 188 193 198	
gtg ctc agc tcc ctg ccc aag cgc ctc tgc ctg gtc tgt ggg gac gtg	738
Val Leu Ser Ser Leu Pro Lys Arg Leu Cys Leu Val Cys Gly Asp Val	
199 204 209 214	
gcc tcc ggc tac cac tat ggt gtg gca tcc tgt gag gcc tgc aaa gcc	786
Ala Ser Gly Tyr His Tyr Gly Val Ala Ser Cys Glu Ala Cys Lys Ala	
215 220 225 230	
ttc ttc aag agg acc atc cag ggg agc atc gag tac agc tgt ccg gcc	834
Phe Phe Lys Arg Thr Ile Gln Gly Ser Ile Glu Tyr Ser Cys Pro Ala	
231 236 241 246	
tcc aac gag tgt gag atc acc aag ccg aga cgc aag gcc tgc cag gcc	882
Ser Asn Glu Cys Glu Ile Thr Lys Arg Arg Arg Lys Ala Cys Gln Ala	
247 252 257 262	
tgc cgc ttc acc aag tgc ctg ccg gtg ggc atg ctc aag gag gga gtg	930
Cys Arg Phe Thr Lys Cys Leu Arg Val Gly Met Leu Lys Glu Gly Val	
263 268 273 278	
cgc ctg gac cgc gtc ccg ggt ggg ccg cag aag tac aag ccg ccg ccg	978
Arg Leu Asp Arg Val Arg Gly Gly Arg Gln Lys Tyr Lys Arg Arg Pro	
279 284 289 294	
gag gtg gac cca ctg ccc ttc ccg ggc ccc ttc cct gct ggg ccc ctg	1026
Glu Val Asp Pro Leu Pro Phe Pro Gly Pro Phe Pro Ala Gly Pro Leu	
295 300 305 310	
gca gtc gct gga ggc ccc ccg aag aca gca gcc cca gtg aat gca ctg	1074

Ala Val Ala Gly Gly Pro Arg Lys Thr Ala Ala Pro Val Asn Ala Leu	
311 316 321 326	
gtg tct cat ctg ctg gtg gtt gag cct gag aag ctc tat gcc atg cct	1122
Val Ser His Leu Leu Val Val Glu Pro Glu Lys Leu Tyr Ala Met Pro	
327 332 337 342	
gac ccc gca ggc cct gat ggg cac ctc cca gcc gtg gct acc ctc tgt	1170
Asp Pro Ala Gly Pro Asp Gly His Leu Pro Ala Val Ala Thr Leu Cys	
343 348 353 358	
gac ctc ttt gac cga gag att gtg gtc acc atc agc tgg gcc aag agc	1218
Asp Leu Phe Asp Arg Glu Ile Val Val Thr Ile Ser Trp Ala Lys Ser	
359 364 369 374	
atc cca ggc ttc tca tcg ctg tcg ctg tct gac cag atg tca gta ctg	1266
Ile Pro Gly Phe Ser Ser Leu Ser Leu Ser Asp Gln Met Ser Val Leu	
375 380 385 390	
cag agc gtg tgg atg gag gtg ctg gtg ctg ggt gtg gcc cag cgc tca	1314
Gln Ser Val Trp Met Glu Val Leu Val Leu Gly Val Ala Gln Arg Ser	
391 396 401 406	
ctg cca ctg cag gat gag ctg gcc ttc gct gag gac tta gtc ctg gat	1362
Leu Pro Leu Gln Asp Glu Leu Ala Phe Ala Glu Asp Leu Val Leu Asp	
407 412 417 422	
gaa gag ggg gca cgg gca gct ggc ctg ggg gaa ctg ggg gct gcc ctg	1410
Glu Glu Gly Ala Arg Ala Ala Gly Leu Gly Glu Leu Gly Ala Ala Leu	
423 428 433 438	
ctg caa cta gtg cgg cgg ctg cag gcc ctg cgg ctg gag cga gag gag	1458
Leu Gln Leu Val Arg Arg Leu Gln Ala Leu Arg Leu Glu Arg Glu Glu	
439 444 449 454	
tat gtt cta cta aag gcc ttg gcc ctt gcc aat tca gac tct gtg cac	1506
Tyr Val Leu Leu Lys Ala Leu Ala Leu Ala Asn Ser Asp Ser Val His	
455 460 465 470	
atc gaa gat gcc gag gct gtg gag cag ctg cga gaa gct ctg cac gag	1554
Ile Glu Asp Ala Glu Ala Val Glu Gln Leu Arg Glu Ala Leu His Glu	
471 476 481 486	
gcc ctg ctg gag tat gaa gcc ggc cgg gct ggc ccc gga ggg ggt gct	1602
Ala Leu Leu Glu Tyr Glu Ala Gly Arg Ala Gly Pro Gly Gly Gly Ala	
487 492 497 502	
gag cgg cgg cgg gcg ggc agg ctg ctg ctc acg cta ccg ctc ctc cgc	1650
Glu Arg Arg Arg Ala Gly Arg Leu Leu Leu Thr Leu Pro Leu Leu Arg	
503 508 513 518	
cag aca gcg ggc aaa gtg ctg gcc cat ttc tat ggg gtg aag ctg gag	1698
Gln Thr Ala Gly Lys Val Leu Ala His Phe Tyr Gly Val Lys Leu Glu	
519 524 529 534	
ggc aag gtg ccc atg cac aag ctg ttc ttg gag atg ctc gag gcc atg	1746
Gly Lys Val Pro Met His Lys Leu Phe Leu Glu Met Leu Glu Ala Met	

535	540	545	550	
atg gac tga ggcaagg ggtgggactg gtgggggttc tggcaggacc tgcctagcat				1802
Met Asp *				
551				
ggggtcagcc ccaagggctg gggcggagct ggggtctggg cagtgccaca gcctgctggc				1862
agggccaggg caatgccatc agcccttggg aacaggcccc acgccctctc ctccccctcc				1922
tagggggtgt cagaagctgg gaacgtgtgt ccaggctctg ggcacagtgc tgccccctgc				1982
aagccataac gtgccccag agtgtagggg gccttgcgga agccataggg ggctgcacgg				2042
gatgctggg aggcagaaac ctatctcagg gaggaaggg gatggaggcc agagtctccc				2102
agtgggtgat gcttttgctg ctgcttaatc ctaccccctc ttcaaagcag agtgggactt				2162
ggagagcaaa ggcccatgcc cccttcgctc ctctctcat catttgcat gggcattagt				2222
gtccccctt gaagcaataa ctccaagcag actccagccc ctggaccctt ggggtggcca				2282
gggcttcccc atcagctccc aacgagcctc ctcaggggtt aggagagcac tgctctatg				2342
ccctgcagag caataacact atatttattt ttgggtttgg ccaggggaggc gcagggacat				2402
ggggcaagcc agggcccaga gcccttggct gtacagagac tctattttaa tgtatatttg				2462
ctgcaaagag aaaccgcttt tggtttttaa cctttaatga gaaaaaata tataataccg				2522
agctcaaaaa aaaaaaa				2539

<210> 455
 <211> 1875
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (196)..(1158)

<400> 455

gagattcgca cgaggtaatc ggctgtcagc ctccctggct gtagtacct tctttcccg	60
agtcctggtc cagagttgg atttactgct gtcgcggtg ggcctcacgc cattccctgt	120
ccctcgcccc cctgagttag tccggtctcc cggcgaaagt gagcgagggt tgcccggagc	180
gcgcacgagg ggaaa atg cct aaa aaa aag act ggt gcg agg aag aag gct	231
Met Pro Lys Lys Lys Thr Gly Ala Arg Lys Lys Ala	
1 5 10	
gag aac cgc cga gaa cgt gaa aaa caa cta aga gca tca aga agc act	279
Glu Asn Arg Arg Glu Arg Glu Lys Gln Leu Arg Ala Ser Arg Ser Thr	

13	18	23	28	
ata gat tta gct aaa cat cca tgt aat gcc tca atg gaa tgt gac aag Ile Asp Leu Ala Lys His Pro Cys Asn Ala Ser Met Glu Cys Asp Lys 29 34 39 44				327
tgt cag agg cgg cag aag aat aga gca ttt tgc tac ttt tgt aat tct Cys Gln Arg Arg Gln Lys Asn Arg Ala Phe Cys Tyr Phe Cys Asn Ser 45 50 55 60				375
gta cag aag tta cca att tgt gca cag tgt ggg aaa aca aag tgc atg Val Gln Lys Leu Pro Ile Cys Ala Gln Cys Gly Lys Thr Lys Cys Met 61 66 71 76				423
atg aag tct tca gac tgt gtc ata aag cat gct ggt gta tac agt act Met Lys Ser Ser Asp Cys Val Ile Lys His Ala Gly Val Tyr Ser Thr 77 82 87 92				471
ggc ctt gca atg gtg ggt gca ata tgt gac ttc tgt gaa gct tgg gtt Gly Leu Ala Met Val Gly Ala Ile Cys Asp Phe Cys Glu Ala Trp Val 93 98 103 108				519
tgc cat ggg agg aag tgt ctc agt aca cat gcc tgt gcc tgc cct ctc Cys His Gly Arg Lys Cys Leu Ser Thr His Ala Cys Ala Cys Pro Leu 109 114 119 124				567
act gat gct gag tgt gtt gaa tgt gaa cga ggc gtg tgg gac cat gga Thr Asp Ala Glu Cys Val Glu Cys Glu Arg Gly Val Trp Asp His Gly 125 130 135 140				615
ggc aga ata ttc agt tgt tct ttt tgc cat aac ttt ctc tgt gaa gat Gly Arg Ile Phe Ser Cys Ser Phe Cys His Asn Phe Leu Cys Glu Asp 141 146 151 156				663
gat caa ttt gag cat caa gcc agc tgc cag gtt tta gag gca gaa aca Asp Gln Phe Glu His Gln Ala Ser Cys Gln Val Leu Glu Ala Glu Thr 157 162 167 172				711
ttt aaa tgt gtt tca tgc aat cgg ctt ggt cag cac tca tgt ctc cgt Phe Lys Cys Val Ser Cys Asn Arg Leu Gly Gln His Ser Cys Leu Arg 173 178 183 188				759
tgt aag gct tgt ttc tgt gat gat cat aca agg agc aaa gtg ttt aag Cys Lys Ala Cys Phe Cys Asp Asp His Thr Arg Ser Lys Val Phe Lys 189 194 199 204				807
caa gaa aaa gga aaa cag cct cct tgt cct aaa tgt ggg cat gaa act Gln Glu Lys Gly Lys Gln Pro Pro Cys Pro Lys Cys Gly His Glu Thr 205 210 215 220				855
cag gag act aag gac ctt agc atg tca aca cgc tcc ctg aaa ttt ggc Gln Glu Thr Lys Asp Leu Ser Met Ser Thr Arg Ser Leu Lys Phe Gly 221 226 231 236				903
agg cag act gga ggt gaa gag gga gat gga gct tct ggg tat gat gct Arg Gln Thr Gly Gly Glu Glu Gly Asp Gly Ala Ser Gly Tyr Asp Ala 237 242 247 252				951

tat tgg aag aac ctt tca tct gat aag tat ggt gat acc agc tac cac	999
Tyr Trp Lys Asn Leu Ser Ser Asp Lys Tyr Gly Asp Thr Ser Tyr His	
253 258 263 268	
gat gag gag gag gat gag tat gaa gca gag gat gat gaa gag gaa gaa	1047
Asp Glu Glu Glu Asp Glu Tyr Glu Ala Glu Asp Asp Glu Glu Glu Glu	
269 274 279 284	
gat gaa ggc aga aag gat tca gat act gag tca tca gat ttg ttt act	1095
Asp Glu Gly Arg Lys Asp Ser Asp Thr Glu Ser Ser Asp Leu Phe Thr	
285 290 295 300	
aat ttg aat tta gga agg acc tat gct agt ggc tat ³ gct cac tat gag	1143
Asn Leu Asn Leu Gly Arg Thr Tyr Ala Ser Gly Tyr Ala His Tyr Glu	
301 306 311 316	
gaa caa gag aac tag gggagctgct ctgggtggccg tgtgtgagag gagcaggagt	1198
Glu Gln Glu Asn *	
317	
gagtgtgtgt gcttgatgaa ttgtgtgtgg ttgttcaaaa gtaccttagc cacttagcct	1258
tgtgcagaag actagttaca cttaatgggc caagcaatag ggtgtagcgt ttttatagaa	1318
ctgataatca ggcttatggc ataagaaaaa tgagtttcaa atttaagatg tttattgatc	1378
gaagcaattg aagtatcatg gattggattg ttactgattt cagtaaagta tgttttgcca	1438
attagatata tatatacaag ataaaggaat aggatggtaa tatatttggt tgaaattaa	1498
ttactgtttt tattaataaaa tactgcttca ttgggctgat tttgtaaaat gtaatgagta	1558
aaatgaatta ctgtatTTTT ccttttatgt ccacagaatg agagtcatat gttgttatat	1618
tctaaatTTT cattaaatat tcatgtcacc ttgagttgtc atgataagta tgttttagta	1678
tttgacttat ttttctcttt cttcacaatg tatgtcctca gtggtacctt ttattgatgc	1738
cttaaatgta ttgataagggt gactagttag ccatttttca gagatacagt atcagaaata	1798
gtattattac agaagcttta ccaggacat tttatttctc tttgaataaa tctattattt	1858
cacttaaaaa aaaaaaa	1875

<210> 456
 <211> 3300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (25) .. (576)

<400> 456

taagcttgcg gccgcggagg gacg	atg cgc gag tac aaa gtg gtg gtg ctg	51
	Met Arg Glu Tyr Lys Val Val Val Leu	
	1 5	
ggc tcg ggc ggg gta ggc aaa tcc gcc ctg acc gtg cag ttc gtg acc	99	
Gly Ser Gly Gly Val Gly Lys Ser Ala Leu Thr Val Gln Phe Val Thr		
10 15 20 25		
ggc acc ttc atc gag aaa tac gac ccc acc atc gag gac ttc tac cgc	147	
Gly Thr Phe Ile Glu Lys Tyr Asp Pro Thr Ile Glu Asp Phe Tyr Arg		
26 31 36 41		
aag gag atc gag gtg gat tgc tgc ccg tgc gtg ctg gag atc ctg gac	195	
Lys Glu Ile Glu Val Asp Ser Ser Pro Ser Val Leu Glu Ile Leu Asp		
42 47 52 57		
acg gcg ggc acc gag cag ttc gcg tcc atg cgg gac ctg tac atc aag	243	
Thr Ala Gly Thr Glu Gln Phe Ala Ser Met Arg Asp Leu Tyr Ile Lys		
58 63 68 73		
aac ggc cag ggc ttc atc ctc gtc tac agc ctc gtc aac cag cag agc	291	
Asn Gly Gln Gly Phe Ile Leu Val Tyr Ser Leu Val Asn Gln Gln Ser		
74 79 84 89		
ttc cag gac atc aag ccc atg cgg gac cag atc atc cgc gtg aag cgg	339	
Phe Gln Asp Ile Lys Pro Met Arg Asp Gln Ile Ile Arg Val Lys Arg		
90 95 100 105		
tat gag aaa gtg cca gtc atc ttg gtt ggg aac aaa gtg gac ctg gaa	387	
Tyr Glu Lys Val Pro Val Ile Leu Val Gly Asn Lys Val Asp Leu Glu		
106 111 116 121		
agt gag aga gaa gta tgc tcc agc gaa ggc aga gcc ctt gct gaa gag	435	
Ser Glu Arg Glu Val Ser Ser Ser Glu Gly Arg Ala Leu Ala Glu Glu		
122 127 132 137		
tgg ggc tgc ccc ttt atg gaa act tcc gct aag agt aaa aca atg gtg	483	
Trp Gly Cys Pro Phe Met Glu Thr Ser Ala Lys Ser Lys Thr Met Val		
138 143 148 153		
gac gaa ctc ttt gca gaa att gtg agg cag atg aac tat gct gct cag	531	
Asp Glu Leu Phe Ala Glu Ile Val Arg Gln Met Asn Tyr Ala Ala Gln		
154 159 164 169		
cct gac aaa gat gac cca tgc tgt tct gca tgt aac ata caa tag cat	579	
Pro Asp Lys Asp Asp Pro Cys Cys Ser Ala Cys Asn Ile Gln *		
170 175 180		
ccaaatatgg ctgtcctgga tgggatttgc ccaatgtcgt aggtgataga aaactcgcct	639	
actccactgc agaacttgca gaatgcgtgg tgttaatcta cagagaactg cagcccttat	699	
tcagaattga gcagtgattg tcagttgata totctgagta acatttgggt tcagtaacta	759	
cagttttcac catttgcct cagtctcctt tatgcattctg caactttaag gcatagtcca	819	

tcgatctaca gggatgatctc atttgaaagc tatgatggca ttgtcgctga gttgacagaa	879
gcaactattg tacaaattaa aaataacccat aagggagaaa ccagaagaat tcctctgacc	939
acttacaatt aaaatatattt gtcttcttta aaaaaataag taaaggagaa atattttcct	999
acaagagtac tgaatttcag gaaatgggat agagcttcta accagtgtat tccgtcaagt	1059
aagataataa cagctgacct gccaacagca ttacagggag attctttgct cagctaacac	1119
atttctgttt ttcaaaattg atgcttaatt gtagctgtta ttctaatttg tgacatggaa	1179
ctaactcatg cttcaatcct tgatagagca aaactcagaa cagggttatgt aaaaatatag	1239
tctggcttta gaatttgta attcacctgc tttgccacag aaaatggagg ctttcacaag	1299
ggtttgatca gaattaaaac cccaaacccg ccctctgtta ggggtggtct ttataacttt	1359
actgaacaag aggggaagcaa ctgtgatggg aagagattac ctagccttac taacaagaag	1419
cattctaata gataaactag taccatcatg taaggaagat gaagccatgt tgcattccaca	1479
tgttcccggt tgcagaaacc tcacaggaca gtacgaatat ctggcatttt taagttcatt	1539
aaagcagcaa attccttctc gcctttaagg gctatgggtg tagtgtgacc cgtgggctaac	1599
ctgctttcaa aatcaagtat ttgctgtagc agagctttat tgcaggcatt ttaaaaattg	1659
aataaccatg tgaaataatt tgggcttaaa agtgaacata aattatagag tggaaggtaa	1719
gggacaaaag ccttttacct ttaattttcc tggagaatta tataaagggtt ttcttagaac	1779
aattttgccc tgattactga agcgtcaaata aaagctggag tgaaaatttt gttttgaaaa	1839
gggtgctcaag ctctgacatt tttgggtttc atagtcgtga agtatattatc atttgcatga	1899
ctaattggcac aggaaaaacc tattcataag ttttacaatc aagtatagag gggctctcag	1959
ctaacttagt tatacataaa tgctgaaaag attatcttga gctgggcctt gggagaagaa	2019
tttggccttc agaactgcaa tatcactgag cctgcgatct atacaccacc ccacattttg	2079
ttggtttcac agtcttgtgc aagtaacctc tgggtcttacg tgtgtaactg agagaagagt	2139
gtgtgtttgt gtgtgcatgt gtgtttattg ttctaagaa tttggcaciaa gtcagagata	2199
attgcctata ctaagaatct atactgcaga atatagtgtg tcaaaaactt ttttctttta	2259
aattattaaa gtgtctttta tacttttatg aaatcattgg tagccccca agtgtttaat	2319
aactggcatt aagcttagag ggtgaaaaaa aaaaaaaga ttgatagtat ttttcataat	2379
gaaaaaactg aagagatacg tgaatgaaac caggccatag ctgtcataaa tctttgactt	2439
ttgaatatatt acattcttca gtataatttt ttataatcct caattatgaa ccaccttggt	2499
tataggacaa aaaaatttaa ccaattttat tgaaacgaat ttcactgtgt aaaagttggt	2559

```

ttgattcaaa catgtagaga agttgtagat tcaagatata tgatttctct atggaaataa 2619
aaatatttgt tagtgaattg gttgagtttt gattcctcta acttctcaga atgattcttt 2679
agaattctat aattcatagc aatttttgac aagtaagatt gcaaaataga aatatctata 2739
aagattccac agtttgacat tatggcttgc tatgcagatg tgaaaatagg ttaaataata 2799
tgaaagatat ggcagaatgt aaagtggaaa agatgacctt aaattttgag ttgtattaat 2859
agttaaaaac atttgtgtca gatgacaggg tgggctttta ctgtcaagac atgaataaga 2919
actgatctgg ctgcctgatg agtggtttcca cgcagccctg catatttagt gaccaaggca 2979
tcaaggacat cccgaaactg gaaattcata tccatctggg atgaatatat aactcagctg 3039
ggcaaagtaa tgtgtttggt gagatattac agtaataaaa cacttaagaa caggaagatt 3099
acatttggtg ggcctacggg aaccttagtg gctacagaag aaagttgacc ttgtgtcact 3159
atatttttta tgccctgatc agactagcca cttagataag tgaaagtttt tctaacctgc 3219
ccttaaaata tttggttttg tccaaagacc cactttttct ttagccttgt ggtaggattt 3279
ccattattta cttttatact a 3300

```

```

<210> 457
<211> 3577
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (177) .. (1835)

```

```

<400> 457
agtcggaat tcccggtcg acgatttcgt cgcctagga gaaaacgtct gactccagcc 60
accggccttc aaggcacggc tttttattcc ttcggctggt cggcctctcg cccttcagct 120
acctgtgcgt ccctccgtcc cgccccgtcc cggggtcacc cggagcctg tccgct 176
atg cgg ctg cct cta gcc cca ggt cgg ctg cgg cgg ggc agc ccc 224
Met Arg Leu Leu Pro Leu Ala Pro Gly Arg Leu Arg Arg Gly Ser Pro
1 5 10 15
cgc cac ctg ccc tcc tgc agc cca gcg ctg cta ctg ctg gtg ctg ggc 272
Arg His Leu Pro Ser Cys Ser Pro Ala Leu Leu Leu Leu Val Leu Gly
17 22 27 32
ggc tgc ctg ggg gtc ttc ggg gtg gct gcg gga acc cgg agg ccc aac 320
Gly Cys Leu Gly Val Phe Gly Val Ala Ala Gly Thr Arg Arg Pro Asn
33 38 43 48

```

gtg gtg ctg ctc ctc acg gac gac cag gac gaa gtg ctc ggc ggc atg	368
Val Val Leu Leu Leu Thr Asp Asp Gln Asp Glu Val Leu Gly Gly Met	
49 54 59 64	
aca cca cta aag aaa acc aaa gct ctc atc gga gag atg ggg atg act	416
Thr Pro Leu Lys Lys Thr Lys Ala Leu Ile Gly Glu Met Gly Met Thr	
65 70 75 80	
ttt tcc agt gct tat gtg cca agt gct ctc tgc tgc ccc agc aga gcc	464
Phe Ser Ser Ala Tyr Val Pro Ser Ala Leu Cys Cys Pro Ser Arg Ala	
81 86 91 96	
agt atc ctg aca gga aag tac cca cat aat cat cac gtt gtg aac aac	512
Ser Ile Leu Thr Gly Lys Tyr Pro His Asn His His Val Val Asn Asn	
97 102 107 112	
act ctg gag ggg aac tgc agt agt aag tcc tgg cag aag atc caa gaa	560
Thr Leu Glu Gly Asn Cys Ser Ser Lys Ser Trp Gln Lys Ile Gln Glu	
113 118 123 128	
cca aat act ttc cca gca att ctc aga tca atg tgt ggt tat cag acc	608
Pro Asn Thr Phe Pro Ala Ile Leu Arg Ser Met Cys Gly Tyr Gln Thr	
129 134 139 144	
ttt ttt gca ggg aaa tat tta aat gag tac gga gcc cca gat gca ggt	656
Phe Phe Ala Gly Lys Tyr Leu Asn Glu Tyr Gly Ala Pro Asp Ala Gly	
145 150 155 160	
gga cta gaa cac gtt cct ctg ggt tgg agt tac tgg tat gcc ttg gaa	704
Gly Leu Glu His Val Pro Leu Gly Trp Ser Tyr Trp Tyr Ala Leu Glu	
161 166 171 176	
aag aat tct aag tat tat aat tac acc ctg tct atc aat ggg aag gca	752
Lys Asn Ser Lys Tyr Tyr Asn Tyr Thr Leu Ser Ile Asn Gly Lys Ala	
177 182 187 192	
cgg aag cat ggt gaa aac tat agt gtg gac tac ctg aca gat gtt ttg	800
Arg Lys His Gly Glu Asn Tyr Ser Val Asp Tyr Leu Thr Asp Val Leu	
193 198 203 208	
gct aat gtc tcc ttg gac ttt ctg gac tac aag tcc aac ttt gag ccc	848
Ala Asn Val Ser Leu Asp Phe Leu Asp Tyr Lys Ser Asn Phe Glu Pro	
209 214 219 224	
ttc ttc atg atg atc gcc act cca gcg cct cat tcg cct tgg aca gct	896
Phe Phe Met Met Ile Ala Thr Pro Ala Pro His Ser Pro Trp Thr Ala	
225 230 235 240	
gca cct cag tac cag aag gct ttc cag aat gtc ttt gca cca aga aac	944
Ala Pro Gln Tyr Gln Lys Ala Phe Gln Asn Val Phe Ala Pro Arg Asn	
241 246 251 256	
aag aac ttc aac atc cat gga acg aac aag cac tgg tta att agg caa	992
Lys Asn Phe Asn Ile His Gly Thr Asn Lys His Trp Leu Ile Arg Gln	
257 262 267 272	
gcc aag act cca atg act aat tct tca ata cag ttt tta gat aat gca	1040

Ala Lys Thr Pro Met Thr Asn Ser Ser Ile Gln Phe Leu Asp Asn Ala	
273 278 283 288	
ttt agg aaa agg tgg caa act ctc ctc tca gtt gat gac ctt gtg gag	1088
Phe Arg Lys Arg Trp Gln Thr Leu Leu Ser Val Asp Asp Leu Val Glu	
289 294 299 304	
aaa ctg gtc aag agg ctg gag ttc act ggg gag ctc aac aac act tac	1136
Lys Leu Val Lys Arg Leu Glu Phe Thr Gly Glu Leu Asn Asn Thr Tyr	
305 310 315 320	
atc ttc tat acc tca gac aat ggc tat cac aca gga cag ttt tcc ttg	1184
Ile Phe Tyr Thr Ser Asp Asn Gly Tyr His Thr Gly Gln Phe Ser Leu	
321 326 331 336	
cca ata gac aag aga cag ctg tat gag ttt gat atc aaa gtt cca ctg	1232
Pro Ile Asp Lys Arg Gln Leu Tyr Glu Phe Asp Ile Lys Val Pro Leu	
337 342 347 352	
ttg gtt cga gga cct ggg atc aaa cca aat cag aca agc aag atg ctg	1280
Leu Val Arg Gly Pro Gly Ile Lys Pro Asn Gln Thr Ser Lys Met Leu	
353 358 363 368	
gtt gcc aac att gac ttg ggt cct act att ttg gac att gct ggc tac	1328
Val Ala Asn Ile Asp Leu Gly Pro Thr Ile Leu Asp Ile Ala Gly Tyr	
369 374 379 384	
gac cta aat aag aca cag atg gat ggg atg tcc tta ttg ccc att ttg	1376
Asp Leu Asn Lys Thr Gln Met Asp Gly Met Ser Leu Leu Pro Ile Leu	
385 390 395 400	
aga ggt gcc agt aac ttg acc tgg cga tca gat gtc ctg gtg gaa tac	1424
Arg Gly Ala Ser Asn Leu Thr Trp Arg Ser Asp Val Leu Val Glu Tyr	
401 406 411 416	
caa gga gaa ggc cgt aac gtc act gac cca aca tgc cct tcc ctg agt	1472
Gln Gly Glu Gly Arg Asn Val Thr Asp Pro Thr Cys Pro Ser Leu Ser	
417 422 427 432	
cct ggc gta tct caa tgc ttc cca gac tgt gta tgt gaa gat gct tat	1520
Pro Gly Val Ser Gln Cys Phe Pro Asp Cys Val Cys Glu Asp Ala Tyr	
433 438 443 448	
aac aat acc tat gcc tgt gtg agg aca atg tca gca ttg tgg aat ttg	1568
Asn Asn Thr Tyr Ala Cys Val Arg Thr Met Ser Ala Leu Trp Asn Leu	
449 454 459 464	
cag tat tgc gag ttt gat gac cag gag gtg ttt gta gaa gtc tat aat	1616
Gln Tyr Cys Glu Phe Asp Asp Gln Glu Val Phe Val Glu Val Tyr Asn	
465 470 475 480	
ctg act gca gac cca gac cag atc act aac att gct aaa acc ata gac	1664
Leu Thr Ala Asp Pro Asp Gln Ile Thr Asn Ile Ala Lys Thr Ile Asp	
481 486 491 496	
cca gag ctt tta gga aag atg aac tat cgg tta atg atg tta cag tcc	1712
Pro Glu Leu Leu Gly Lys Met Asn Tyr Arg Leu Met Met Leu Gln Ser	

497	502	507	512	
tgt tct ggg cca acc	tgt cgc act cca ggg	gtt ttt gac ccc gga	tac	1760
Cys Ser Gly Pro Thr	Cys Arg Thr Pro Gly	Val Phe Asp Pro Gly	Tyr	
513	518	523	528	
agg ttt gac ccc cgt	ctc atg ttc agc aat	cgc ggc agt gtc agg	act	1808
Arg Phe Asp Pro Arg	Leu Met Phe Ser Asn	Arg Gly Ser Val Arg	Thr	
529	534	539	544	
cga aga ttt tcc aaa	cat ctt ctg tag cgacc	tcacacagcc tctgcagatg		1860
Arg Arg Phe Ser Lys	His Leu Leu *			
545	550			
gatccctgca cgccctctttc	tgatgaagtg attgtagtag	gtgtotgtag ctagtcttca		1920
agaccacacc tggaagagtt	tctgggctgg ctttaagtcc	tgtttgaaaa agcaaccag		1980
tcagctgact tcctcgtgca	atgtgttaaa ctgtgaactc	tgcccatgtg tcaggagtgg		2040
ctgtctctgg tctcttcott	tagctgacaa ggacactcct	gaggctctttg ttctcactgt		2100
attcttttta tcctggggcc	acagttcttg attattcttc	ttgtgggttaa agactgaatt		2160
tgtaaaccce ttacagataaa	tggcagtact ttaggacaça	cacaaacaca cagatacacc		2220
ttttgatatg taagcttgac	ctaaagtcaa aggacctgtg	tagcatttca gattgagcac		2280
ttcactatca aaaatactaa	catcacatgg cttgaagagt	aaccatcaga gctgaatcat		2340
ccaagtaaga acaagtacca	ttgttgattg ataagtagag	atacattttt tatgatgttc		2400
atcacagtgt ggtaagggtg	caaattcaaa acatgtcacc	caagctctgt tcatgttttt		2460
gtgaattcta ggctgggtgt	gcactgaaat agagcagtaa	gcttgtgata aaggccaatt		2520
ccaggtagct cttgaagggtg	atagccatct actttccagt	ggctgccaac cacagggagt		2580
gccagttaac actggaagga	ttaaggcaag gtcccttctc	ttgagactcc cctctgagat		2640
ctgaaaaatg aagtggctta	ggaacatcag cagtgaagaa	ctgccaagag ttggtgaagg		2700
ttgtctcttc cgagggcctt	ctgaagacag ggctcttgaa	cagacaagtg gaagggctgt		2760
accagggata aaggaaagaa	gtgcctgtcc agcagggagc	ttgaatttaa gttccatgta		2820
tgaagtcatt ggctctatct	gcatttttct gtcattctct	tcatttgttt taagggtggaa		2880
aattttctta cagttgatgc	aaagtatcaa ctactttacc	ctaccttctc cctttttaga		2940
tggtttcttc ctgagttttg	gagtccttgta tgattatcag	tattcccttg tcaaaatcaa		3000
atctattcag gtttcttcac	tggttgagaac acctaaatgt	ttttattttt gagaagtggg		3060
gacagagtct cactatgtca	cccaggctgg agtgcaatgg	catgatctca gctcactgca		3120
accttcgcct cctgggttca	agcgattctc ctgcctccgc	ctcctgagta gctgggatta		3180

```

taggcacaca ccaccacgcc cagctaattt tttgtatttt tagtagagac agagtttcac 3240
catgttggcc aggctgggtct tgaactcctg accttgtgat ccaccacct cggcctccca 3300
gagtgtctggg attacaggca tgagccacca cgcttggcta agaacaccta aatttttatg 3360
tttcttggct caaaaaccag ttccatttct aatgttgtcc tcacaagaag gctaattggg 3420
ggtagagacag caggggagga ggaagagctg tggtttgtaa cttgttcaac tcaggcaata 3480
agcgatttta gctttattta aagtcttctg tccagcttta agcactttgt aagacatggc 3540
tgaaagtagc tttttatatca gaattgcaga tagtcat 3577

```

```

<210> 458
<211> 1520
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (271)..(1161)

```

```

<400> 458
aggggggatt tgtttcatcg cctgcggtac cggcccggaa ttcccgggtc gaccacgcg 60
tccgctgcag ccgagagtcc agagaggagg aagctcctgc cggctgagcg ggcctggagg 120
aagtgagcag cggggctcct gcctcccgcc ctgggtccccg aagaccccag aagaacccgg 180
aacttgcttc cattcggaat ccagggacca ccctttgcac tcagtaggcc tttgttttcc 240
tgcgtggaaa gcggttgggc ttgggaggcg      atg gag ccg gag ttc ttg tac 291
                                   Met Glu Pro Glu Phe Leu Tyr
                                   1               5

gac ctg ctg cag ctc ccc aag ggg gtg gag ccc cca gcg gag gag gag 339
Asp Leu Leu Gln Leu Pro Lys Gly Val Glu Pro Pro Ala Glu Glu Glu
  8               13               18               23

ctc tca aaa gga gga aag aag aaa tac ctg cca ccc act tcc cgg aag 387
Leu Ser Lys Gly Gly Lys Lys Lys Tyr Leu Pro Pro Thr Ser Arg Lys
 24               29               34               39

gac ccc aaa ttt gaa gaa ctg cag aag ctg cag gtg ttg atg gag tgg 435
Asp Pro Lys Phe Glu Glu Leu Gln Lys Leu Gln Val Leu Met Glu Trp
 40               45               50               55

atc aat gcc act ctt ctc ccc gag cac att gtg gtc cgc agc ctg gag 483
Ile Asn Ala Thr Leu Leu Pro Glu His Ile Val Val Arg Ser Leu Glu
 56               61               66               71

gag gac atg ttc gac ggg ctc atc cta cac cac cta ttc cag agg ctg 531

```

Glu Asp Met Phe Asp Gly Leu Ile Leu His His Leu Phe Gln Arg Leu	
72 77 82 87	
gcg gcg ctc aag ctg gaa gca gag gac atc gcc ctg aca gcc aca agc	579
Ala Ala Leu Lys Leu Glu Ala Glu Asp Ile Ala Leu Thr Ala Thr Ser	
88 93 98 103	
cag aag cac aag ctc aca gtg gtg ctg gag gcc gtg aac cgg agt ctg	627
Gln Lys His Lys Leu Thr Val Val Leu Glu Ala Val Asn Arg Ser Leu	
104 109 114 119	
cag ctg gag gag tgg cag gcc aag tgg agc gtg gag agc atc ttc aac	675
Gln Leu Glu Glu Trp Gln Ala Lys Trp Ser Val Glu Ser Ile Phe Asn	
120 125 130 135	
aag gac ctg ttg tct acc ctg cac ctc ctt gtg gcc ctg gcc aag cgc	723
Lys Asp Leu Leu Ser Thr Leu His Leu Leu Val Ala Leu Ala Lys Arg	
136 141 146 151	
ttc cag ccc gac ctc tcc ctc cca acc aac gtc cag gtg gag gtc atc	771
Phe Gln Pro Asp Leu Ser Leu Pro Thr Asn Val Gln Val Glu Val Ile	
152 157 162 167	
act atc gag agc acc aaa agt ggt ctg aag tca gag aag ttg gtg gaa	819
Thr Ile Glu Ser Thr Lys Ser Gly Leu Lys Ser Glu Lys Leu Val Glu	
168 173 178 183	
cag ctc act gaa tac agc aca gac aag gac gag cct cca aag gac gtc	867
Gln Leu Thr Glu Tyr Ser Thr Asp Lys Asp Glu Pro Pro Lys Asp Val	
184 189 194 199	
ttt gat gaa tta ttt aag ctg gct cgg gag aaa gtg aac gca gtg aaa	915
Phe Asp Glu Leu Phe Lys Leu Ala Pro Glu Lys Val Asn Ala Val Lys	
200 205 210 215	
gag gcc atc gtg aac ttt gtc aac cag aag ctg gac cgc ctg ggc ctg	963
Glu Ala Ile Val Asn Phe Val Asn Gln Lys Leu Asp Arg Leu Gly Leu	
216 221 226 231	
tct gtg cag aat ctg gac acc cag ttt gca gat ggg gtc atc tta ctc	1011
Ser Val Gln Asn Leu Asp Thr Gln Phe Ala Asp Gly Val Ile Leu Leu	
232 237 242 247	
ttg ctg att gga caa ctt gaa ggc ttc ttc ctg cac tta aag gaa ttc	1059
Leu Leu Ile Gly Gln Leu Glu Gly Phe Phe Leu His Leu Lys Glu Phe	
248 253 258 263	
tac ctc act ccc aac tct cct gca gaa atg ctg cac aac gtc acc ctg	1107
Tyr Leu Thr Pro Asn Ser Pro Ala Glu Met Leu His Asn Val Thr Leu	
264 269 274 279	
gcg ctg gag ctg cct gaa gga cga ggg cct gct cag ctg ccc tgt cag	1155
Ala Leu Glu Leu Pro Glu Gly Arg Gly Pro Ala Gln Leu Pro Cys Gln	
280 285 290 295	
ccc tga agatatcgtg aacaaggatg ccaagagcac actgcgggtg ctctatggtc	1211
Pro *	

296

tgttctgcaa gcacacgcag aaggcacaca gggacaggac gcccctatgga gcccgaatt 1271
gacctcact gcctccaaag cccagagcct gcctgtcagc ccagctggag ggcccaggc 1331
tgcaggggtgt cctcccacag tcccgtgtt tcctgtgcat tcgtgaccgc cttccctccc 1391
accctgtctc ctgtctccat cgttggatta tctttgaacc cccttgtgtg gatcattttg 1451
agccgcctgg ccttgctcag tttattttta taaaagtatt tctgggaggg attctggaaa 1511
aaaaaaaaa 1520

<210> 459
<211> 6223
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (59)..(4132)

<400> 459

ctcgtgcct gcggtaccgg tccggaattc ccgggtcgac gatttcgtcc acgggagc 58
atg gcg gac acc gac ctg ttc atg gaa tgt gag gag gag gag ttg gag 106
Met Ala Asp Thr Asp Leu Phe Met Glu Cys Glu Glu Glu Glu Leu Glu
1 5 10 15
cca tgg cag aaa atc agt gat gtc att gag gac tct gta gtt gaa gat 154
Pro Trp Gln Lys Ile Ser Asp Val Ile Glu Asp Ser Val Val Glu Asp
17 22 27 32
tat aat tca gtg gat aaa act acc aca gct ggc aat cct ttg gtc cag 202
Tyr Asn Ser Val Asp Lys Thr Thr Thr Ala Gly Asn Pro Leu Val Gln
33 38 43 48
caa ggt gga cag cca ctc atc ctg acc cag aat cca gcc cca ggt ctg 250
Gln Gly Gly Gln Pro Leu Ile Leu Thr Gln Asn Pro Ala Pro Gly Leu
49 54 59 64
ggc aca atg gtt act caa cca gta ttg agg cct gtt cag gtc atg cag 298
Gly Thr Met Val Thr Gln Pro Val Leu Arg Pro Val Gln Val Met Gln
65 70 75 80
aat gcc aat cat gtg act agt tcc cct gtg gcc tca caa cca ata ttt 346
Asn Ala Asn His Val Thr Ser Ser Pro Val Ala Ser Gln Pro Ile Phe
81 86 91 96
atc act acg cag gga ttt cct gta agg aat gtc cgg cct gta caa aat 394
Ile Thr Thr Gln Gly Phe Pro Val Arg Asn Val Arg Pro Val Gln Asn
97 102 107 112
gca atg aat cag gtt ggg att gtg ctg aac gta cag caa ggc caa acg 442

Ala Met Asn Gln Val Gly Ile Val Leu Asn Val Gln Gln Gly Gln Thr	
113 118 123 128	
gtt aga cca att aca cta gtt cca gcc cca ggt acc cag ttt gtt aag	490
Val Arg Pro Ile Thr Leu Val Pro Ala Pro Gly Thr Gln Phe Val Lys	
129 134 139 144	
ccg aca gtt gga gtt cca caa gtg ttc tcc cag atg acc cct gtg agg	538
Pro Thr Val Gly Val Pro Gln Val Phe Ser Gln Met Thr Pro Val Arg	
145 150 155 160	
cca ggc tcc aca atg cct gtg agg ccc acc acc aac acc ttc acc acc	586
Pro Gly Ser Thr Met Pro Val Arg Pro Thr Thr Asn Thr Phe Thr Thr	
161 166 171 176	
gtc atc ccg gcc act ctt acc att cga agc acc gtc cca cag tcc cag	634
Val Ile Pro Ala Thr Leu Thr Ile Arg Ser Thr Val Pro Gln Ser Gln	
177 182 187 192	
tcc cag cag acc aag tcc act ccc agc act tct acc act ccc act gcc	682
Ser Gln Gln Thr Lys Ser Thr Pro Ser Thr Ser Thr Thr Pro Thr Ala	
193 198 203 208	
aca cag cca acc tca ctg ggg caa cta gct gtt cag tct cca ggc cag	730
Thr Gln Pro Thr Ser Leu Gly Gln Leu Ala Val Gln Ser Pro Gly Gln	
209 214 219 224	
tca aac cag acc acg aat ccc aag cta gct ccc tcc ttc ccc tct cca	778
Ser Asn Gln Thr Thr Asn Pro Lys Leu Ala Pro Ser Phe Pro Ser Pro	
225 230 235 240	
cct gca gtg agc att gcc agc ttt gtc act gtg aag cga cct ggt gtt	826
Pro Ala Val Ser Ile Ala Ser Phe Val Thr Val Lys Arg Pro Gly Val	
241 246 251 256	
aca ggc gaa aat agc aat gaa gtg gcc aaa ttg gtg aat acc ctt aac	874
Thr Gly Glu Asn Ser Asn Glu Val Ala Lys Leu Val Asn Thr Leu Asn	
257 262 267 272	
acc atc cct tcc ctg ggc cag agt cct ggg cca gtg gtg gtg tcc aac	922
Thr Ile Pro Ser Leu Gly Gln Ser Pro Gly Pro Val Val Val Ser Asn	
273 278 283 288	
aac agc tct gct cat ggc tct caa aga acc agc gga cct gag tct tca	970
Asn Ser Ser Ala His Gly Ser Gln Arg Thr Ser Gly Pro Glu Ser Ser	
289 294 299 304	
atg aaa gtg acc tct tcc atc cca gta ttt gac ctc cag gat ggt gga	1018
Met Lys Val Thr Ser Ser Ile Pro Val Phe Asp Leu Gln Asp Gly Gly	
305 310 315 320	
cgg aaa ata tgt cca cga tgt aat gct caa ttt cgt gtt act gaa gct	1066
Arg Lys Ile Cys Pro Arg Cys Asn Ala Gln Phe Arg Val Thr Glu Ala	
321 326 331 336	
ttg aga ggt cac atg tgt tac tgt tgc cca gaa atg gtt gaa tac cag	1114
Leu Arg Gly His Met Cys Tyr Cys Cys Pro Glu Met Val Glu Tyr Gln	

337	342	347	352	
aag aaa gga aag tcc ctg gat tca gaa ccc agt gtc cca tca gca gca				1162
Lys Lys Gly Lys Ser Leu Asp Ser Glu Pro Ser Val Pro Ser Ala Ala				
353	358	363	368	
aag ccc cca tcc cct gag aaa aca gct cct gtt gct tcc aca ccc tct				1210
Lys Pro Pro Ser Pro Glu Lys Thr Ala Pro Val Ala Ser Thr Pro Ser				
369	374	379	384	
tct aca cct att cct gct ctg tca ccg cct acc aaa gta cca gaa cca				1258
Ser Thr Pro Ile Pro Ala Leu Ser Pro Pro Thr Lys Val Pro Glu Pro				
385	390	395	400	
aat gag aac gtg ggc gat gcc gtc cag acc aaa ctc att atg ctt gta				1306
Asn Glu Asn Val Gly Asp Ala Val Gln Thr Lys Leu Ile Met Leu Val				
401	406	411	416	
gat gac ttc tac tat gga cgg gat ggt ggc aaa gta gcc cag ctc aca				1354
Asp Asp Phe Tyr Tyr Gly Arg Asp Gly Gly Lys Val Ala Gln Leu Thr				
417	422	427	432	
aat ttc cct aag gtc gcc aca tct ttc cga tgc cca cat tgt acc aaa				1402
Asn Phe Pro Lys Val Ala Thr Ser Phe Arg Cys Pro His Cys Thr Lys				
433	438	443	448	
agg cta aaa aac aat att cga ttc atg aac cat atg aaa cac cac gta				1450
Arg Leu Lys Asn Asn Ile Arg Phe Met Asn His Met Lys His His Val				
449	454	459	464	
gaa ctc gat cag cag aac ggt gag gta gat ggt cac act atc tgc cag				1498
Glu Leu Asp Gln Gln Asn Gly Glu Val Asp Gly His Thr Ile Cys Gln				
465	470	475	480	
cac tgt tac cgc cag ttt tcc act ccc ttc cag ctt cag tgc cac ttg				1546
His Cys Tyr Arg Gln Phe Ser Thr Pro Phe Gln Leu Gln Cys His Leu				
481	486	491	496	
gaa aat gtt cat agt ccc tat gaa tct act acc aag tgc aag atc tgt				1594
Glu Asn Val His Ser Pro Tyr Glu Ser Thr Thr Lys Cys Lys Ile Cys				
497	502	507	512	
gaa tgg gcg ttt gaa agt gag cca cta ttt ctc cag cat atg aag gat				1642
Glu Trp Ala Phe Glu Ser Glu Pro Leu Phe Leu Gln His Met Lys Asp				
513	518	523	528	
act cat aag cct gga gag atg cct tat gtt tgc cag gtg tgt caa tat				1690
Thr His Lys Pro Gly Glu Met Pro Tyr Val Cys Gln Val Cys Gln Tyr				
529	534	539	544	
cgc tcc tca ctc tac tct gag gta gat gtc cat ttt cgg atg atc cat				1738
Arg Ser Ser Leu Tyr Ser Glu Val Asp Val His Phe Arg Met Ile His				
545	550	555	560	
gag gat acc cgg cat ctg ctc tgc cct tat tgc ctg aag gtc ttc aaa				1786
Glu Asp Thr Arg His Leu Leu Cys Pro Tyr Cys Leu Lys Val Phe Lys				
561	566	571	576	

aat ggc aat gca ttc caa cag cat tac atg agg cac cag aag aga aat	1834
Asn Gly Asn Ala Phe Gln Gln His Tyr Met Arg His Gln Lys Arg Asn	
577 582 587 592	
ggt tat cac tgc aac aaa tgc cgg ctg cag ttt ctc ttt gcc aag gac	1882
Val Tyr His Cys Asn Lys Cys Arg Leu Gln Phe Leu Phe Ala Lys Asp	
593 598 603 608	
aaa att gaa cac aag ctt caa cac cat aaa acc ttc cgt aaa ccc aag	1930
Lys Ile Glu His Lys Leu Gln His His Lys Thr Phe Arg Lys Pro Lys	
609 614 619 624	
cag ctg gag ggc ttg aaa cca ggc acc aag gtg aca atc cgg gct tcc	1978
Gln Leu Glu Gly Leu Lys Pro Gly Thr Lys Val Thr Ile Arg Ala Ser	
625 630 635 640	
cga ggg cag cca cga act gtt cct gta tcc tct aat gat aca cct ccc	2026
Arg Gly Gln Pro Arg Thr Val Pro Val Ser Ser Asn Asp Thr Pro Pro	
641 646 651 656	
agc gcc ttg cag gag gca gca ccg ctg acc tcc tca atg gac cct ctg	2074
Ser Ala Leu Gln Glu Ala Ala Pro Leu Thr Ser Ser Met Asp Pro Leu	
657 662 667 672	
cct gtc ttc ctt tat ccc cct gtc cag cgc agc atc cag aag aga gct	2122
Pro Val Phe Leu Tyr Pro Pro Val Gln Arg Ser Ile Gln Lys Arg Ala	
673 678 683 688	
ggt agg aaa atg agt gtc atg ggc cgg cag aca tgc ctg gag tgc agc	2170
Val Arg Lys Met Ser Val Met Gly Arg Gln Thr Cys Leu Glu Cys Ser	
689 694 699 704	
ttc gag atc cca gac ttc cct aat cat ttc cct act tac gta cac tgc	2218
Phe Glu Ile Pro Asp Phe Pro Asn His Phe Pro Thr Tyr Val His Cys	
705 710 715 720	
tct ctg tgt cgc tat agc acc tgc tgt tct cga gct tat gcc aac cac	2266
Ser Leu Cys Arg Tyr Ser Thr Cys Cys Ser Arg Ala Tyr Ala Asn His	
721 726 731 736	
atg atc aac aat cat gtt cca cgg aag agc ccc aag tat ttg gct ttg	2314
Met Ile Asn Asn His Val Pro Arg Lys Ser Pro Lys Tyr Leu Ala Leu	
737 742 747 752	
ttt aaa aat tct gtg agt gga atc aag ctg gcc tgc act tca tgt acc	2362
Phe Lys Asn Ser Val Ser Gly Ile Lys Leu Ala Cys Thr Ser Cys Thr	
753 758 763 768	
ttt gtt acc tct gtg ggc gat gct atg gcc aag cat ttg gta ttc aac	2410
Phe Val Thr Ser Val Gly Asp Ala Met Ala Lys His Leu Val Phe Asn	
769 774 779 784	
ccc tct cac aga tcc agc agc atc ctg cca cgg gga ctc act tgg ata	2458
Pro Ser His Arg Ser Ser Ser Ile Leu Pro Arg Gly Leu Thr Trp Ile	
785 790 795 800	

gct cac tca agg cat ggc cag act cgt gac cga gtg cat gac cgg aac	2506
Ala His Ser Arg His Gly Gln Thr Arg Asp Arg Val His Asp Arg Asn	
801 806 811 816	
gtg aag aat atg tac cct cct cct tcc ttc ccc act aac aaa gct gcc	2554
Val Lys Asn Met Tyr Pro Pro Pro Ser Phe Pro Thr Asn Lys Ala Ala	
817 822 827 832	
act gtg aaa tct gcg ggg gcc acc cca gct gag cct gaa gag cta cta	2602
Thr Val Lys Ser Ala Gly Ala Thr Pro Ala Glu Pro Glu Glu Leu Leu	
833 838 843 848	
act ccc tta gcc cca gca ctc cca tca cca gcc tca act gca acc cca	2650
Thr Pro Leu Ala Pro Ala Leu Pro Ser Pro Ala Ser Thr Ala Thr Pro	
849 854 859 864	
cca cca acc ccc act cac ccg cag gct tta gcc ctt cca ccg ctg gct	2698
Pro Pro Thr Pro Thr His Pro Gln Ala Leu Ala Leu Pro Pro Leu Ala	
865 870 875 880	
aca gag gga gcc gaa tgt ctg aat gtt gat gat cag gat gaa ggg agc	2746
Thr Glu Gly Ala Glu Cys Leu Asn Val Asp Asp Gln Asp Glu Gly Ser	
881 886 891 896	
cca gtc acc caa gaa cct gag cta gca tca ggt ggt ggt ggt agt ggt	2794
Pro Val Thr Gln Glu Pro Glu Leu Ala Ser Gly Gly Gly Gly Ser Gly	
897 902 907 912	
gga gtt ggc aaa aag gag cag ctg tct gtg aag aag ctt cga gta gta	2842
Gly Val Gly Lys Lys Glu Gln Leu Ser Val Lys Lys Leu Arg Val Val	
913 918 923 928	
ctg ttt gct cta tgc tgc aat aca gaa cag gca gct gaa cac ttc cga	2890
Leu Phe Ala Leu Cys Cys Asn Thr Glu Gln Ala Ala Glu His Phe Arg	
929 934 939 944	
aat ccc cag cga cgt att cgc cgt tgg ctt cga cgt ttc cag gcc tcc	2938
Asn Pro Gln Arg Arg Ile Arg Arg Trp Leu Arg Arg Phe Gln Ala Ser	
945 950 955 960	
cag ggg gag aat cta gag ggc aaa tat ctg agc ttt gag gca gaa gag	2986
Gln Gly Glu Asn Leu Glu Gly Lys Tyr Leu Ser Phe Glu Ala Glu Glu	
961 966 971 976	
aaa ctg gct gag tgg gtg cta acc cag cgc gaa caa cag cta cct gta	3034
Lys Leu Ala Glu Trp Val Leu Thr Gln Arg Glu Gln Gln Leu Pro Val	
977 982 987 992	
aat gag gag acc ttg ttc cag aag gcc acc aaa ata gga cgt tct ttg	3082
Asn Glu Glu Thr Leu Phe Gln Lys Ala Thr Lys Ile Gly Arg Ser Leu	
993 998 1003 1008	
gaa ggg ggg ttt aag atc tcc tat gag tgg gct gtg cgt ttc atg ctg	3130
Glu Gly Gly Phe Lys Ile Ser Tyr Glu Trp Ala Val Arg Phe Met Leu	
1009 1014 1019 1024	
cgg cac cac ctg act ccc cat gcc cgg cga gct gtg gcc cac acc cta	3178

[illegible]

1249	1254	1259	1264	
cta gtt cag cgc tcc ttc ctg gtg gct agt gtt ctg cct ggc ccc gat				3898
Leu Val Gln Arg Ser Phe Leu Val Ala Ser Val Leu Pro Gly Pro Asp				
1265	1270	1275	1280	
ggc aac att aac tca cct aca aga aat gct gac atg cag gag gag cta				3946
Gly Asn Ile Asn Ser Pro Thr Arg Asn Ala Asp Met Gln Glu Glu Leu				
1281	1286	1291	1296	
att gcc tcc cta gag gag caa ctg aag ctg agt ggg gaa cat tct gag				3994
Ile Ala Ser Leu Glu Glu Gln Leu Lys Leu Ser Gly Glu His Ser Glu				
1297	1302	1307	1312	
tct tcc act cca cga ccc aga tca tct cct gaa gag aca att gag cct				4042
Ser Ser Thr Pro Arg Pro Arg Ser Ser Pro Glu Glu Thr Ile Glu Pro				
1313	1318	1323	1328	
gaa agt ctt cac cag ctc ttt gag ggt gaa agt gag acc gag tct ttc				4090
Glu Ser Leu His Gln Leu Phe Glu Gly Glu Ser Glu Thr Glu Ser Phe				
1329	1334	1339	1344	
tat ggc ttt gaa gaa gct gac cta gat ctg atg gag att tga gtgttg				4139
Tyr Gly Phe Glu Glu Ala Asp Leu Asp Leu Met Glu Ile *				
1345	1350	1355		
ggatcatgagg ggggtgtggag tgggggtggg aacatgtgag ggagggtaaa ggggcttagg				4199
gaaaaggggg cataccaggt ggggtatttg gtttctattt tttaatttta taccaccact				4259
ccccctgaa gttgacttac acttcctgt ggatttgtgg attaattagg aaaaccaata				4319
gtaatcacgt ctgagccaag gagctggccc attgggtcatt cacttctgct aaaaacaggt				4379
ttttgtgact tttttttttt ttaaatttaa atcactgtgt ttggtatttt tctgacaaaa				4439
ttaagaaaaa gaaaaaaaat tatttgtggg caaatgttaa atttttttgt tccccctttt				4499
acctcaattg tatcatagta ctgggttttt ttgtttgttt tattgtgtgg ccaatgtctt				4559
tgggcatgat gctatctaatt cattgttaat gtgagaacat ttctgaagat gggaaagaca				4619
aattatgtag ctacaaaact ggtttattat atatatggat aaaaaacttt ttccattgtg				4679
gtcttaacac ttttatataa aaatgaaaat ggaaaaaaag tccactgaa ctctctcttc				4739
cttctctctt tctttccttc cctctccaga gatgttggtt tctacagcaa cctagatat				4799
aaaattgtgg ctttaaaaaat gcatgaaacc accttaatt atccagaatg aatagatttg				4859
tcttttcttc accaccttcc ctccaaaaca tgacataaac aatatttttt gcacttgtga				4919
tccttgcccc ctttcccat tctcaacacc atccatccct ctggacaaag gatcatacag				4979
gtgttattag caagcaagag atactgaagc gatcaaacag ttttaggggtg gaagccattc				5039
ccagtttgag tcttcatcct gtaagcccc aggggcagtc cctgctttac tgaacttcat				5099

```

cctgttagat ggagagcatg cctgtttaag ggattactgg tcctacagcc aggagctaata 5159
tggtcaagaa gtgttgaact ttaaaaagac aagaccactt gttgaaatcc agcgtgctct 5219
gtggctttcc cctattttctc ttaatactta gggaagaatc tgacaggaag aagcgcacag 5279
gggtgtgcac aaagaaaatg acatgaatct ttattttttca ctgccagctt caaggaaaga 5339
aaattttttc tacaatttgc atgagggatt tttttaattg tatgtactca tggttgtaaa 5399
ccaaaacgta ctgtaccgta cagagaaaag gagcaaaaaa ccaagtcttc tgtttatcct 5459
gaggttttcc acaatgttcc cctcctgtga gccaaaggagg caaactgcac aagcttgtaa 5519
atggttcgctc tttaaaatgt acataagtgg aacatttaata aaaatgaggg gaaatggatt 5579
tataaacttg ttttttttct aggtgaccct gtttaatagg ctttcacaga ctggggaatg 5639
ctcaagatgt gatgggcctg gtggtacagg tgtgacattt gttaccaccc atttctccca 5699
ccccaccctg cttttttgtt tgtttgtttt ttcattcccc agcacactat aatatagtga 5759
actggaaaag tcccttccag aaacagcttg gccagctttg tgaacctttg acatctgaaa 5819
acaaccaagg atccatctgg gcttctcttc cccagctttt tgccctgatgc cattttattg 5879
acagacaatg gactttgaag tcagcctttg cctttgagaa agttcaagaa ctatgggttg 5939
tcacgtctat ctacaaccta atcctactct ttggtagtct ctgcagcagc cacagcctta 5999
gcagagctgg gggttcctgtc ttctgcacac gattgacttt cttgatgggt aatttttttt 6059
aagattatac caacagtgga tcagctgggt tttggccagg aagttgtctt tgtggactct 6119
gctgcatgg ctttagtagta gaaggaaatt tttttttggt tttgtttttt ataattcagt 6179
ttaatcaata aacatgtatt tattgactgt taaaaaaaaa aaaa 6223

```

```

<210> 460
<211> 6382
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (59) .. (4291)

```

```

<400> 460
ctcgtcgcct gcggtaccgg tccggaatcc ccgggtcgac gatttcgtcc accgggagc 58
atg gcg gac acc gac ctg ttc atg gaa tgt gag gag gag gag ttg gag 106
Met Ala Asp Thr Asp Leu Phe Met Glu Cys Glu Glu Glu Glu Leu Glu
1 5 10 15

```

cca tgg cag aaa atc agt gat gtc att gag gac tct gta gtt gaa gat	154
Pro Trp Gln Lys Ile Ser Asp Val Ile Glu Asp Ser Val Val Glu Asp	
17 22 27 32	
tat aat tca gtg gat aaa act acc aca gtt tct gtg agc cag cag cca	202
Tyr Asn Ser Val Asp Lys Thr Thr Thr Val Ser Val Ser Gln Gln Pro	
33 38 43 48	
gtc tcg gct cca gtg ccc atc gct gcc cat gct tct gtt gct ggg cac	250
Val Ser Ala Pro Val Pro Ile Ala Ala His Ala Ser Val Ala Gly His	
49 54 59 64	
ctc tct aca tcc acc acc gtt agt agc agc ggg gca cag aac agc gac	298
Leu Ser Thr Ser Thr Thr Val Ser Ser Ser Gly Ala Gln Asn Ser Asp	
65 70 75 80	
agt aca aag aag act ctt gtc aca cta att gcc aac aac aat gct ggc	346
Ser Thr Lys Lys Thr Leu Val Thr Leu Ile Ala Asn Asn Asn Ala Gly	
81 86 91 96	
aat cct ttg gtc cag caa ggt gga cag cca ctc atc ctg acc cag aat	394
Asn Pro Leu Val Gln Gln Gly Gly Gln Pro Leu Ile Leu Thr Gln Asn	
97 102 107 112	
cca gcc cca ggt ctg ggc aca atg gtt act caa cca gta ttg agg cct	442
Pro Ala Pro Gly Leu Gly Thr Met Val Thr Gln Pro Val Leu Arg Pro	
113 118 123 128	
gtt cag gtc atg cag aat gcc aat cat gtg act agt tcc cct gtg gcc	490
Val Gln Val Met Gln Asn Ala Asn His Val Thr Ser Ser Pro Val Ala	
129 134 139 144	
tca caa cca ata ttt atc act acg cag gga ttt cct gta agg aat gtc	538
Ser Gln Pro Ile Phe Ile Thr Thr Gln Gly Phe Pro Val Arg Asn Val	
145 150 155 160	
cgg cct gta caa aat gca atg aat cag gtt ggg att gtg ctg aac gta	586
Arg Pro Val Gln Asn Ala Met Asn Gln Val Gly Ile Val Leu Asn Val	
161 166 171 176	
cag caa ggc caa acg gtt aga cca att aca cta gtt cca gcc cca ggt	634
Gln Gln Gly Gln Thr Val Arg Pro Ile Thr Leu Val Pro Ala Pro Gly	
177 182 187 192	
acc cag ttt gtt aag ccg aca gtt gga gtt cca caa gtg ttc tcc cag	682
Thr Gln Phe Val Lys Pro Thr Val Gly Val Pro Gln Val Phe Ser Gln	
193 198 203 208	
atg acc cct gtg agg cca ggc tcc aca atg cct gtg agg ccc acc acc	730
Met Thr Pro Val Arg Pro Gly Ser Thr Met Pro Val Arg Pro Thr Thr	
209 214 219 224	
aac acc ttc acc acc gtc atc ccg gcc act ctt acc att cga agc acc	778
Asn Thr Phe Thr Thr Val Ile Pro Ala Thr Leu Thr Ile Arg Ser Thr	
225 230 235 240	
gtc cca cag tcc cag tcc cag cag acc aag tcc act ccc agc act tct	826

Val	Pro	Gln	Ser	Gln	Ser	Gln	Gln	Thr	Lys	Ser	Thr	Pro	Ser	Thr	Ser	
241					246					251					256	
acc	act	ccc	act	gcc	aca	cag	cca	acc	tca	ctg	ggg	caa	cta	gct	gtt	874
Thr	Thr	Pro	Thr	Ala	Thr	Gln	Pro	Thr	Ser	Leu	Gly	Gln	Leu	Ala	Val	
257					262					267					272	
cag	tct	cca	ggc	cag	tca	aac	cag	acc	acg	aat	ccc	aag	cta	gct	ccc	922
Gln	Ser	Pro	Gly	Gln	Ser	Asn	Gln	Thr	Thr	Asn	Pro	Lys	Leu	Ala	Pro	
273					278					283					288	
tcc	ttc	ccc	tct	cca	cct	gca	gtg	agc	att	gcc	agc	ttt	gtc	act	gtg	970
Ser	Phe	Pro	Ser	Pro	Pro	Ala	Val	Ser	Ile	Ala	Ser	Phe	Val	Thr	Val	
289					294					299					304	
aag	cga	cct	ggg	gtt	aca	ggc	gaa	aat	agc	aat	gaa	gtg	gcc	aaa	ttg	1018
Lys	Arg	Pro	Gly	Val	Thr	Gly	Glu	Asn	Ser	Asn	Glu	Val	Ala	Lys	Leu	
305					310					315					320	
gtg	aat	acc	ctt	aac	acc	atc	cct	tcc	ctg	ggc	cag	agt	cct	ggg	cca	1066
Val	Asn	Thr	Leu	Asn	Thr	Ile	Pro	Ser	Leu	Gly	Gln	Ser	Pro	Gly	Pro	
321					326					331					336	
gtg	gtg	gtg	tcc	aac	aac	agc	tct	gct	cat	ggc	tct	caa	aga	acc	agc	1114
Val	Val	Val	Ser	Asn	Asn	Ser	Ser	Ala	His	Gly	Ser	Gln	Arg	Thr	Ser	
337					342					347					352	
gga	cct	gag	tct	tca	atg	aaa	gtg	acc	tct	tcc	atc	cca	gta	ttt	gac	1162
Gly	Pro	Glu	Ser	Ser	Met	Lys	Val	Thr	Ser	Ser	Ile	Pro	Val	Phe	Asp	
353					358					363					368	
ctc	cag	gat	ggg	gga	cgg	aaa	ata	tgt	cca	cga	tgt	aat	gct	caa	ttt	1210
Leu	Gln	Asp	Gly	Gly	Arg	Lys	Ile	Cys	Pro	Arg	Cys	Asn	Ala	Gln	Phe	
369					374					379					384	
cgt	gtt	act	gaa	gct	ttg	aga	ggg	cac	atg	tgt	tac	tgt	tgc	cca	gaa	1258
Arg	Val	Thr	Glu	Ala	Leu	Arg	Gly	His	Met	Cys	Tyr	Cys	Cys	Pro	Glu	
385					390					395					400	
atg	gtt	gaa	tac	cag	aag	aaa	gga	aag	tcc	ctg	gat	tca	gaa	ccc	agt	1306
Met	Val	Glu	Tyr	Gln	Lys	Lys	Gly	Lys	Ser	Leu	Asp	Ser	Glu	Pro	Ser	
401					406					411					416	
gtc	cca	tca	gca	gca	aag	ccc	cca	tcc	cct	gag	aaa	aca	gct	cct	gtt	1354
Val	Pro	Ser	Ala	Ala	Lys	Pro	Pro	Ser	Pro	Glu	Lys	Thr	Ala	Pro	Val	
417					422					427					432	
gct	tcc	aca	ccc	tct	tct	aca	cct	att	cct	gct	ctg	tca	ccg	cct	acc	1402
Ala	Ser	Thr	Pro	Ser	Ser	Thr	Pro	Ile	Pro	Ala	Leu	Ser	Pro	Pro	Thr	
433					438					443					448	
aaa	gta	cca	gaa	cca	aat	gag	aac	gtg	ggc	gat	gcc	gtc	cag	acc	aaa	1450
Lys	Val	Pro	Glu	Pro	Asn	Glu	Asn	Val	Gly	Asp	Ala	Val	Gln	Thr	Lys	
449					454					459					464	
ctc	att	atg	ctt	gta	gat	gac	ttc	tac	tat	gga	cgg	gat	ggg	ggc	aaa	1498
Leu	Ile	Met	Leu	Val	Asp	Asp	Phe	Tyr	Tyr	Gly	Arg	Asp	Gly	Gly	Lys	

465	470	475	480	
gta gcc cag ctc aca aat ttc cct aag gtc gcc aca tct ttc cga tgc				1546
Val Ala Gln Leu Thr Asn Phe Pro Lys Val Ala Thr Ser Phe Arg Cys				
481	486	491	496	
cca cat tgt acc aaa agg cta aaa aac aat att cga ttc atg aac cat				1594
Pro His Cys Thr Lys Arg Leu Lys Asn Asn Ile Arg Phe Met Asn His				
497	502	507	512	
atg aaa cac cac gta gaa ctc gat cag cag aac ggt gag gta gat ggt				1642
Met Lys His His Val Glu Leu Asp Gln Gln Asn Gly Glu Val Asp Gly				
513	518	523	528	
cac act atc tgc cag cac tgt tac cgc cag ttt tcc act ccc ttc cag				1690
His Thr Ile Cys Gln His Cys Tyr Arg Gln Phe Ser Thr Pro Phe Gln				
529	534	539	544	
ctt cag tgc cac ttg gaa aat gtt cat agt ccc tat gaa tct act acc				1738
Leu Gln Cys His Leu Glu Asn Val His Ser Pro Tyr Glu Ser Thr Thr				
545	550	555	560	
aag tgc aag atc tgt gaa tgg gcg ttt gaa agt gag cca cta ttt ctc				1786
Lys Cys Lys Ile Cys Glu Trp Ala Phe Glu Ser Glu Pro Leu Phe Leu				
561	566	571	576	
cag cat atg aag gat act cat aag cct gga gag atg cct tat gtt tgc				1834
Gln His Met Lys Asp Thr His Lys Pro Gly Glu Met Pro Tyr Val Cys				
577	582	587	592	
cag gtg tgt caa tat cgc tcc tca ctc tac tct gag gta gat gtc cat				1882
Gln Val Cys Gln Tyr Arg Ser Ser Leu Tyr Ser Glu Val Asp Val His				
593	598	603	608	
ttt cgg atg atc cat gag gat acc cgg cat ctg ctc tgc cct tat tgc				1930
Phe Arg Met Ile His Glu Asp Thr Arg His Leu Leu Cys Pro Tyr Cys				
609	614	619	624	
ctg aag gtc ttc aaa aat ggc aat gca ttc caa cag cat tac atg agg				1978
Leu Lys Val Phe Lys Asn Gly Asn Ala Phe Gln Gln His Tyr Met Arg				
625	630	635	640	
cac cag aag aga aat gtt tat cac tgc aac aaa tgc cgg ctg cag ttt				2026
His Gln Lys Arg Asn Val Tyr His Cys Asn Lys Cys Arg Leu Gln Phe				
641	646	651	656	
ctc ttt gcc aag gac aaa att gaa cac aag ctt caa cac cat aaa acc				2074
Leu Phe Ala Lys Asp Lys Ile Glu His Lys Leu Gln His His Lys Thr				
657	662	667	672	
ttc cgt aaa ccc aag cag ctg gag ggc ttg aaa cca ggc acc aag gtg				2122
Phe Arg Lys Pro Lys Gln Leu Glu Gly Leu Lys Pro Gly Thr Lys Val				
673	678	683	688	
aca atc cgg gct tcc cga ggg cag cca cga act gtt cct gta tcc tct				2170
Thr Ile Arg Ala Ser Arg Gly Gln Pro Arg Thr Val Pro Val Ser Ser				
689	694	699	704	

aat gat aca cct ccc agc gcc ttg cag gag gca gca ccg ctg acc tcc	2218
Asn Asp Thr Pro Pro Ser Ala Leu Gln Glu Ala Ala Pro Leu Thr Ser	
705 710 715 720	
tca atg gac cct ctg cct gtc ttc ctt tat ccc cct gtc cag cgc agc	2266
Ser Met Asp Pro Leu Pro Val Phe Leu Tyr Pro Pro Val Gln Arg Ser	
721 726 731 736	
atc cag aag aga gct gtt agg aaa atg agt gtc atg ggc cgg cag aca	2314
Ile Gln Lys Arg Ala Val Arg Lys Met Ser Val Met Gly Arg Gln Thr	
737 742 747 752	
tgc ctg gag tgc agc ttc gag atc cca gac ttc cct ¹ aat cat ttc cct	2362
Cys Leu Glu Cys Ser Phe Glu Ile Pro Asp Phe Pro Asn His Phe Pro	
753 758 763 768	
act tac gta cac tgc tct ctg tgt cgc tat agc acc tgc tgt tct cga	2410
Thr Tyr Val His Cys Ser Leu Cys Arg Tyr Ser Thr Cys Cys Ser Arg	
769 774 779 784	
gct tat gcc aac cac atg atc aac aat cat gtt cca cgg aag agc ccc	2458
Ala Tyr Ala Asn His Met Ile Asn Asn His Val Pro Arg Lys Ser Pro	
785 790 795 800	
aag tat ttg gct ttg ttt aaa aat tct gtg agt gga atc aag ctg gcc	2506
Lys Tyr Leu Ala Leu Phe Lys Asn Ser Val Ser Gly Ile Lys Leu Ala	
801 806 811 816	
tgc act tca tgt acc ttt gtt acc tct gtg ggc gat gct atg gcc aag	2554
Cys Thr Ser Cys Thr Phe Val Thr Ser Val Gly Asp Ala Met Ala Lys	
817 822 827 832	
cat ttg gta ttc aac ccc tct cac aga tcc agc agc atc ctg cca cgg	2602
His Leu Val Phe Asn Pro Ser His Arg Ser Ser Ser Ile Leu Pro Arg	
833 838 843 848	
gga ctc act tgg ata gct cac tca agg cat ggc cag act cgt gac cga	2650
Gly Leu Thr Trp Ile Ala His Ser Arg His Gly Gln Thr Arg Asp Arg	
849 854 859 864	
gtg cat gac cgg aac gtg aag aat atg tac cct cct cct tcc ttc ccc	2698
Val His Asp Arg Asn Val Lys Asn Met Tyr Pro Pro Pro Ser Phe Pro	
865 870 875 880	
act aac aaa gct gcc act gtg aaa tct gcg ggg gcc acc cca gct gag	2746
Thr Asn Lys Ala Ala Thr Val Lys Ser Ala Gly Ala Thr Pro Ala Glu	
881 886 891 896	
cct gaa gag cta cta act ccc tta gcc cca gca ctc cca tca cca gcc	2794
Pro Glu Glu Leu Leu Thr Pro Leu Ala Pro Ala Leu Pro Ser Pro Ala	
897 902 907 912	
tca act gca acc cca cca cca acc ccc act cac ccg cag gct tta gcc	2842
Ser Thr Ala Thr Pro Pro Pro Thr Pro Thr His Pro Gln Ala Leu Ala	
913 918 923 928	

ctt cca ccg ctg gct aca gag gga gcc gaa tgt ctg aat gtt gat gat	2890
Leu Pro Pro Leu Ala Thr Glu Gly Ala Glu Cys Leu Asn Val Asp Asp	
929 934 939 944	
cag gat gaa ggg agc cca gtc acc caa gaa cct gag cta gca tca ggt	2938
Gln Asp Glu Gly Ser Pro Val Thr Gln Glu Pro Glu Leu Ala Ser Gly	
945 950 955 960	
ggg ggt ggt agt ggt gga gtt ggc aaa aag gag cag ctg tct gtg aag	2986
Gly Gly Gly Ser Gly Gly Val Gly Lys Lys Glu Gln Leu Ser Val Lys	
961 966 971 976	
aag ctt cga gta gta ctg ttt gct cta tgc tgc aat aca gaa cag gca	3034
Lys Leu Arg Val Val Leu Phe Ala Leu Cys Cys Asn Thr Glu Gln Ala	
977 982 987 992	
gct gaa cac ttc cga aat ccc cag cga cgt att cgc cgt tgg ctt cga	3082
Ala Glu His Phe Arg Asn Pro Gln Arg Arg Ile Arg Arg Trp Leu Arg	
993 998 1003 1008	
cgt ttc cag gcc tcc cag ggg gag aat cta gag ggc aaa tat ctg agc	3130
Arg Phe Gln Ala Ser Gln Gly Glu Asn Leu Glu Gly Lys Tyr Leu Ser	
1009 1014 1019 1024	
ttt gag gca gaa gag aaa ctg gct gag tgg gtg cta acc cag cgc gaa	3178
Phe Glu Ala Glu Glu Lys Leu Ala Glu Trp Val Leu Thr Gln Arg Glu	
1025 1030 1035 1040	
caa cag cta cct gta aat gag gag acc ttg ttc cag aag gcc acc aaa	3226
Gln Gln Leu Pro Val Asn Glu Glu Thr Leu Phe Gln Lys Ala Thr Lys	
1041 1046 1051 1056	
ata gga cgt tct ttg gaa ggg ggg ttt aag atc tcc tat gag tgg gct	3274
Ile Gly Arg Ser Leu Glu Gly Gly Phe Lys Ile Ser Tyr Glu Trp Ala	
1057 1062 1067 1072	
gtg cgt ttc atg ctg cgg cac cac ctg act ccc cat gcc cgg cga gct	3322
Val Arg Phe Met Leu Arg His His Leu Thr Pro His Ala Arg Arg Ala	
1073 1078 1083 1088	
gtg gcc cac acc cta cct aag gat gta gca gag aat gca gga ctc ttc	3370
Val Ala His Thr Leu Pro Lys Asp Val Ala Glu Asn Ala Gly Leu Phe	
1089 1094 1099 1104	
att gat ttt gta caa cgg cag att cac aac cag gac tta ccc ttg tct	3418
Ile Asp Phe Val Gln Arg Gln Ile His Asn Gln Asp Leu Pro Leu Ser	
1105 1110 1115 1120	
atg att gtg gct att gat gag atc tct ttg ttc ctg gat aca gag gtg	3466
Met Ile Val Ala Ile Asp Glu Ile Ser Leu Phe Leu Asp Thr Glu Val	
1121 1126 1131 1136	
ctg agc agt gat gat cga aag gag aat gcc ctg cag aca gtg ggc aca	3514
Leu Ser Ser Asp Asp Arg Lys Glu Asn Ala Leu Gln Thr Val Gly Thr	
1137 1142 1147 1152	
ggg gaa cct tgg tgt gat gta gtc cta gcc att ctg gca gat ggc act	3562

Gly Glu Pro Trp Cys Asp Val Val Leu Ala Ile Leu Ala Asp Gly Thr	
1153 1158 1163 1168	
gtc ctt ccc acc ctg gtt ttc tac aga ggg cag atg gat cag cct gct	3610
Val Leu Pro Thr Leu Val Phe Tyr Arg Gly Gln Met Asp Gln Pro Ala	
1169 1174 1179 1184	
aac atg cca gac tcc ata ttg cta gag gca aag gag agt ggc tac agt	3658
Asn Met Pro Asp Ser Ile Leu Leu Glu Ala Lys Glu Ser Gly Tyr Ser	
1185 1190 1195 1200	
gat gac gag atc atg gag ctg tgg tca act cga gtg tgg cag aag cac	3706
Asp Asp Glu Ile Met Glu Leu Trp Ser Thr Arg Val Trp Gln Lys His	
1201 1206 1211 1216	
aca gct tgc cag cgc agc aaa ggc atg ctt gtg atg gac tgt cat cgc	3754
Thr Ala Cys Gln Arg Ser Lys Gly Met Leu Val Met Asp Cys His Arg	
1217 1222 1227 1232	
act cac ttg tca gaa gag gta ctg gct atg ctt agt gcc tct agc act	3802
Thr His Leu Ser Glu Glu Val Leu Ala Met Leu Ser Ala Ser Ser Thr	
1233 1238 1243 1248	
ttg cct gca gtg gtc cca gca ggc tgt agc tcc aaa att cag cca tta	3850
Leu Pro Ala Val Val Pro Ala Gly Cys Ser Ser Lys Ile Gln Pro Leu	
1249 1254 1259 1264	
gat gta tgc atc aaa aga act gtc aag aac ttc ctg cat aaa aaa tgg	3898
Asp Val Cys Ile Lys Arg Thr Val Lys Asn Phe Leu His Lys Lys Trp	
1265 1270 1275 1280	
aag gaa cag gct cgg gaa atg gca gat act gca tgt gat tct gat gtc	3946
Lys Glu Gln Ala Arg Glu Met Ala Asp Thr Ala Cys Asp Ser Asp Val	
1281 1286 1291 1296	
ctg ctt cag ctg gtg ctt gtc tgg ctg ggt gaa gtg cta ggt gtc att	3994
Leu Leu Gln Leu Val Leu Val Trp Leu Gly Glu Val Leu Gly Val Ile	
1297 1302 1307 1312	
ggg gac tgt cca gag cta gtt cag cgc tcc ttc ctg gtg gct agt gtt	4042
Gly Asp Cys Pro Glu Leu Val Gln Arg Ser Phe Leu Val Ala Ser Val	
1313 1318 1323 1328	
ctg cct ggc ccc gat ggc aac att aac tca cct aca aga aat gct gac	4090
Leu Pro Gly Pro Asp Gly Asn Ile Asn Ser Pro Thr Arg Asn Ala Asp	
1329 1334 1339 1344	
atg cag gag gag cta att gcc tcc cta gag gag caa ctg aag ctg agt	4138
Met Gln Glu Glu Leu Ile Ala Ser Leu Glu Glu Gln Leu Lys Leu Ser	
1345 1350 1355 1360	
ggg gaa cat tct gag tct tcc act cca cga ccc aga tca tct cct gaa	4186
Gly Glu His Ser Glu Ser Ser Thr Pro Arg Pro Arg Ser Ser Pro Glu	
1361 1366 1371 1376	
gag aca att gag cct gaa agt ctt cac cag ctc ttt gag ggt gaa agt	4234
Glu Thr Ile Glu Pro Glu Ser Leu His Gln Leu Phe Glu Gly Glu Ser	

1377	1382	1387	1392	
gag acc gag tct ttc tat ggc ttt gaa gaa gct gac cta gat ctg atg				4282
Glu Thr Glu Ser Phe Tyr Gly Phe Glu Glu Ala Asp Leu Asp Leu Met				
1393	1398	1403	1408	
gag att tga gtgttgg ggtcatgagg ggggtgtggag tgggggtggg aacatgtgag				4338
Glu Ile *				
1409				
ggaggggtaaa ggggcttagg gaaaaggggg cataccaggt ggggtatttg gtttctatatt				4398
tttaatttta taccaccact ccccccctgaa gttgacttac acttccctgt ggatttgtgg				4458
attaattagg aaaaccaata gtaatcacgt ctgagccaag gagctggccc attggtcatt				4518
cacttctgct aaaaacaggt ttttgtgact tttttttttt ttaaatttaa atcactgtgt				4578
ttgggtatttt tctgacaaaa ttaagaaaaa gaaaaaaaat tatttgtggg caaatgttaa				4638
atTTTTTgt tccccTTTT acctcaattg tatcatagta ctgggttttt ttgtttgttt				4698
tattgtgtgg ccaatgtctt tgggcatgat gctatctaatt cattgttaatt gtgagaacat				4758
ttctgaagat gggaaagaca aattatgtag ctacaaaact gggtttattat atatatggat				4818
aaaaaacttt tttoattgtg gtcttaacac ttttatataa aaatgaaaat ggaaaaaaag				4878
tcccactgaa ctctctcttc cttctccttt tctttccttc cctctccaga gatgttggtt				4938
tctacagcaa cctagatat aaaattgtgg ctttaaaaaat gcatgaaacc acctttaatt				4998
atccagaatg aatagatttg tcttttcctc accaccttcc ctccaaaaca tgacataaac				5058
aatatttttt gcaattgtga tccttgggcc ctttcccat tctcaacacc atccatccct				5118
ctggacaaag gatcatacag gtgttattag caagcaagag atactgaagc gatcaaacag				5178
ttttaggggtg gaagccattc ccagtttgag tcttcatcct gtaagcccc aggggcagtc				5238
cctgctttac tgaacttcat cctgttagat ggagagcatg cctgtttaag ggattactgg				5298
tcctacagcc aggagctaatt tgttcaagaa gtgttgaact ttaaaaagac aagaccattt				5358
gttgaaatcc agcgtgctct gtggctttcc cctatttctc ttaatactta gggaagaatc				5418
tgacaggaag aagcgcacag ggggtgtgcac aaagaaaatg acatgaatct ttatttttca				5478
ctgccagctt caaggaaaga aaattttttc tacaatttgc atgagggatt tttttaattg				5538
tatgtactca tggttgtaaa ccaaaacgta ctgtaccgta cagagaaaag gagcaaaaaa				5598
ccaagtcttc tgtttatcct gaggccttcc acaatgttcc cctcctgtga gccaaaggagg				5658
caaactgcac aagcttgtaa atgggttcgtc tttaaaatgt acataagtgg aacatttaatt				5718
aaaatgaggg gaaatggatt tataaacttg ttttttttct aggtgaccct gtttaatagg				5778

```

ctttcacaga ctggggaatg ctcaagatgt gatgggcctg gtggtacagg tgtgacattt 5838
gttaccaccc atttctccca cccaccctg cttttttgtt tgtttgttt ttcatccccc 5898
agcacactat aatatagtga actggaaaag tcccttcag aaacagcttg gccagctttg 5958
tgaacctttg acatctgaaa acaaccaagg atccatctgg gcttctcttc cccagctttt 6018
tgctgatgc cattttattg acagacaatg gactttgaag tcagcctttg cctttgagaa 6078
agttcaagaa ctatggttgg tcacgtctat ctacaacctt atcctactct ttggtagtct 6138
ctgcagcagc cacagcctta gcagagctgg gggtcctgtc ttctgcacac gattgaactt 6198
cttgatgggt aatttttttt aagattatac caacagtgga tcagctgggt tttggccagg 6258
aagttgtctt tgtggactct gctgcatgg cttagtagta gaaggaaatt tttttttggt 6318
tttgtttttt ataattcagt ttaatcaata aacatgtatt tattgactgt taaaaaaaaa 6378
aaaa 6382

```

```

<210> 461
<211> 6304
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (59) .. (4213)

```

```

<400> 461
ctcgtcgcct gcggtaccgg tccggaattc cggggtcgac gatttcgtcc acgggagc 58
atg gcg gac acc gac ctg ttc atg gaa tgt gag gag gag gag ttg gag 106
Met Ala Asp Thr Asp Leu Phe Met Glu Cys Glu Glu Glu Glu Leu Glu
1 5 10 15

cca tgg cag aaa atc agt gat gtc att gag gac tct gta gtt gaa gat 154
Pro Trp Gln Lys Ile Ser Asp Val Ile Glu Asp Ser Val Val Glu Asp
17 22 27 32

tat aat tca gtg gat aaa act acc aca gct ggc aat cct ttg gtc cag 202
Tyr Asn Ser Val Asp Lys Thr Thr Thr Ala Gly Asn Pro Leu Val Gln
33 38 43 48

caa ggt gga cag cca ctc atc ctg acc cag aat cca gcc cca ggt ctg 250
Gln Gly Gly Gln Pro Leu Ile Leu Thr Gln Asn Pro Ala Pro Gly Leu
49 54 59 64

ggc aca atg gtt act caa cca gta ttg agg cct gtt cag gtc atg cag 298
Gly Thr Met Val Thr Gln Pro Val Leu Arg Pro Val Gln Val Met Gln
65 70 75 80

```

aat gcc aat cat gtg act agt tcc cct gtg gcc tca caa cca ata ttt	346
Asn Ala Asn His Val Thr Ser Ser Pro Val Ala Ser Gln Pro Ile Phe	
81 86 91 96	
atc act acg cag gga ttt cct gta agg aat gtc cgg cct gta caa aat	394
Ile Thr Thr Gln Gly Phe Pro Val Arg Asn Val Arg Pro Val Gln Asn	
97 102 107 112	
gca atg aat cag gtt ggg att gtg ctg aac gta cag caa ggc caa acg	442
Ala Met Asn Gln Val Gly Ile Val Leu Asn Val Gln Gln Gly Gln Thr	
113 118 123 128	
gtt aga cca att aca cta gtt cca gcc cca ggt acc cag ttt gtt aag	490
Val Arg Pro Ile Thr Leu Val Pro Ala Pro Gly Thr Gln Phe Val Lys	
129 134 139 144	
ccg aca gtt gga gtt cca caa gtg ttc tcc cag atg acc cct gtg agg	538
Pro Thr Val Gly Val Pro Gln Val Phe Ser Gln Met Thr Pro Val Arg	
145 150 155 160	
cca ggc tcc aca atg cct gtg agg ccc acc acc aac acc ttc acc acc	586
Pro Gly Ser Thr Met Pro Val Arg Pro Thr Thr Asn Thr Phe Thr Thr	
161 166 171 176	
gtc atc ccg gcc act ctt acc att cga agc acc gtc cca cag tcc cag	634
Val Ile Pro Ala Thr Leu Thr Ile Arg Ser Thr Val Pro Gln Ser Gln	
177 182 187 192	
tcc cag cag acc aag tcc act ccc agc act tct acc act ccc act gcc	682
Ser Gln Gln Thr Lys Ser Thr Pro Ser Thr Ser Thr Thr Pro Thr Ala	
193 198 203 208	
aca cag cca acc tca ctg ggg caa cta gct gtt cag tct cca ggc cag	730
Thr Gln Pro Thr Ser Leu Gly Gln Leu Ala Val Gln Ser Pro Gly Gln	
209 214 219 224	
tca aac cag acc acg aat ccc aag cta ggt aag gct tcg gaa gag gag	778
Ser Asn Gln Thr Thr Asn Pro Lys Leu Gly Lys Ala Ser Glu Glu Glu	
225 230 235 240	
atg gca gag cca ggt tgg gat ggt ggg tgg aga aca gat gat tat cac	826
Met Ala Glu Pro Gly Trp Asp Gly Gly Trp Arg Thr Asp Asp Tyr His	
241 246 251 256	
ttg gtc acc gta gct ccc tcc ttc ccc tct cca cct gca gtg agc att	874
Leu Val Thr Val Ala Pro Ser Phe Pro Ser Pro Pro Ala Val Ser Ile	
257 262 267 272	
gcc agc ttt gtc act gtg aag cga cct ggt gtt aca ggc gaa aat agc	922
Ala Ser Phe Val Thr Val Lys Arg Pro Gly Val Thr Gly Glu Asn Ser	
273 278 283 288	
aat gaa gtg gcc aaa ttg gtg aat acc ctt aac acc atc cct tcc ctg	970
Asn Glu Val Ala Lys Leu Val Asn Thr Leu Asn Thr Ile Pro Ser Leu	
289 294 299 304	
ggc cag agt cct ggg cca gtg gtg gtg tcc aac aac agc tct gct cat	1018

Gly	Gln	Ser	Pro	Gly	Pro	Val	Val	Val	Ser	Asn	Asn	Ser	Ser	Ala	His	
305					310					315					320	
ggc	tct	caa	aga	acc	agc	gga	cct	gag	tct	tca	atg	aaa	gtg	acc	tct	1066
Gly	Ser	Gln	Arg	Thr	Ser	Gly	Pro	Glu	Ser	Ser	Met	Lys	Val	Thr	Ser	
321					326					331					336	
tcc	atc	cca	gta	ttt	gac	ctc	cag	gat	ggc	gga	cgg	aaa	ata	tgt	cca	1114
Ser	Ile	Pro	Val	Phe	Asp	Leu	Gln	Asp	Gly	Gly	Arg	Lys	Ile	Cys	Pro	
337					342					347					352	
cga	tgt	aat	gct	caa	ttt	cgt	gtt	act	gaa	gct	ttg	aga	ggc	cac	atg	1162
Arg	Cys	Asn	Ala	Gln	Phe	Arg	Val	Thr	Glu	Ala	Leu	Arg	Gly	His	Met	
353					358					363					368	
tgt	tac	tgt	tgc	cca	gaa	atg	gtt	gaa	tac	cag	aag	aaa	gga	aag	tcc	1210
Cys	Tyr	Cys	Cys	Pro	Glu	Met	Val	Glu	Tyr	Gln	Lys	Lys	Gly	Lys	Ser	
369					374					379					384	
ctg	gat	tca	gaa	ccc	agt	gtc	cca	tca	gca	gca	aag	ccc	cca	tcc	cct	1258
Leu	Asp	Ser	Glu	Pro	Ser	Val	Pro	Ser	Ala	Ala	Lys	Pro	Pro	Ser	Pro	
385					390					395					400	
gag	aaa	aca	gct	cct	gtt	gct	tcc	aca	ccc	tct	tct	aca	cct	att	cct	1306
Glu	Lys	Thr	Ala	Pro	Val	Ala	Ser	Thr	Pro	Ser	Ser	Thr	Pro	Ile	Pro	
401					406					411					416	
gct	ctg	tca	ccg	cct	acc	aaa	gta	cca	gaa	cca	aat	gag	aac	gtg	ggc	1354
Ala	Leu	Ser	Pro	Pro	Thr	Lys	Val	Pro	Glu	Pro	Asn	Glu	Asn	Val	Gly	
417					422					427					432	
gat	gcc	gtc	cag	acc	aaa	ctc	att	atg	ctt	gta	gat	gac	ttc	tac	tat	1402
Asp	Ala	Val	Gln	Thr	Lys	Leu	Ile	Met	Leu	Val	Asp	Asp	Phe	Tyr	Tyr	
433					438					443					448	
gga	cgg	gat	ggc	ggc	aaa	gta	gcc	cag	ctc	aca	aat	ttc	cct	aag	gtc	1450
Gly	Arg	Asp	Gly	Gly	Lys	Val	Ala	Gln	Leu	Thr	Asn	Phe	Pro	Lys	Val	
449					454					459					464	
gcc	aca	tct	ttc	cga	tgc	cca	cat	tgt	acc	aaa	agg	cta	aaa	aac	aat	1498
Ala	Thr	Ser	Phe	Arg	Cys	Pro	His	Cys	Thr	Lys	Arg	Leu	Lys	Asn	Asn	
465					470					475					480	
att	cga	ttc	atg	aac	cat	atg	aaa	cac	cac	gta	gaa	ctc	gat	cag	cag	1546
Ile	Arg	Phe	Met	Asn	His	Met	Lys	His	His	Val	Glu	Leu	Asp	Gln	Gln	
481					486					491					496	
aac	ggc	gag	gta	gat	ggc	cac	act	atc	tgc	cag	cac	tgt	tac	cgc	cag	1594
Asn	Gly	Glu	Val	Asp	Gly	His	Thr	Ile	Cys	Gln	His	Cys	Tyr	Arg	Gln	
497					502					507					512	
ttt	tcc	act	ccc	ttc	cag	ctt	cag	tgc	cac	ttg	gaa	aat	gtt	cat	agt	1642
Phe	Ser	Thr	Pro	Phe	Gln	Leu	Gln	Cys	His	Leu	Glu	Asn	Val	His	Ser	
513					518					523					528	
ccc	tat	gaa	tct	act	acc	aag	tgc	aag	atc	tgt	gaa	tgg	gcg	ttt	gaa	1690
Pro	Tyr	Glu	Ser	Thr	Thr	Lys	Cys	Lys	Ile	Cys	Glu	Trp	Ala	Phe	Glu	

529	534	539	544	
agt gag cca cta ttt ctc cag cat atg aag gat act cat aag cct gga				1738
Ser Glu Pro Leu Phe Leu Gln His Met Lys Asp Thr His Lys Pro Gly				
545	550	555	560	
gag atg cct tat gtt tgc cag gtg tgt caa tat cgc tcc tca ctc tac				1786
Glu Met Pro Tyr Val Cys Gln Val Cys Gln Tyr Arg Ser Ser Leu Tyr				
561	566	571	576	
tct gag gta gat gtc cat ttt cgg atg atc cat gag gat acc cgg cat				1834
Ser Glu Val Asp Val His Phe Arg Met Ile His Glu Asp Thr Arg His				
577	582	587	592	
ctg ctc tgc cct tat tgc ctg aag gtc ttc aaa aat ggc aat gca ttc				1882
Leu Leu Cys Pro Tyr Cys Leu Lys Val Phe Lys Asn Gly Asn Ala Phe				
593	598	603	608	
caa cag cat tac atg agg cac cag aag aga aat gtt tat cac tgc aac				1930
Gln Gln His Tyr Met Arg His Gln Lys Arg Asn Val Tyr His Cys Asn				
609	614	619	624	
aaa tgc cgg ctg cag ttt ctc ttt gcc aag gac aaa att gaa cac aag				1978
Lys Cys Arg Leu Gln Phe Leu Phe Ala Lys Asp Lys Ile Glu His Lys				
625	630	635	640	
ctt caa cac cat aaa acc ttc cgt aaa ccc aag cag ctg gag ggc ttg				2026
Leu Gln His His Lys Thr Phe Arg Lys Pro Lys Gln Leu Glu Gly Leu				
641	646	651	656	
aaa cca ggc acc aag gtg aca atc cgg gct tcc cga ggg cag cca cga				2074
Lys Pro Gly Thr Lys Val Thr Ile Arg Ala Ser Arg Gly Gln Pro Arg				
657	662	667	672	
act gtt cct gta tcc tct aat gat aca cct ccc agc gcc ttg cag gag				2122
Thr Val Pro Val Ser Ser Asn Asp Thr Pro Pro Ser Ala Leu Gln Glu				
673	678	683	688	
gca gca ccg ctg acc tcc tca atg gac cct ctg cct gtc ttc ctt tat				2170
Ala Ala Pro Leu Thr Ser Ser Met Asp Pro Leu Pro Val Phe Leu Tyr				
689	694	699	704	
ccc cct gtc cag cgc agc atc cag aag aga gct gtt agg aaa atg agt				2218
Pro Pro Val Gln Arg Ser Ile Gln Lys Arg Ala Val Arg Lys Met Ser				
705	710	715	720	
gtc atg ggc cgg cag aca tgc ctg gag tgc agc ttc gag atc cca gac				2266
Val Met Gly Arg Gln Thr Cys Leu Glu Cys Ser Phe Glu Ile Pro Asp				
721	726	731	736	
ttc cct aat cat ttc cct act tac gta cac tgc tct ctg tgt cgc tat				2314
Phe Pro Asn His Phe Pro Thr Tyr Val His Cys Ser Leu Cys Arg Tyr				
737	742	747	752	
agc acc tgc tgt tct cga gct tat gcc aac cac atg atc aac aat cat				2362
Ser Thr Cys Cys Ser Arg Ala Tyr Ala Asn His Met Ile Asn Asn His				
753	758	763	768	

gtt cca cgg aag agc ccc aag tat ttg gct ttg ttt aaa aat tct gtg	2410
Val Pro Arg Lys Ser Pro Lys Tyr Leu Ala Leu Phe Lys Asn Ser Val	
769 774 779 784	
agt gga atc aag ctg gcc tgc act tca tgt acc ttt gtt acc tct gtg	2458
Ser Gly Ile Lys Leu Ala Cys Thr Ser Cys Thr Phe Val Thr Ser Val	
785 790 795 800	
ggc gat gct atg gcc aag cat ttg gta ttc aac ccc tct cac aga tcc	2506
Gly Asp Ala Met Ala Lys His Leu Val Phe Asn Pro Ser His Arg Ser	
801 806 811 816	
agc agc atc ctg cca cgg gga ctc act tgg ata gct cac tca agg cat	2554
Ser Ser Ile Leu Pro Arg Gly Leu Thr Trp Ile Ala His Ser Arg His	
817 822 827 832	
ggc cag act cgt gac cga gtg cat gac cgg aac gtg aag aat atg tac	2602
Gly Gln Thr Arg Asp Arg Val His Asp Arg Asn Val Lys Asn Met Tyr	
833 838 843 848	
cct cct cct tcc ttc ccc act aac aaa gct gcc act gtg aaa tct gcg	2650
Pro Pro Pro Ser Phe Pro Thr Asn Lys Ala Ala Thr Val Lys Ser Ala	
849 854 859 864	
ggg gcc acc cca gct gag cct gaa gag cta cta act ccc tta gcc cca	2698
Gly Ala Thr Pro Ala Glu Pro Glu Glu Leu Leu Thr Pro Leu Ala Pro	
865 870 875 880	
gca ctc cca tca cca gcc tca act gca acc cca cca cca acc ccc act	2746
Ala Leu Pro Ser Pro Ala Ser Thr Ala Thr Pro Pro Pro Thr Pro Thr	
881 886 891 896	
cac ccg cag gct tta gcc ctt cca ccg ctg gct aca gag gga gcc gaa	2794
His Pro Gln Ala Leu Ala Leu Pro Pro Leu Ala Thr Glu Gly Ala Glu	
897 902 907 912	
tgt ctg aat gtt gat gat cag gat gaa ggg agc cca gtc acc caa gaa	2842
Cys Leu Asn Val Asp Asp Gln Asp Glu Gly Ser Pro Val Thr Gln Glu	
913 918 923 928	
cct gag cta gca tca ggt ggt ggt ggt agt ggt gga gtt ggc aaa aag	2890
Pro Glu Leu Ala Ser Gly Gly Gly Gly Ser Gly Gly Val Gly Lys Lys	
929 934 939 944	
gag cag ctg tct gtg aag aag ctt cga gta gta ctg ttt gct cta tgc	2938
Glu Gln Leu Ser Val Lys Lys Leu Arg Val Val Leu Phe Ala Leu Cys	
945 950 955 960	
tgc aat aca gaa cag gca gct gaa cac ttc cga aat ccc cag cga cgt	2986
Cys Asn Thr Glu Gln Ala Ala Glu His Phe Arg Asn Pro Gln Arg Arg	
961 966 971 976	
att cgc cgt tgg ctt cga cgt ttc cag gcc tcc cag ggg gag aat cta	3034
Ile Arg Arg Trp Leu Arg Arg Phe Gln Ala Ser Gln Gly Glu Asn Leu	
977 982 987 992	

gag ggc aaa tat ctg agc ttt gag gca gaa gag aaa ctg gct gag tgg	3082
Glu Gly Lys Tyr Leu Ser Phe Glu Ala Glu Glu Lys Leu Ala Glu Trp	
993 998 1003 1008	
gtg cta acc cag cgc gaa caa cag cta cct gta aat gag gag acc ttg	3130
Val Leu Thr Gln Arg Glu Gln Gln Leu Pro Val Asn Glu Glu Thr Leu	
1009 1014 1019 1024	
ttc cag aag gcc acc aaa ata gga cgt tct ttg gaa ggg ggg ttt aag	3178
Phe Gln Lys Ala Thr Lys Ile Gly Arg Ser Leu Glu Gly Gly Phe Lys	
1025 1030 1035 1040	
atc tcc tat gag tgg gct gtg cgt ttc atg ctg cgg cac cac ctg act	3226
Ile Ser Tyr Glu Trp Ala Val Arg Phe Met Leu Arg His His Leu Thr	
1041 1046 1051 1056	
ccc cat gcc cgg cga gct gtg gcc cac acc cta cct aag gat gta gca	3274
Pro His Ala Arg Arg Ala Val Ala His Thr Leu Pro Lys Asp Val Ala	
1057 1062 1067 1072	
gag aat gca gga ctc ttc att gat ttt gta caa cgg cag att cac aac	3322
Glu Asn Ala Gly Leu Phe Ile Asp Phe Val Gln Arg Gln Ile His Asn	
1073 1078 1083 1088	
cag gac tta ccc ttg tct atg att gtg gct att gat gag atc tct ttg	3370
Gln Asp Leu Pro Leu Ser Met Ile Val Ala Ile Asp Glu Ile Ser Leu	
1089 1094 1099 1104	
ttc ctg gat aca gag gtg ctg agc agt gat gat cga aag gag aat gcc	3418
Phe Leu Asp Thr Glu Val Leu Ser Ser Asp Asp Arg Lys Glu Asn Ala	
1105 1110 1115 1120	
ctg cag aca gtg ggc aca ggg gaa cct tgg tgt gat gta gtc cta gcc	3466
Leu Gln Thr Val Gly Thr Gly Glu Pro Trp Cys Asp Val Val Leu Ala	
1121 1126 1131 1136	
att ctg gca gat ggc act gtc ctt ccc acc ctg gtt ttc tac aga ggg	3514
Ile Leu Ala Asp Gly Thr Val Leu Pro Thr Leu Val Phe Tyr Arg Gly	
1137 1142 1147 1152	
cag atg gat cag cct gct aac atg cca gac tcc ata ttg cta gag gca	3562
Gln Met Asp Gln Pro Ala Asn Met Pro Asp Ser Ile Leu Leu Glu Ala	
1153 1158 1163 1168	
aag gag agt ggc tac agt gat gac gag atc atg gag ctg tgg tca act	3610
Lys Glu Ser Gly Tyr Ser Asp Asp Glu Ile Met Glu Leu Trp Ser Thr	
1169 1174 1179 1184	
cga gtg tgg cag aag cac aca gct tgc cag cgc agc aaa ggc atg ctt	3658
Arg Val Trp Gln Lys His Thr Ala Cys Gln Arg Ser Lys Gly Met Leu	
1185 1190 1195 1200	
gtg atg gac tgt cat cgc act cac ttg tca gaa gag gta ctg gct atg	3706
Val Met Asp Cys His Arg Thr His Leu Ser Glu Glu Val Leu Ala Met	
1201 1206 1211 1216	
ctt agt gcc tct agc act ttg cct gca gtg gtc cca gca ggc tgt agc	3754

Leu Ser Ala Ser Ser Thr Leu Pro Ala Val Val Pro Ala Gly Cys Ser	
1217	1222 1227 1232
tcc aaa att cag cca tta gat gta tgc atc aaa aga act gtc aag aac	3802
Ser Lys Ile Gln Pro Leu Asp Val Cys Ile Lys Arg Thr Val Lys Asn	
1233	1238 1243 1248
ttc ctg cat aaa aaa tgg aag gaa cag gct cgg gaa atg gca gat act	3850
Phe Leu His Lys Lys Trp Lys Glu Gln Ala Arg Glu Met Ala Asp Thr	
1249	1254 1259 1264
gca tgt gat tct gat gtc ctg ctt cag ctg gtg ctt gtc tgg ctg ggt	3898
Ala Cys Asp Ser Asp Val Leu Leu Gln Leu Val Leu Val Trp Leu Gly	
1265	1270 1275 1280
gaa gtg cta ggt gtc att ggg gac tgt cca gag cta gtt cag cgc tcc	3946
Glu Val Leu Gly Val Ile Gly Asp Cys Pro Glu Leu Val Gln Arg Ser	
1281	1286 1291 1296
ttc ctg gtg gct agt gtt ctg cct ggc ccc gat ggc aac att aac tca	3994
Phe Leu Val Ala Ser Val Leu Pro Gly Pro Asp Gly Asn Ile Asn Ser	
1297	1302 1307 1312
cct aca aga aat gct gac atg cag gag gag cta att gcc tcc cta gag	4042
Pro Thr Arg Asn Ala Asp Met Gln Glu Glu Leu Ile Ala Ser Leu Glu	
1313	1318 1323 1328
gag caa ctg aag ctg agt ggg gaa cat tct gag tct tcc act cca cga	4090
Glu Gln Leu Lys Leu Ser Gly Glu His Ser Glu Ser Ser Thr Pro Arg	
1329	1334 1339 1344
ccc aga tca tct cct gaa gag aca att gag cct gaa agt ctt cac cag	4138
Pro Arg Ser Ser Pro Glu Glu Thr Ile Glu Pro Glu Ser Leu His Gln	
1345	1350 1355 1360
ctc ttt gag ggt gaa agt gag acc gag tct ttc tat ggc ttt gaa gaa	4186
Leu Phe Glu Gly Glu Ser Glu Thr Glu Ser Phe Tyr Gly Phe Glu Glu	
1361	1366 1371 1376
gct gac cta gat ctg atg gag att tga gtggtt ggggtcatga gggggtgtgg	4238
Ala Asp Leu Asp Leu Met Glu Ile *	
1377	1382
agtgggggtg ggaacatgtg agggagggtg aaggggctta gggaaaaggg ggcataccag	4298
gtgggggtatt tggtttctat tttttaattt tataccacca ctccccctg aagttgactt	4358
acacttccct gtggatttgt ggattaatta ggaaaaccaa tagtaatcac gtctgagcca	4418
aggagctggc ccattggcca ttcacttctg ctaaaaacag gtttttgtga cttttttttt	4478
ttttaaatat aaatcactgt gtttggtatt tttctgacaa aattaagaaa aagaaaaaaa	4538
attatttgtg ggcaaatgtt aaattttttt gtttccctt ttacctcaat tgtatcatag	4598
tactgggttt ttttggttgt tttatttgtt ggccaatgtc tttgggcatg atgctatcta	4658

atcattgtta atgtgagaac atttctgaag atgggaaaga caaattatgt agctcacaaa	4718
ctggtttatt atatatatgg ataaaaaact tttttcattg tggctttaac acttttatat	4778
aaaaatgaaa atggaaaaaa agtcccactg aactctctct tccttctoct tttctttcct	4838
tcctctotcca gagatgttgg tttctacagc aaccctagat ataaaattgt ggcttttaaaa	4898
atgcatgaaa ccacctttaa ttatccagaa tgaatagatt tgtcttttcc tcaccacctt	4958
ccctccaaaa catgacataa acaatatttt ttgcacttgt gatccttgge ccctttcccc	5018
attctcaaca ccatccatcc ctctggacaa aggatcatac aggtgttatt agcaagcaag	5078
agatactgaa gcatcaaac agtttttaggg tggaagccat tcccagtttg agtcttcac	5138
ctgtaagccc ccaggggcag tccttctttt actgaacttc atcctgttag atggagagca	5198
tgctgtttta agggattact ggtcctacag ccaggagcta attgttcaag aagtgttgaa	5258
ctttaaaaag acaagaccac ttgttgaaat ccagcgtgct ctgtggcttt cccctatttc	5318
tottaatact tagggaagaa tctgacagga agaagcgac aggggtgtgc acaaagaaaa	5378
tgacatgaat ctttattttt cactgccagc ttcaaggaaa gaaaattttt tctacaattt	5438
gcatgagggg tttttttaat tgtatgtact catggttgta aaccaaaccg tactgtaccg	5498
tacagagaaa aggagcaaaa aaaccaagtct tctgtttatc ctgaggcttt ccacaatgtt	5558
cccctctgt gagccaagga ggcaactgc acaagcttgt aaatggttcg tctttaaaat	5618
gtacataagt ggaacattta ataaaatgag gggaaatgga tttataaact tgtttttttt	5678
ctaggtgacc ctgtttaata ggctttcaca gactggggaa tgctcaagat gtgatgggcc	5738
tggtggtaca ggtgtgacat ttgttaccac ccattttctc caccacccc tgcttttttg	5798
tttgtttgtt ttttcatccc ccagcacact ataatatagt gaactggaaa agtcccttc	5858
agaaacagct tggccagctt tgtgaacctt tgacatctga aaacaaccaa ggatccatct	5918
gggcttctct tccccagctt tttgctgat gccattttat tgacagacaa tggactttga	5978
agtcagcctt tgcctttgag aaagttcaag aactatgggt ggtcacgtct atctacaacc	6038
taatcctact ctttggtagt ctctgcagca gccacagcct tagcagagct ggggttctg	6098
tcttctgcac acgattgact ttcttgatgg gtaatttttt ttaagattat accaacagtg	6158
gatcagctgg gttttggcca ggaagttgtc tttgtggact ctgcctgcat ggcttagtag	6218
tagaaggaaa tttttttttg gttttgtttt ttataattca gtttaatcaa taaacatgta	6278
tttattgact gttaaaaaaa aaaaaa	6304

<210> 462
 <211> 1946
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (13)..(1404)

<220>
 <221> misc_feature
 <222> (1)...(1946)
 <223> n = a,t,c or g

<400> 462

```

ggtggtgnatt ga      atg cgt tca cct gat tac gcc aag ctt ggc acg agg      48
                    Met Arg Ser Pro Asp Tyr Ala Lys Leu Gly Thr Arg
                      1              5              10

gtg ccc gga acc cgg aag tgc gag ctg gcg cgc agc tgc agt ctg gga      96
Val Pro Gly Thr Arg Lys Cys Glu Leu Ala Arg Ser Cys Ser Leu Gly
  13              18              23              28

gtc ttt gga gta aga atg gcc ttg gaa ggg atg agc aaa cgg aag aga      144
Val Phe Gly Val Arg Met Ala Leu Glu Gly Met Ser Lys Arg Lys Arg
  29              34              39              44

aag aga agt gtc cag gag gga gag aat cct gac gac ggc gtt cgc ggg      192
Lys Arg Ser Val Gln Glu Gly Glu Asn Pro Asp Asp Gly Val Arg Gly
  45              50              55              60

agt ccg ccg gaa gac tac agg ctt gga cag gtc gcc agt agc tta ttt      240
Ser Pro Pro Glu Asp Tyr Arg Leu Gly Gln Val Ala Ser Ser Leu Phe
  61              66              71              76

cgc ggc gaa cac cat tcc aga ggt ggc acc ggt cgg ctg gcg tcc ctc      288
Arg Gly Glu His His Ser Arg Gly Gly Thr Gly Arg Leu Ala Ser Leu
  77              82              87              92

ttc agt tct ctg gag ccc cag att caa ccc gtg tac gtg cct gtg cct      336
Phe Ser Ser Leu Glu Pro Gln Ile Gln Pro Val Tyr Val Pro Val Pro
  93              98              103             108

aaa caa acc atc aaa aaa acg aaa cgg aat gag gag gaa gaa agt aca      384
Lys Gln Thr Ile Lys Lys Thr Lys Arg Asn Glu Glu Glu Glu Ser Thr
  109             114             119             124

tcc cag att gaa aga cca ctt tcg caa gaa cct gcc aaa aaa gtg aaa      432
Ser Gln Ile Glu Arg Pro Leu Ser Gln Glu Pro Ala Lys Lys Val Lys
  125             130             135             140

gcg aag aag aaa cac act aac gca gaa aaa aag ttg gca gac agg gaa      480
Ala Lys Lys Lys His Thr Asn Ala Glu Lys Lys Leu Ala Asp Arg Glu
  141             146             151             156

```

agc gct cta gcg agt gct gat tta gaa gaa gaa att cac cag aaa caa	528
Ser Ala Leu Ala Ser Ala Asp Leu Glu Glu Glu Ile His Gln Lys Gln	
157 162 167 172	
ggg cag aaa agg aaa aat tct caa cct ggt gtt aaa gta gca gat aga	576
Gly Gln Lys Arg Lys Asn Ser Gln Pro Gly Val Lys Val Ala Asp Arg	
173 178 183 188	
aaa ata ctt gat gac aca gaa gac aca gtt gtc agt caa aga aag aaa	624
Lys Ile Leu Asp Asp Thr Glu Asp Thr Val Val Ser Gln Arg Lys Lys	
189 194 199 204	
att caa atc aac caa gaa gaa gag aga tta aag aat gag aga act gtg	672
Ile Gln Ile Asn Gln Glu Glu Glu Arg Leu Lys Asn Glu Arg Thr Val	
205 210 215 220	
ttt gtt ggg aat ttg cct gtt aca tgt aat aag aag aag ctg aag tcg	720
Phe Val Gly Asn Leu Pro Val Thr Cys Asn Lys Lys Lys Leu Lys Ser	
221 226 231 236	
ttt ttt aaa gag tat gga caa ata gaa tct gta cga ttt cgt tct ctg	768
Phe Phe Lys Glu Tyr Gly Gln Ile Glu Ser Val Arg Phe Arg Ser Leu	
237 242 247 252	
att cca gca gag gga acg cta tcc aaa aag ttg gca gca ata aaa cgt	816
Ile Pro Ala Glu Gly Thr Leu Ser Lys Lys Leu Ala Ala Ile Lys Arg	
253 258 263 268	
aaa att cat cct gat cag aaa aat att aat gcc tat gtt gtg ttt aag	864
Lys Ile His Pro Asp Gln Lys Asn Ile Asn Ala Tyr Val Val Phe Lys	
269 274 279 284	
gag gag agt gct gcc acg caa gca ttg aaa aga aat ggg gcc cag att	912
Glu Glu Ser Ala Ala Thr Gln Ala Leu Lys Arg Asn Gly Ala Gln Ile	
285 290 295 300	
gca gat gga ttt cgt att aga gtt gat ctc gca tct gag acc tca tct	960
Ala Asp Gly Phe Arg Ile Arg Val Asp Leu Ala Ser Glu Thr Ser Ser	
301 306 311 316	
aga gac aag aga tcg gtt ttt gtg ggg aat ctc cct tat aaa gtt gaa	1008
Arg Asp Lys Arg Ser Val Phe Val Gly Asn Leu Pro Tyr Lys Val Glu	
317 322 327 332	
gaa tct gcc att gag aag cac ttt ctg gac tgt gga agt atc atg gcc	1056
Glu Ser Ala Ile Glu Lys His Phe Leu Asp Cys Gly Ser Ile Met Ala	
333 338 343 348	
gtg agg att gtg aga gac aaa atg aca ggc atc ggc aaa ggg ttt ggc	1104
Val Arg Ile Val Arg Asp Lys Met Thr Gly Ile Gly Lys Gly Phe Gly	
349 354 359 364	
tat gtg ctc ttt gag aat aca gat tct gtt cat ctt gct ctg aaa tta	1152
Tyr Val Leu Phe Glu Asn Thr Asp Ser Val His Leu Ala Leu Lys Leu	
365 370 375 380	
aat aat tct gaa ctc atg ggg aga aaa ctc aga gtc atg cgt tct gtt	1200

acgcgcactt gtcggagtga cgggccctgc ggaagaggag gtgcggccca gggcgcaggg	180
gagccctcgg gagcggggccc ggccctcagc gccgcccgg cegtgtcccg gaggagcggc	240
ctgcgcggcc gcgcgagagg aagcaccag gc atg tgg aat atg ctc ata gtg	293
Met Trp Asn Met Leu Ile Val	
1 5	
gcg atg tgc ttg gcc ctt ctg ggc tgc ctg caa gcc cag gag ctc cag	341
Ala Met Cys Leu Ala Leu Leu Gly Cys Leu Gln Ala Gln Glu Leu Gln	
8 13 18 23	
gga cat gtc tcc ata atc ctg ctg gga gca act ggg gac ctg gct aag	389
Gly His Val Ser Ile Ile Leu Leu Gly Ala Thr Gly Asp Leu Ala Lys	
24 29 34 39	
aag tac tta tgg cag gga ctg ttc cag ctg tac ctg gat gaa gcg ggg	437
Lys Tyr Leu Trp Gln Gly Leu Phe Gln Leu Tyr Leu Asp Glu Ala Gly	
40 45 50 55	
agg ggt cac agt ttt agc ttc cat gga gct gct ctg aca gcc ccc aag	485
Arg Gly His Ser Phe Ser Phe His Gly Ala Ala Leu Thr Ala Pro Lys	
56 61 66 71	
cag ggt caa gag ctc atg gcc aag gcc ctg gaa tcc ctc tcc tgc ccc	533
Gln Gly Gln Glu Leu Met Ala Lys Ala Leu Glu Ser Leu Ser Cys Pro	
72 77 82 87	
aag gac atg gca ccc agt cac tgt gca gag cac aag gat cag ttc ctg	581
Lys Asp Met Ala Pro Ser His Cys Ala Glu His Lys Asp Gln Phe Leu	
88 93 98 103	
cag ctg agc cag tac cgc caa ctg aag acg gcc gag gac tat cag gcc	629
Gln Leu Ser Gln Tyr Arg Gln Leu Lys Thr Ala Glu Asp Tyr Gln Ala	
104 109 114 119	
ctg aac aag gac atc gag gca cag ctc cag cac gca ggc ctc cgg gag	677
Leu Asn Lys Asp Ile Glu Ala Gln Leu Gln His Ala Gly Leu Arg Glu	
120 125 130 135	
gct ggc agg atc ttc tac ttc tca gtg cca ccc ttc gcc tat gaa gac	725
Ala Gly Arg Ile Phe Tyr Phe Ser Val Pro Pro Phe Ala Tyr Glu Asp	
136 141 146 151	
att gcc cgc aac atc aac agt agc tgc cgg cca ggc ccg ggc gcc tgg	773
Ile Ala Arg Asn Ile Asn Ser Ser Cys Arg Pro Gly Pro Gly Ala Trp	
152 157 162 167	
ctg cgg gtt gtc ctt gag aaa ccc ttt ggc cat gac cac ttc tca gcc	821
Leu Arg Val Val Leu Glu Lys Pro Phe Gly His Asp His Phe Ser Ala	
168 173 178 183	
cag cag ctg gcc aca gaa ctc ggg acc ttt ttc cag gag gag gag atg	869
Gln Gln Leu Ala Thr Glu Leu Gly Thr Phe Phe Gln Glu Glu Glu Met	
184 189 194 199	

tac cgg gtg gac cat tac tta ggc aag cag gct gtg gcg cag atc ctg	917
Tyr Arg Val Asp His Tyr Leu Gly Lys Gln Ala Val Ala Gln Ile Leu	
200 205 210 215	
cct ttc cga gac cag aac cgc aag gct ttg gac ggc ctc tgg aac cgg	965
Pro Phe Arg Asp Gln Asn Arg Lys Ala Leu Asp Gly Leu Trp Asn Arg	
216 221 226 231	
cac cat gtg gag cgg gtg gag atc atc atg aaa gag acc gtg gat gct	1013
His His Val Glu Arg Val Glu Ile Ile Met Lys Glu Thr Val Asp Ala	
232 237 242 247	
gaa ggc cgc acc agc ttc tat gag gag tac ggt gtc att cgc gac gtc	1061
Glu Gly Arg Thr Ser Phe Tyr Glu Glu Tyr Gly Val Ile Arg Asp Val	
248 253 258 263	
ctc cag aac cat ctg acg gag gtc ctc acc ctc gtg gcc atg gag ctg	1109
Leu Gln Asn His Leu Thr Glu Val Leu Thr Leu Val Ala Met Glu Leu	
264 269 274 279	
ccc cac aat gtc agc agt gcg gag gct gtg ctg cgg cac aag ctt cag	1157
Pro His Asn Val Ser Ser Ala Glu Ala Val Leu Arg His Lys Leu Gln	
280 285 290 295	
gtc ttc cag gcg ctg cgg ggc ctg cag agg ggc agt gcc gtc gtg ggc	1205
Val Phe Gln Ala Leu Arg Gly Leu Gln Arg Gly Ser Ala Val Val Gly	
296 301 306 311	
cag tac cag tct tac agt gag cag gtg cgc aga gag ctg cag aag cca	1253
Gln Tyr Gln Ser Tyr Ser Glu Gln Val Arg Arg Glu Leu Gln Lys Pro	
312 317 322 327	
gac agc ttc cac agc ctg acg ccg acc ttc gca ggt gtc cta gtg cac	1301
Asp Ser Phe His Ser Leu Thr Pro Thr Phe Ala Gly Val Leu Val His	
328 333 338 343	
att gac aac ctt cgc tgg gag ggc gtg cct ttc atc ctg atg tct ggc	1349
Ile Asp Asn Leu Arg Trp Glu Gly Val Pro Phe Ile Leu Met Ser Gly	
344 349 354 359	
aaa gcc ttg gac gag aga gtg ggc tac gct cgg atc ttg ttc aag aac	1397
Lys Ala Leu Asp Glu Arg Val Gly Tyr Ala Arg Ile Leu Phe Lys Asn	
360 365 370 375	
cag gcc tgc tgt gtg cag agc gaa aag cac tgg gcc gcg gcg cag agc	1445
Gln Ala Cys Cys Val Gln Ser Glu Lys His Trp Ala Ala Ala Gln Ser	
376 381 386 391	
cag tgc ctg ccc cgg cag ctc gtc ttc cac atc ggc cat ggc gac ctg	1493
Gln Cys Leu Pro Arg Gln Leu Val Phe His Ile Gly His Gly Asp Leu	
392 397 402 407	
ggc agc cct gcc gtg ctg gtc agc agg aac ctg ttc agg ccc tcc ctg	1541
Gly Ser Pro Ala Val Leu Val Ser Arg Asn Leu Phe Arg Pro Ser Leu	
408 413 418 423	
ccc tcc agc tgg aag gaa atg gag gga cca cct ggg ctc cgc ctt ttc	1589

Pro Ser Ser Trp Lys Glu Met Glu Gly Pro Pro Gly Leu Arg Leu Phe	
424 429 434 439	
ggc agc cct ctg tcc gat tac tac gcc tac agc cct gtg cgg gag cgg	1637
Gly Ser Pro Leu Ser Asp Tyr Tyr Ala Tyr Ser Pro Val Arg Glu Arg	
440 445 450 455	
gac gcc cac tcc gtc ctc tta tcc cat atc ttc cat ggc cgg aag aat	1685
Asp Ala His Ser Val Leu Leu Ser His Ile Phe His Gly Arg Lys Asn	
456 461 466 471	
ttc ttc atc acc aca gag aac ttg ctg gcc tcc tgg aac ttc tgg acc	1733
Phe Phe Ile Thr Thr Glu Asn Leu Leu Ala Ser Trp Asn Phe Trp Thr	
472 477 482 487	
cct ctg ctg gag agc ctg gcc cat aag gcc cca cgc ctc tac cct gga	1781
Pro Leu Leu Glu Ser Leu Ala His Lys Ala Pro Arg Leu Tyr Pro Gly	
488 493 498 503	
gga gct gag aat ggc cgt ctg ttg gac ttt gag ttc agt agc ggc cgg	1829
Gly Ala Glu Asn Gly Arg Leu Leu Asp Phe Glu Phe Ser Ser Gly Arg	
504 509 514 519	
ttg ttc ttt tcc cag cag cag ccg gag cag ctg gtg cca ggg cca ggg	1877
Leu Phe Phe Ser Gln Gln Gln Pro Glu Gln Leu Val Pro Gly Pro Gly	
520 525 530 535	
ccg gcc cca atg ccc agt gac ttc cag gtc ctc agg gcc aag tac cga	1925
Pro Ala Pro Met Pro Ser Asp Phe Gln Val Leu Arg Ala Lys Tyr Arg	
536 541 546 551	
gag agc ccg ctg gtc tcc gcc tgg tcc gag gag ctg atc tct aag ctg	1973
Glu Ser Pro Leu Val Ser Ala Trp Ser Glu Glu Leu Ile Ser Lys Leu	
552 557 562 567	
gct aat gac atc gag gcc acc gct gtg cga gcc gtg cgg cgc ttt ggc	2021
Ala Asn Asp Ile Glu Ala Thr Ala Val Arg Ala Val Arg Arg Phe Gly	
568 573 578 583	
cag ttc cac ctg gca ctg tcg ggg ggc tcg agc ccc gtg gcc ctg ttc	2069
Gln Phe His Leu Ala Leu Ser Gly Gly Ser Ser Pro Val Ala Leu Phe	
584 589 594 599	
cag cag ctg gcc acg gcg cac tat ggc ttc ccc tgg gcc cac acg cac	2117
Gln Gln Leu Ala Thr Ala His Tyr Gly Phe Pro Trp Ala His Thr His	
600 605 610 615	
ctg tgg ctg gtt gac gag cgc tgc gtc cca ctc tca gac ccg gag tcc	2165
Leu Trp Leu Val Asp Glu Arg Cys Val Pro Leu Ser Asp Pro Glu Ser	
616 621 626 631	
aac ttc cag ggc ctg cag gcc cac ctg ctg cag cac gtc cgg atc ccc	2213
Asn Phe Gln Gly Leu Gln Ala His Leu Leu Gln His Val Arg Ile Pro	
632 637 642 647	
tac tac aac atc cac ccc atg cct gtg cac ctg cag cag cgg ctc tgc	2261
Tyr Tyr Asn Ile His Pro Met Pro Val His Leu Gln Gln Arg Leu Cys	

648	653	658	663	
gcc gag gag gac cag ggc gcc cag atc tat gcc agg gag atc tca gcc				2309
Ala Glu Glu Asp Gln Gly Ala Gln Ile Tyr Ala Arg Glu Ile Ser Ala				
664	669	674	679	
ctg ggg gcc aac agc agc ttc gac ctg gtg ctg ctg ggc atg ggt gcc				2357
Leu Gly Ala Asn Ser Ser Phe Asp Leu Val Leu Leu Gly Met Gly Ala				
680	685	690	695	
gac ggg cac aca gcc tcc ctc ttc cca cag tca ccc act ggc ctg gat				2405
Asp Gly His Thr Ala Ser Leu Phe Pro Gln Ser Pro Thr Gly Leu Asp				
696	701	706	711	
ggc gag cag ctg gtc gtg ctg acc acg agc ccc tcc cag cca cac cgc				2453
Gly Glu Gln Leu Val Val Leu Thr Thr Ser Pro Ser Gln Pro His Arg				
712	717	722	727	
cgc atg agc ctt agc ctg cct ctc atc aac cgc gcc aag aag gtg gca				2501
Arg Met Ser Leu Ser Leu Pro Leu Ile Asn Arg Ala Lys Lys Val Ala				
728	733	738	743	
gtc ctg gtc atg ggc agg atg aag cgt gag atc acc acg ctg gtg agc				2549
Val Leu Val Met Gly Arg Met Lys Arg Glu Ile Thr Thr Leu Val Ser				
744	749	754	759	
cgg gtg ggc cat gag ccc aag aag tgg ccc atc tcg ggt gtc ctg ccg				2597
Arg Val Gly His Glu Pro Lys Lys Trp Pro Ile Ser Gly Val Leu Pro				
760	765	770	775	
cac tcc ggc cag ctg gtg tgg tac atg gac tac gac gcc ttc ctg gga				2645
His Ser Gly Gln Leu Val Trp Tyr Met Asp Tyr Asp Ala Phe Leu Gly				
776	781	786	791	
tga gggc gcctgtgcc cttgcccgtc tcgctcctgt gctttccttc gcccggtct				2702
*				
792				
tcctccctt ctggccccg ccacctgcc agcgtgccct ggctctccag aaccttctat				2762
cccacagtca ggccccagag agggcaggac aagccttgtc ccgatgcctt tgaccggcag				2822
ctctgtgtat tgggtgatag atgcagaaac a				2853

<210> 464
 <211> 4648
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (452) .. (3730)

<400> 464

gaa gaa ata aac ttg ttt agt gaa aac aag tta cag tta aag cag atg	1000
Glu Glu Ile Asn Leu Phe Ser Glu Asn Lys Leu Gln Leu Lys Gln Met	
168 173 178 183	
ggt gac cag ttg atc aag gcc agc aac aaa tca aga gca gct gag atc	1048
Gly Asp Gln Leu Ile Lys Ala Ser Asn Lys Ser Arg Ala Ala Glu Ile	
184 189 194 199	
gat gac aag ctc aac aaa att aac gat cgt tgg caa cat ctt ttt gat	1096
Asp Asp Lys Leu Asn Lys Ile Asn Asp Arg Trp Gln His Leu Phe Asp	
200 205 210 215	
gtc atc gga tca agg gtg aag aag ctg aag gag acc ttt gct ttt att	1144
Val Ile Gly Ser Arg Val Lys Lys Leu Lys Glu Thr Phe Ala Phe Ile	
216 221 226 231	
cag cag ttg gac aaa aac atg agc aac ctt cgc acc tgg ttg gct cga	1192
Gln Gln Leu Asp Lys Asn Met Ser Asn Leu Arg Thr Trp Leu Ala Arg	
232 237 242 247	
att gag tct gag ctt tcc aag cct gtt gtt tat gat gtc tgc gat gat	1240
Ile Glu Ser Glu Leu Ser Lys Pro Val Val Tyr Asp Val Cys Asp Asp	
248 253 258 263	
caa gag atc cag aag agg ctc gct gag cag cag gat cta cag cga gat	1288
Gln Glu Ile Gln Lys Arg Leu Ala Glu Gln Gln Asp Leu Gln Arg Asp	
264 269 274 279	
att gaa caa cac agc gca ggg gtg gag tcc gtg ttt aac atc tgt gac	1336
Ile Glu Gln His Ser Ala Gly Val Glu Ser Val Phe Asn Ile Cys Asp	
280 285 290 295	
gtc cta ctg cac gac tcc gat gcc tgt gca aat gag acc gag tgt gac	1384
Val Leu Leu His Asp Ser Asp Ala Cys Ala Asn Glu Thr Glu Cys Asp	
296 301 306 311	
tcg atc cag cag acc acc agg agc ctg gac aga cgc tgg agg aac att	1432
Ser Ile Gln Gln Thr Thr Arg Ser Leu Asp Arg Arg Trp Arg Asn Ile	
312 317 322 327	
tgt gcc atg tcc atg gag cgg cgc atg aaa atc gag gag acg tgg cgc	1480
Cys Ala Met Ser Met Glu Arg Arg Met Lys Ile Glu Glu Thr Trp Arg	
328 333 338 343	
ctg tgg cag aag ttt tta gac gac tat tct cgc ttt gag gac tgg ctc	1528
Leu Trp Gln Lys Phe Leu Asp Asp Tyr Ser Arg Phe Glu Asp Trp Leu	
344 349 354 359	
aag tca gct gag agg acg gca gcc tgc cca aat tcc tca gag gtg ttg	1576
Lys Ser Ala Glu Arg Thr Ala Ala Cys Pro Asn Ser Ser Glu Val Leu	
360 365 370 375	
tac acg agt gcc aaa gag gaa ctg aag agg ttt gag gcc ttt cag cgg	1624
Tyr Thr Ser Ala Lys Glu Glu Leu Lys Arg Phe Glu Ala Phe Gln Arg	
376 381 386 391	

cag att cat gag cgg ctc act cag ctg gag ctc atc aac aag cag tac	1672
Gln Ile His Glu Arg Leu Thr Gln Leu Glu Leu Ile Asn Lys Gln Tyr	
392 397 402 407	
cgg cgg ctg gcc cgg gag aac cgc aca gac acg gcc agc agg ctg aag	1720
Arg Arg Leu Ala Arg Glu Asn Arg Thr Asp Thr Ala Ser Arg Leu Lys	
408 413 418 423	
cag atg gtc cac gag ggc aac cag cgc tgg gac aac ctt cag agg cgg	1768
Gln Met Val His Glu Gly Asn Gln Arg Trp Asp Asn Leu Gln Arg Arg	
424 429 434 439	
gtc aca gcc gtc ctg cgg aga ctc agg cat ttc acc aac cag agg gaa	1816
Val Thr Ala Val Leu Arg Arg Leu Arg His Phe Thr Asn Gln Arg Glu	
440 445 450 455	
gaa ttt gag ggc acc agg gag agc att ctg gtg tgg ctc aca gag atg	1864
Glu Phe Glu Gly Thr Arg Glu Ser Ile Leu Val Trp Leu Thr Glu Met	
456 461 466 471	
gac ctg cag ctg acc aac gtg gag cac ttc tca gag agt gac gcc gat	1912
Asp Leu Gln Leu Thr Asn Val Glu His Phe Ser Glu Ser Asp Ala Asp	
472 477 482 487	
gac aag atg cgc caa ctg aat ggc ttc caa cag gaa att aca tta aat	1960
Asp Lys Met Arg Gln Leu Asn Gly Phe Gln Gln Glu Ile Thr Leu Asn	
488 493 498 503	
acc aac aag att gat cag ctc att gtg ttt ggg gag cag ctg att cag	2008
Thr Asn Lys Ile Asp Gln Leu Ile Val Phe Gly Glu Gln Leu Ile Gln	
504 509 514 519	
aag agc gag ccc ctg gat gct gtg ctg att gag gat gag ctg gag gaa	2056
Lys Ser Glu Pro Leu Asp Ala Val Leu Ile Glu Asp Glu Leu Glu Glu	
520 525 530 535	
ctc cac cgc tac tgc cag gag gtg ttt gga agg gtc tcc cgg ttc cac	2104
Leu His Arg Tyr Cys Gln Glu Val Phe Gly Arg Val Ser Arg Phe His	
536 541 546 551	
cgg cgg ctc acc tcc tgc act ccg ggc ttg gaa gat gaa aag gag gcc	2152
Arg Arg Leu Thr Ser Cys Thr Pro Gly Leu Glu Asp Glu Lys Glu Ala	
552 557 562 567	
tct gag aat gaa aca gac atg gaa gac ccc aga gaa atc cag act gat	2200
Ser Glu Asn Glu Thr Asp Met Glu Asp Pro Arg Glu Ile Gln Thr Asp	
568 573 578 583	
tct tgg cgt aaa cgg gga gag agc gag gaa ccg tca tct cct cag tcc	2248
Ser Trp Arg Lys Arg Gly Glu Ser Glu Glu Pro Ser Ser Pro Gln Ser	
584 589 594 599	
ctg tgt cat cta gtg gcc cca ggg cac gag cgg tct ggc tgc gag acc	2296
Leu Cys His Leu Val Ala Pro Gly His Glu Arg Ser Gly Cys Glu Thr	
600 605 610 615	
cct gtc agc gtg gac tcc atc ccc ctg gag tgg gac cac aca ggc gac	2344

Pro	Val	Ser	Val	Asp	Ser	Ile	Pro	Leu	Glu	Trp	Asp	His	Thr	Gly	Asp	
616					621					626					631	
gtg	ggg	ggc	tcc	tcc	tct	cac	gaa	gag	gac	gag	gag	ggc	cca	tac	tac	2392
Val	Gly	Gly	Ser	Ser	Ser	His	Glu	Glu	Asp	Glu	Glu	Gly	Pro	Tyr	Tyr	
632					637					642					647	
agc	gca	ctg	tca	ggc	aaa	tcc	att	tgc	gat	ggc	cac	tgc	tgg	cat	gtt	2440
Ser	Ala	Leu	Ser	Gly	Lys	Ser	Ile	Ser	Asp	Gly	His	Ser	Trp	His	Val	
648					653					658					663	
ccc	gac	agc	cct	tcc	tgt	ccc	gag	cat	cac	tac	aag	caa	atg	gaa	ggc	2488
Pro	Asp	Ser	Pro	Ser	Cys	Pro	Glu	His	His	Tyr	Lys	Gln	Met	Glu	Gly	
664					669					674					679	
gac	agg	aat	gtt	cca	cct	gtt	ccc	cct	gcg	tcc	agc	acc	cct	tat	aaa	2536
Asp	Arg	Asn	Val	Pro	Pro	Val	Pro	Pro	Ala	Ser	Ser	Thr	Pro	Tyr	Lys	
680					685					690					695	
cca	ccc	tat	gga	aag	cta	cta	tta	cct	cca	ggc	acg	gat	ggc	ggc	aaa	2584
Pro	Pro	Tyr	Gly	Lys	Leu	Leu	Leu	Pro	Pro	Gly	Thr	Asp	Gly	Gly	Lys	
696					701					706					711	
gaa	ggc	ccg	cga	gtc	ctg	aat	ggc	aac	cca	cag	cag	gaa	gac	ggg	gga	2632
Glu	Gly	Pro	Arg	Val	Leu	Asn	Gly	Asn	Pro	Gln	Gln	Glu	Asp	Gly	Gly	
712					717					722					727	
ctg	gcc	ggc	atc	aca	gag	cag	cag	tca	ggc	gcc	ttc	gac	aga	tgg	gag	2680
Leu	Ala	Gly	Ile	Thr	Glu	Gln	Gln	Ser	Gly	Ala	Phe	Asp	Arg	Trp	Glu	
728					733					738					743	
atg	att	caa	gca	cag	gag	ctt	cac	aat	aag	ctc	aaa	ata	aaa	caa	aat	2728
Met	Ile	Gln	Ala	Gln	Glu	Leu	His	Asn	Lys	Leu	Lys	Ile	Lys	Gln	Asn	
744					749					754					759	
ttg	caa	cag	ctg	aac	tct	gat	atc	agc	gcc	atc	act	act	tgg	ctg	aaa	2776
Leu	Gln	Gln	Leu	Asn	Ser	Asp	Ile	Ser	Ala	Ile	Thr	Thr	Trp	Leu	Lys	
760					765					770					775	
aaa	act	gaa	gca	gag	ctg	gaa	atg	tta	aag	atg	gca	aag	cct	ccc	tct	2824
Lys	Thr	Glu	Ala	Glu	Leu	Glu	Met	Leu	Lys	Met	Ala	Lys	Pro	Pro	Ser	
776					781					786					791	
gat	atc	cag	gaa	ata	gaa	ctg	aga	gtg	aag	aga	ctg	cag	gag	ata	ctg	2872
Asp	Ile	Gln	Glu	Ile	Glu	Leu	Arg	Val	Lys	Arg	Leu	Gln	Glu	Ile	Leu	
792					797					802					807	
aaa	gcc	ttt	gac	act	tac	aag	gca	tta	gtg	gtc	tct	gtc	aac	gtg	agc	2920
Lys	Ala	Phe	Asp	Thr	Tyr	Lys	Ala	Leu	Val	Val	Ser	Val	Asn	Val	Ser	
808					813					818					823	
agc	aag	gaa	ttt	ctg	caa	acc	gag	agc								

840	845	850	855	
gtg gac agc tgg aga ggg ggc tta cga cag tgc ctc atg cag tgc cag Val Asp Ser Trp Arg Gly Gly Leu Arg Gln Ser Leu Met Gln Cys Gln 856 861 866 871				3064
gac ttc cac cag ttg agt caa aat ctg ctg ctg tgg tta gcg agt gcc Asp Phe His Gln Leu Ser Gln Asn Leu Leu Leu Trp Leu Ala Ser Ala 872 877 882 887				3112
aag aac cgg agg cag aag gct cat gtc acc gat cca aag gca gac ccc Lys Asn Arg Arg Gln Lys Ala His Val Thr Asp Pro Lys Ala Asp Pro 888 893 898 903				3160
cgg gct ctc cta gag tgt cgg agg gaa cta atg caa ctg gaa aag gag Arg Ala Leu Leu Glu Cys Arg Arg Glu Leu Met Gln Leu Glu Lys Glu 904 909 914 919				3208
ctg gta gaa cgt caa cct caa gtg gac atg tta cag gag att tca aac Leu Val Glu Arg Gln Pro Gln Val Asp Met Leu Gln Glu Ile Ser Asn 920 925 930 935				3256
agc ctt ctc att aag gga cat gga gaa gac tgt att gaa gct gaa gaa Ser Leu Leu Ile Lys Gly His Gly Glu Asp Cys Ile Glu Ala Glu Glu 936 941 946 951				3304
aag gtg cat gtt att gag aag aaa ctc aaa cag tta cgg gag caa gtg Lys Val His Val Ile Glu Lys Lys Leu Lys Gln Leu Arg Glu Gln Val 952 957 962 967				3352
tcc caa gat tta atg gcc ttg cag gga acc cag aac cca gcc tca ccc Ser Gln Asp Leu Met Ala Leu Gln Gly Thr Gln Asn Pro Ala Ser Pro 968 973 978 983				3400
ctg ccc agc ttc gac gag gta gac tgc ggg gac cag cct cct gca aca Leu Pro Ser Phe Asp Glu Val Asp Ser Gly Asp Gln Pro Pro Ala Thr 984 989 994 999				3448
tcc gtg cca gct ccc cga gca aag cag ttc aga gca gtg aga act aca Ser Val Pro Ala Pro Arg Ala Lys Gln Phe Arg Ala Val Arg Thr Thr 1000 1005 1010 1015				3496
gaa ggc gag gag gag aca gag agc agg gtc ccc ggc agc aca cgg cca Glu Gly Glu Glu Glu Thr Glu Ser Arg Val Pro Gly Ser Thr Arg Pro 1016 1021 1026 1031				3544
cag cgc tcc ttc ctc tca agg gtg gtc cgg gca gcc cta ccc ctg cag Gln Arg Ser Phe Leu Ser Arg Val Val Arg Ala Ala Leu Pro Leu Gln 1032 1037 1042 1047				3592
ctg ctc ctc ctg ctg ctg ctg ctc ctg gcc tgc ctg ctg ccc tcc tcc Leu Leu Leu Leu Leu Leu Leu Leu Leu Ala Cys Leu Leu Pro Ser Ser 1048 1053 1058 1063				3640
gaa gaa gac tac agc tgc act cag gcc aac aac ttt gcc cgg tcc ttt Glu Glu Asp Tyr Ser Cys Thr Gln Ala Asn Asn Phe Ala Arg Ser Phe 1064 1069 1074 1079				3688

tac ccc atg ctg agg tac acc aat ggg cca ccc ccc aca tag agggcat 3737
 Tyr Pro Met Leu Arg Tyr Thr Asn Gly Pro Pro Pro Thr *
 1080 1085 1090

agctggccac agtgctacac caoctgcctg attgccaaagg gtgcccagca cgtggcccca 3797
 gaccaatctg agtgacttag tgttggcaag gtcccgggac ctgtgcagac ttcttctggg 3857
 cttacacagc acgggctccc tggagcccag ggcagctttc agattgtgtt cctccccagg 3917
 agcagggAAC ctgtgtggca ggtgccccgg gtactttggc agaactagtt gattagttta 3977
 gggatctctg gaaatgtcag tttcctgaag agccaagcac tttgtgaatt ctggtttgtt 4037
 tgtaaaacag cattattata atgtaggtat ggtcaatgag cagtgggtgtc catcacatat 4097
 attatagaag caagcgagca cattccacc tagaaatggg tcagaaactc ataggcacc 4157
 ttagctgatg gaaacaatca atcatattta atacgcttag aatcagtttt actccaatca 4217
 gctggcaatt ttgagctgcc gggtatacac caaaatgttc tgttcagtac ctagctctgc 4277
 tcttttatat tgctttaaat ttttaaagaa attatattgc atggatgtgg ttatttgtgc 4337
 atatttttta acaatgccc atctgtatga ataatgtaaa cttcgatttt tttttaaaaa 4397
 aattagattt tagctggagc ttttgactaa tgtaaagtaa atgccaaact accgacttga 4457
 tagggatgtt tttgtaagtt aattttctaa gactttttca catccaaagt gatgctttgc 4517
 tttgggtttt aactgtttgg ccacggcggg ggtgggggCG ggggggttgg acaaaaactt 4577
 gaagctgttt gtgatatgta caactcagat gtttctcatt aaaaaacaaa attagccaga 4637
 aaaaaaaaaa a 4648

<210> 465
 <211> 1185
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (198)..(1133)

<400> 465
 gaattcccgg gtgcacgatt tcgtgagcgc ggcagcccgc gcagccggtg actgggggac 60
 tgggtttgga gtaggacctg cggcgtgctc gagactccga cttcgggtctt gcggcgcgct 120
 cgcgcccgcg ggccatgccc cactgactct aagtgggcac tgccccggct ccgggagggc 180
 gagaccgagc gccggcc atg gga agc ttc cag ctg gaa gac ttt gcg gcg 230

Met Gly Ser Phe Gln Leu Glu Asp Phe Ala Ala
1 5

ggc tgg atc gga ggt gca gcc agt gtc atc gtc ggc cac cct ctg gac Gly Trp Ile Gly Gly Ala Ala Ser Val Ile Val Gly His Pro Leu Asp 12 17 22 27	278
aca gtc aag act cgc ctg cag gct ggc gtt ggc tac gga aac acc ctc Thr Val Lys Thr Arg Leu Gln Ala Gly Val Gly Tyr Gly Asn Thr Leu 28 33 38 43	326
agc tgc atc cgc gtg gtg tac agg agg gag agt atg ttc ggc ttc ttc Ser Cys Ile Arg Val Val Tyr Arg Arg Glu Ser Met Phe Gly Phe Phe 44 49 54 59	374
aag ggc atg tcc ttc ccc ctc gcc agc att gcc gtc tac aac tcc gtg Lys Gly Met Ser Phe Pro Leu Ala Ser Ile Ala Val Tyr Asn Ser Val 60 65 70 75	422
gtg ttt ggg gtc ttc agt aac acg cag cgg ttc ctc agc cag cac cgc Val Phe Gly Val Phe Ser Asn Thr Gln Arg Phe Leu Ser Gln His Arg 76 81 86 91	470
tgc ggg gag cca gag gcc agt cct ccc cgc acg ctg tca gac ctg ctc Cys Gly Glu Pro Glu Ala Ser Pro Pro Arg Thr Leu Ser Asp Leu Leu 92 97 102 107	518
ctg gcc agc atg gtg gcc ggc gtg gtc tct gtc ggg ctg gga ggg ccc Leu Ala Ser Met Val Ala Gly Val Val Ser Val Gly Leu Gly Gly Pro 108 113 118 123	566
gtg gac ctc atc aag atc cgg ttg cag atg cag aca caa ccg ttt cgg Val Asp Leu Ile Lys Ile Arg Leu Gln Met Gln Thr Gln Pro Phe Arg 124 129 134 139	614
gac gcc aac ctc ggt ttg aag tcc agg gca gtg gct cct gca gag cag Asp Ala Asn Leu Gly Leu Lys Ser Arg Ala Val Ala Pro Ala Glu Gln 140 145 150 155	662
cca gca tac cag ggg cca gtg cac tgc att aca acc att gtg agg aat Pro Ala Tyr Gln Gly Pro Val His Cys Ile Thr Thr Ile Val Arg Asn 156 161 166 171	710
gag ggc ctg gcg ggg cta tac cgg ggg gcc agt gcc atg ctg ctg agg Glu Gly Leu Ala Gly Leu Tyr Arg Gly Ala Ser Ala Met Leu Leu Arg 172 177 182 187	758
gat gtc cca ggc tat tgc ctc tac ttc atc ccc tac gtg ttc ctg agt Asp Val Pro Gly Tyr Cys Leu Tyr Phe Ile Pro Tyr Val Phe Leu Ser 188 193 198 203	806
gag tgg atc aca cct gag gcc tgc aca ggc ccc agc ccc tgt gct gtg Glu Trp Ile Thr Pro Glu Ala Cys Thr Gly Pro Ser Pro Cys Ala Val 204 209 214 219	854
tgg ctg gcg ggc ggc atg gca gga gca att tct tgg ggg aca gcg act Trp Leu Ala Gly Gly Met Ala Gly Ala Ile Ser Trp Gly Thr Ala Thr 224 229 234 239	902

220	225	230	235	
cct atg gat gtc gtg aaa agt cga ctc caa gct gat ggg gtt tat tta				950
Pro Met Asp Val Val Lys Ser Arg Leu Gln Ala Asp Gly Val Tyr Leu				
236	241	246	251	
aac aaa tat aaa ggt gtc ctg gac tgt atc tcc cag agt tac cag aag				998
Asn Lys Tyr Lys Gly Val Leu Asp Cys Ile Ser Gln Ser Tyr Gln Lys				
252	257	262	267	
gaa ggt ctt aaa gtg ttt ttc aga ggc atc act gtg aac gcg gtg cgg				1046
Glu Gly Leu Lys Val Phe Phe Arg Gly Ile Thr Val Asn Ala Val Arg				
268	273	278	283	
ggc ttc ccc atg agt gcg gcc atg ttc ctt ggg tac gag ctg tcg ctg				1094
Gly Phe Pro Met Ser Ala Ala Met Phe Leu Gly Tyr Glu Leu Ser Leu				
284	289	294	299	
cag gct atc cgc ggg gac cac gca gtg acg agc cca taa gcgccaggtc				1143
Gln Ala Ile Arg Gly Asp His Ala Val Thr Ser Pro *				
300	305	310		
tttgctcagg ctgtcccctc tgccctgacat cctcttctcg ct				1185

<210> 466
 <211> 907
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (240)..(779)

<220>
 <221> misc_feature
 <222> (1)...(907)
 <223> n = a,t,c or g

atttgccct cgaggcanag aattcggcac gaggagagac tttcgcttcc ggctgccgca	60
cgcttcgctg gtgcaggtaa gctccgcaca ctctcggccg gtcccgagtc cgactccctc	120
aagggtgacg cgagctctgc cctttaaccg gaaacgtctc cctgctcacc ccacccccgc	180
gcagacgcag tgctgagcac acagctaccg gacaaagagt gacgcccgga gctggagtt	239
atg gcg gct acg gag ccg atc ttg gcg gcc act ggg agt ccc gcg gcg	287
Met Ala Ala Thr Glu Pro Ile Leu Ala Ala Thr Gly Ser Pro Ala Ala	
1 5 10 15	
gtg cca ccg gag aaa ctg gaa gga gcc ggt tcg agc tca gcc cct gag	335
Val Pro Pro Glu Lys Leu Glu Gly Ala Gly Ser Ser Ser Ala Pro Glu	
17 22 27 32	

cgt aac tgt gtg ggc tcc tcg ctg cca gag gcc tca ccg cct gcc cct	383
Arg Asn Cys Val Gly Ser Ser Leu Pro Glu Ala Ser Pro Pro Ala Pro	
33 38 43 48	
gag cct tcc agt ccc aac gcc gcg gtc cct gaa gcc atc cct acg ccc	431
Glu Pro Ser Ser Pro Asn Ala Ala Val Pro Glu Ala Ile Pro Thr Pro	
49 54 59 64	
cga gct gcg gcc tcc gcg gcc ctg gag ctg cct ctc ggg ccc gca ccc	479
Arg Ala Ala Ala Ser Ala Ala Leu Glu Leu Pro Leu Gly Pro Ala Pro	
65 70 75 80	
gtg agc gta gcg cct cag gcc gaa gct gaa gcg cgc tcc aca cca ggc	527
Val Ser Val Ala Pro Gln Ala Glu Ala Glu Ala Arg Ser Thr Pro Gly	
81 86 91 96	
ccc gcc ggc tct aga ctc ggt ccc gag acg ttc cgc cag cgt ttc cgg	575
Pro Ala Gly Ser Arg Leu Gly Pro Glu Thr Phe Arg Gln Arg Phe Arg	
97 102 107 112	
cag ttc cgc tac cag gat gcg gcg ggt ccc cgg gag gct ttc cgg cag	623
Gln Phe Arg Tyr Gln Asp Ala Ala Gly Pro Arg Glu Ala Phe Arg Gln	
113 118 123 128	
ctg cgg gag ctg tcc cgc cag tgg ctg cgg cct gac atc cgc acc aag	671
Leu Arg Glu Leu Ser Arg Gln Trp Leu Arg Pro Asp Ile Arg Thr Lys	
129 134 139 144	
gag cag atc gtg gag atg ctg gtg caa gag cag ctg ctc gcc atc ctg	719
Glu Gln Ile Val Glu Met Leu Val Gln Glu Gln Leu Leu Ala Ile Leu	
145 150 155 160	
ccc gag gcg gct cgg gcc cgg cgg atc cgc cgc cgc acg gat gtg cgc	767
Pro Glu Ala Ala Arg Ala Arg Arg Ile Arg Arg Arg Thr Asp Val Arg	
161 166 171 176	
atc act ggc tga gcg gtggagctgc gggcgggccag ggccgggcgc tctgtgcgga	822
Ile Thr Gly *	
177	
ctggggccat gatcggggccc gggggcctga gcctgggacc ccaccccgctg ttaatgaaaa	882
atgagttttg gcaaaaaaaaa aaaaa	907

<210> 467
 <211> 1131
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (35) .. (982)

<400> 467

agcgcaggtg ggcccgcgct ctcggccctg caag	atg ccc ctg aag ctg cgg	52
	Met Pro Leu Lys Leu Arg	
	1	
ggg aag aag aag gcc aag tcc aag gag acc gcc ggg ctg gtg gag ggc		100
Gly Lys Lys Lys Ala Lys Ser Lys Glu Thr Ala Gly Leu Val Glu Gly		
7 12 17 22		
gag ccg acg ggc gcg ggc ggc ggg agc ctc tca gcg tcc cgg gct ccc		148
Glu Pro Thr Gly Ala Gly Gly Gly Ser Leu Ser Ala Ser Arg Ala Pro		
23 28 33 38		
gca cgc agg ctg gtc ttc cac gcg cag ctg gcg cac ggt agt gcc acg		196
Ala Arg Arg Leu Val Phe His Ala Gln Leu Ala His Gly Ser Ala Thr		
39 44 49 54		
ggc cga gtg gag ggc ttc tcc agc atc cag gag ctc tac gcc cag atc		244
Gly Arg Val Glu Gly Phe Ser Ser Ile Gln Glu Leu Tyr Ala Gln Ile		
55 60 65 70		
gcg ggc gcg ttt gaa atc tcg ccg tcg gag atc tta tat tgc act tta		292
Ala Gly Ala Phe Glu Ile Ser Pro Ser Glu Ile Leu Tyr Cys Thr Leu		
71 76 81 86		
aac aca cct aaa att gac atg gaa aga ctc tta gga gga caa cta gga		340
Asn Thr Pro Lys Ile Asp Met Glu Arg Leu Leu Gly Gly Gln Leu Gly		
87 92 97 102		
cta gaa gat ttc ata ttt gcc cat gtg aaa gga atc gaa aaa gaa gtg		388
Leu Glu Asp Phe Ile Phe Ala His Val Lys Gly Ile Glu Lys Glu Val		
103 108 113 118		
aat gtg tat aaa tct gag gat tca ctt ggt ctc acc att aca gat aat		436
Asn Val Tyr Lys Ser Glu Asp Ser Leu Gly Leu Thr Ile Thr Asp Asn		
119 124 129 134		
ggt gtt ggc tat gct ttt ata aag aga att aaa gat ggt ggt gtt att		484
Gly Val Gly Tyr Ala Phe Ile Lys Arg Ile Lys Asp Gly Gly Val Ile		
135 140 145 150		
gac tca gtt aaa aca atc tgt gtt ggg gat cat att gaa tcc ata aat		532
Asp Ser Val Lys Thr Ile Cys Val Gly Asp His Ile Glu Ser Ile Asn		
151 156 161 166		
gga gaa aat att gtt ggg tgg cgt cac tat gat gtt gct aag aag tta		580
Gly Glu Asn Ile Val Glu Trp Arg His Tyr Asp Val Ala Lys Lys Leu		
167 172 177 182		
aag gaa tta aaa aag gag gaa ctc ttt act atg aag tta ata gaa cct		628
Lys Glu Leu Lys Lys Glu Glu Leu Phe Thr Met Lys Leu Ile Glu Pro		
183 188 193 198		
aag aag gca ttt gaa ata gag ctg agg tca aag gct gga aag tca tca		676
Lys Lys Ala Phe Glu Ile Glu Leu Arg Ser Lys Ala Gly Lys Ser Ser		
199 204 209 214		
gga gaa aaa att ggt tgt gga agg gca aca ctt cgc ctg aga tca aaa		724

Gly	Glu	Lys	Ile	Gly	Cys	Gly	Arg	Ala	Thr	Leu	Arg	Leu	Arg	Ser	Lys	
215					220					225					230	
ggt	cct	gcc	acc	gtg	gaa	gaa	atg	cct	tct	gaa	acc	aaa	gca	aag	gca	772
Gly	Pro	Ala	Thr	Val	Glu	Glu	Met	Pro	Ser	Glu	Thr	Lys	Ala	Lys	Ala	
231					236					241					246	
att	gaa	aag	att	gat	gat	gtt	ctt	gag	ttg	tac	atg	gga	att	cga	gat	820
Ile	Glu	Lys	Ile	Asp	Asp	Val	Leu	Glu	Leu	Tyr	Met	Gly	Ile	Arg	Asp	
247					252					257					262	
att	gat	tta	gcc	acc	aca	atg	ttt	gaa	gct	gga	aag	gac	aaa	gta	aat	868
Ile	Asp	Leu	Ala	Thr	Thr	Met	Phe	Glu	Ala	Gly	Lys	Asp	Lys	Val	Asn	
263					268					273					278	
cca	gat	gaa	ttt	gct	gtg	gca	ctt	gac	gaa	act	ctt	gga	gac	ttt	gcg	916
Pro	Asp	Glu	Phe	Ala	Val	Ala	Leu	Asp	Glu	Thr	Leu	Gly	Asp	Phe	Ala	
279					284					289					294	
ttc	cca	gac	gaa	ttt	gtc	ttt	gat	gtt	tgg	gga	gtc	att	ggg	gat	gcc	964
Phe	Pro	Asp	Glu	Phe	Val	Phe	Asp	Val	Trp	Gly	Val	Ile	Gly	Asp	Ala	
295					300					305					310	
aaa	cga	aga	gga	tta	tga	tgtgta	cactccatct	ctgaagaaac	aacccatcgt							1018
Lys	Arg	Arg	Gly	Leu	*											
311					316											
tctttttttt	tctctttttt	aaaaagtcct	ataagatctg	tttttggaca	cctttactaa											1078
ctctggttta	atttcatgtg	tatggaatat	attctttgaa	atataaaaaa	aaa											1131

<210> 468
 <211> 862
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (226)..(612)

<400> 468																
gcaaggatcc	ttacttaaat	taatcccccc	cccccccccc	cggcgctgc	tcgctccctt											60
ctcggcagtg	gtacctgttc	ccggtgtccc	tgaggacgtg	cgggccaggt	acggccccga											120
aagtaggaag	cgagggggga	gcaggtttgc	ggggccaagt	gttgcgggca	cgcacctcac											180
gtcgagaatc	gggaggagga	gactgcaagg	ataggcccag	gagta	atg gag tcc											234
					Met Glu Ser											
					1											
aaa	gag	gaa	cga	gcg	tta	aac	aat	ctc	atc	gtg	gaa	aat	gtc	aac	cag	282
Lys	Glu	Glu	Arg	Ala	Leu	Asn	Asn	Leu	Ile	Val	Glu	Asn	Val	Asn	Gln	
4					9					14					19	

gaa aat gat gaa aaa gat gaa aag gag caa gtt gct aat aaa ggg gag	330
Glu Asn Asp Glu Lys Asp Glu Lys Glu Gln Val Ala Asn Lys Gly Glu	
20 25 30 35	
ccc ttg gcc cta cct ttg aat gtt agt gaa tac tgt gtg cct aga gga	378
Pro Leu Ala Leu Pro Leu Asn Val Ser Glu Tyr Cys Val Pro Arg Gly	
36 41 46 51	
aac cgt agg cgg ttc cgc gtt agg cag ccc atc ctg cag tat aga tgg	426
Asn Arg Arg Arg Phe Arg Val Arg Gln Pro Ile Leu Gln Tyr Arg Trp	
52 57 62 67	
gac ata atg cat agg ctt gga gag cca cag gca agg atg aga gag gag	474
Asp Ile Met His Arg Leu Gly Glu Pro Gln Ala Arg Met Arg Glu Glu	
68 73 78 83	
aat atg gaa agg att ggg gag gag gtg aga cag ctg atg gaa aag ctg	522
Asn Met Glu Arg Ile Gly Glu Glu Val Arg Gln Leu Met Glu Lys Leu	
84 89 94 99	
agg gaa aag cag ttg agt cat agt ttg cgg gca gtc agc act gat ccc	570
Arg Glu Lys Gln Leu Ser His Ser Leu Arg Ala Val Ser Thr Asp Pro	
100 105 110 115	
cct cac cat gac cat cac gat gag ttt tgc ctt atg ccc tga atcctga	619
Pro His His Asp His His Asp Glu Phe Cys Leu Met Pro *	
116 121 126	
tggtttccct gaagttaata gggagaccoc tgcttcctaa acttacacat ttgtggtgta	679
cctttgtcgt aaacgttttg atgttaocta tttcttggtg gtctcctatt accagcttct	739
aaatgaatgt tgtttttgac ccagtttgta agtttctgtc agcaggagag ttttacctat	799
tgcattgaaa gatgctcatt atatattgtg aagttaataa aacagtttta aaaagcaaaa	859
aaa	862

<210> 469
 <211> 3362
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (442)..(3108)

<400> 469	
agaaagtgca ttgaatttta atttatttaa agaattcggc aggtgccgcc taaggaagag	60
aaagataaaa acaacgaacc tcatgatgta agaaattttg actatactgc tcgaagttgg	120
actggaaaat ctcccaaaca atttctgatt gattgggtca ggaagaatct tcccaagagt	180

ccaaatcctt cctttgaaaa agttccagta ggtagatact ggaaatgtag ggtagggta	240
atcaagtctg aagatgatgt cctggtagta tgcctacaa tcttaacaga agatggcatg	300
caagctcagc acctgggagc tacttttagcc ctttaccgtt tagttaaagg gcagtcagtt	360
catcagttac ttctctccac ttaccgagat gtttggtcgg agtggagtga tgcagaaaag	420
aaaaggaag aattaaataa a atg gaa acc aat aaa cca cgt gat ctt ttt	471
Met Glu Thr Asn Lys Pro Arg Asp Leu Phe	
1 5	
att gcc aaa ctt ctg aat aaa ctg aaa cag cag caa cag cag caa caa	519
Ile Ala Lys Leu Leu Asn Lys Leu Lys Gln Gln Gln Gln Gln Gln	
11 16 21 26	
cag cat tct gaa aat aag aga gaa aac tct gaa gat ccc gag gaa tct	567
Gln His Ser Glu Asn Lys Arg Glu Asn Ser Glu Asp Pro Glu Glu Ser	
27 32 37 42	
tgg gaa aat tta gtt tgc gat gag gat ttt tct gca ctg tcc ttg gaa	615
Trp Glu Asn Leu Val Ser Asp Glu Asp Phe Ser Ala Leu Ser Leu Glu	
43 48 53 58	
tca gca aat gtg gaa gat ttg gaa cct gtt aga aac ctc ttt aga aag	663
Ser Ala Asn Val Glu Asp Leu Glu Pro Val Arg Asn Leu Phe Arg Lys	
59 64 69 74	
ttg caa agc aca cct aag tat cag aaa ctt cta aag gaa aga caa cag	711
Leu Gln Ser Thr Pro Lys Tyr Gln Lys Leu Leu Lys Glu Arg Gln Gln	
75 80 85 90	
cta cct gta ttt aaa cat cgg gac tca att gtt gaa act ctt aaa agg	759
Leu Pro Val Phe Lys His Arg Asp Ser Ile Val Glu Thr Leu Lys Arg	
91 96 101 106	
cat cgg gta gtg gtt gtg gca ggt gaa aca ggg agt ggt aaa agt act	807
His Arg Val Val Val Val Ala Gly Glu Thr Gly Ser Gly Lys Ser Thr	
107 112 117 122	
cag gta cca cat ttt cta ttg gaa gat ttg ctt cta aat gag tgg gaa	855
Gln Val Pro His Phe Leu Leu Glu Asp Leu Leu Leu Asn Glu Trp Glu	
123 128 133 138	
gca agt aaa tgt aac att gtc tgt acc caa ccc cga aga atc tca gca	903
Ala Ser Lys Cys Asn Ile Val Cys Thr Gln Pro Arg Arg Ile Ser Ala	
139 144 149 154	
gtt agt tta gcc aac aga gta tgt gat gaa ttg ggc tgt gaa aat gga	951
Val Ser Leu Ala Asn Arg Val Cys Asp Glu Leu Gly Cys Glu Asn Gly	
155 160 165 170	
cct gga gga agg aat tcc ttg tgt gga tat cag atc cgg atg gaa tct	999
Pro Gly Gly Arg Asn Ser Leu Cys Gly Tyr Gln Ile Arg Met Glu Ser	
171 176 181 186	

cga gct tgt gaa tct acc agg tta ctc tat tgt aca aca ggg gtt ttg	1047
Arg Ala Cys Glu Ser Thr Arg Leu Leu Tyr Cys Thr Thr Gly Val Leu	
187 192 197 202	
cta agg aaa ctt caa gaa gat ggt ctt cta agt aat gtg tct cat gtt	1095
Leu Arg Lys Leu Gln Glu Asp Gly Leu Leu Ser Asn Val Ser His Val	
203 208 213 218	
att gta gat gag gtt cat gaa aga agt gtc cag tca gac ttc cta cta	1143
Ile Val Asp Glu Val His Glu Arg Ser Val Gln Ser Asp Phe Leu Leu	
219 224 229 234	
att atc ttg aag gaa att tta cag aaa cgt tct gat cta cac ttg att	1191
Ile Ile Leu Lys Glu Ile Leu Gln Lys Arg Ser Asp Leu His Leu Ile	
235 240 245 250	
cta atg agt gcc act gtg gac agc gaa aaa ttt tct aca tat ttc aca	1239
Leu Met Ser Ala Thr Val Asp Ser Glu Lys Phe Ser Thr Tyr Phe Thr	
251 256 261 266	
cac tgc ccc att ctc aga att tca gga aga agt tat cct gtt gag gtt	1287
His Cys Pro Ile Leu Arg Ile Ser Gly Arg Ser Tyr Pro Val Glu Val	
267 272 277 282	
ttt cat ctt gaa gat ata ata gaa gaa aca ggc ttt gta ctg gaa aaa	1335
Phe His Leu Glu Asp Ile Ile Glu Glu Thr Gly Phe Val Leu Glu Lys	
283 288 293 298	
gac tca gaa tat tgt cag aaa ttt ctg gaa gag gaa gaa gaa gta acc	1383
Asp Ser Glu Tyr Cys Gln Lys Phe Leu Glu Glu Glu Glu Val Thr	
299 304 309 314	
att aat gtt aca agc aaa gca ggg gga ata aaa aaa tat cag gaa tac	1431
Ile Asn Val Thr Ser Lys Ala Gly Gly Ile Lys Lys Tyr Gln Glu Tyr	
315 320 325 330	
atc cca gtt cag act gga gca cat gct gat tta aat cca ttt tac caa	1479
Ile Pro Val Gln Thr Gly Ala His Ala Asp Leu Asn Pro Phe Tyr Gln	
331 336 341 346	
aag tac agc agc cgc act cag cat gct att cta tac atg aat cct cat	1527
Lys Tyr Ser Ser Arg Thr Gln His Ala Ile Leu Tyr Met Asn Pro His	
347 352 357 362	
aaa atc aac ctg gat ctc att ttg gaa ctt ctt gca tac tta gat aaa	1575
Lys Ile Asn Leu Asp Leu Ile Leu Glu Leu Leu Ala Tyr Leu Asp Lys	
363 368 373 378	
agt ccc caa ttc aga aat att gaa gga gca gta ttg atc ttt tta cca	1623
Ser Pro Gln Phe Arg Asn Ile Glu Gly Ala Val Leu Ile Phe Leu Pro	
379 384 389 394	
gga ctt gct cat att cag cag ttg tat gat ctt cta tca aat gat aga	1671
Gly Leu Ala His Ile Gln Gln Leu Tyr Asp Leu Leu Ser Asn Asp Arg	
395 400 405 410	
aga ttt tat tct gaa cga tat aaa gtg ata gct ctg cat tct att ctt	1719

Arg Phe Tyr Ser Glu	Arg Tyr Lys Val Ile	Ala Leu His Ser Ile Leu	
411	416	421	426
tca acc caa gat caa gct gca gca ttc aca ctt ccc cct cca gga gtc			1767
Ser Thr Gln Asp Gln	Ala Ala Ala Phe Thr	Leu Pro Pro Pro Gly Val	
427	432	437	442
agg aag att gtt tta gca acc aat att gca gag acg ggt atc act att			1815
Arg Lys Ile Val Leu	Ala Thr Asn Ile Ala	Glu Thr Gly Ile Thr Ile	
443	448	453	458
cct gat gtt gta ttt gta att gat act gga aga aca aaa gaa aat aag			1863
Pro Asp Val Val Phe	Val Ile Asp Thr Gly	Arg Thr Lys Glu Asn Lys	
459	464	469	474
tac cat gaa agc agt cag atg agt tct ttg gtg gag acg ttt gtc agt			1911
Tyr His Glu Ser Ser	Gln Met Ser Ser Leu	Val Glu Thr Phe Val Ser	
475	480	485	490
aaa gcc agt gct ttg cag cgc cag gga aga gct ggg cgg gtc aga gat			1959
Lys Ala Ser Ala Leu	Gln Arg Gln Gly Arg	Ala Gly Arg Val Arg Asp	
491	496	501	506
ggc ttc tgt ttc cga atg tac aca aga gaa aga ttt gaa ggc ttt atg			2007
Gly Phe Cys Phe Arg	Met Tyr Thr Arg Glu	Arg Phe Glu Gly Phe Met	
507	512	517	522
gat tat tct gtt cct gaa atc tta cgt gta cct ttg gag gaa tta tgc			2055
Asp Tyr Ser Val Pro	Glu Ile Leu Arg Val	Pro Leu Glu Glu Leu Cys	
523	528	533	538
ctt cat att atg aaa tgt aat ctt ggt tct cct gaa gat ttc ctc tcc			2103
Leu His Ile Met Lys	Cys Asn Leu Gly Ser	Pro Glu Asp Phe Leu Ser	
539	544	549	554
aaa gcc tta gat cct cct cag ctc caa gtg atc agc aat gca atg aat			2151
Lys Ala Leu Asp Pro	Pro Gln Leu Gln Val	Ile Ser Asn Ala Met Asn	
555	560	565	570
ttg ctc cga aaa att gga gct tgt gaa tta aat gag cct aaa ctg act			2199
Leu Leu Arg Lys Ile	Gly Ala Cys Glu Leu	Asn Glu Pro Lys Leu Thr	
571	576	581	586
cag ttg ggc caa cac ctt gca gct tta cct gtg aat gtc aag att ggc			2247
Pro Leu Gly Gln His	Leu Ala Ala Leu Pro	Val Asn Val Lys Ile Gly	
587	592	597	602
aag atg ctt att ttt ggt gcc ata ttt ggc tgc ctt gac cca gtg gca			2295
Lys Met Leu Ile Phe	Gly Ala Ile Phe Gly	Cys Leu Asp Pro Val Ala	
603	608	613	618
aca cta gct gca gtt atg aca gag aag tct cct ttt acc aca cca att			2343
Thr Leu Ala Ala Val	Met Thr Glu Lys Ser	Pro Phe Thr Thr Pro Ile	
619	624	629	634
ggc cga aaa gat gaa gca gat ctt gca aaa tca gct ttg gcc atg gcg			2391
Gly Arg Lys Asp Glu	Ala Asp Leu Ala Lys	Ser Ala Leu Ala Met Ala	

635	640	645	650	
gat tca gac cac ctg	acg atc tac aat gca	tat cta gga tgg aag aaa		2439
Asp Ser Asp His Leu	Thr Ile Tyr Asn Ala	Tyr Leu Gly Trp Lys Lys		
651	656	661	666	
gca cga caa gaa gga	ggt tat cgt tct gaa	atc aca tac tgc cgg agg		2487
Ala Arg Gln Glu Gly	Gly Tyr Arg Ser Glu	Ile Thr Tyr Cys Arg Arg		
667	672	677	682	
aac ttt ctt aat aga	aca tca ctg tta acc	cta gag gat gta aag cag		2535
Asn Phe Leu Asn Arg	Thr Ser Leu Leu Thr	Leu Glu Asp Val Lys Gln		
683	688	693	698	
gag tta ata aag ttg	gtt aag gca gca gga	ttt tca tct tcc aca act		2583
Glu Leu Ile Lys Leu	Val Lys Ala Ala Gly	Phe Ser Ser Ser Thr Thr		
699	704	709	714	
tct acc agc tgg gaa	gga aac aga gcc tca	cag acc ctc tca ttc caa		2631
Ser Thr Ser Trp Glu	Gly Asn Arg Ala Ser	Gln Thr Leu Ser Phe Gln		
715	720	725	730	
gaa att gcc ctt ctt	aaa gct gta ctg gtg	gct gga ctg tat gac aat		2679
Glu Ile Ala Leu Leu	Lys Ala Val Leu Val	Ala Gly Leu Tyr Asp Asn		
731	736	741	746	
gtg ggg aag ata atc	tat aca aag tca gtg	gat gtt aca gaa aaa ttg		2727
Val Gly Lys Ile Ile	Tyr Thr Lys Ser Val	Asp Val Thr Glu Lys Leu		
747	752	757	762	
gct tgc att gtg gag	acg gcc caa ggc aaa	gca caa gta cac cca tcc		2775
Ala Cys Ile Val Glu	Thr Ala Gln Gly Lys	Ala Gln Val His Pro Ser		
763	768	773	778	
tca gta aat cga gat	ttg caa act cat gga	tgg ctc tta tac cag gag		2823
Ser Val Asn Arg Asp	Leu Gln Thr His Gly	Trp Leu Leu Tyr Gln Glu		
779	784	789	794	
aag ata agg tat gcc	aga gtg tat ttg aga	gaa act acc cta ata acc		2871
Lys Ile Arg Tyr Ala	Arg Val Tyr Leu Arg	Glu Thr Thr Leu Ile Thr		
795	800	805	810	
cct ttt cca gtt tta	ctt ttt ggt ggt gat	ata gaa gtt cag cac cga		2919
Pro Phe Pro Val Leu	Leu Phe Gly Gly Asp	Ile Glu Val Gln His Arg		
811	816	821	826	
gaa cgt ctt ctt tct	att gat ggc tgg atc	tat ttt cag gcc cct gta		2967
Glu Arg Leu Leu Ser	Ile Asp Gly Trp Ile	Tyr Phe Gln Ala Pro Val		
827	832	837	842	
aag ata gct gtc att	ttc aag cag ctg aga	gtt ctc att gat tca gtt		3015
Lys Ile Ala Val Ile	Phe Lys Gln Leu Arg	Val Leu Ile Asp Ser Val		
843	848	853	858	
tta aga aaa aag ctt	gaa aat cca aag atg	tcc ctt gaa aat gac aag		3063
Leu Arg Lys Lys Leu	Glu Asn Pro Lys Met	Ser Leu Glu Asn Asp Lys		
859	864	869	874	

att ctg cag atc att acg gaa ttg ata aaa aca gag aat aac tga aac 3111
 Ile Leu Gln Ile Ile Thr Glu Leu Ile Lys Thr Glu Asn Asn *
 875 880 885

tgaaattcat ggtcaactgc tttaaaaatt aagatgaaga tacagtcacg aaattatctg 3171
 aaaatggggtc atcacattaa gtatttcatt acttaaaatg ttggtactag ccattaactt 3231
 aaagggtgggtg ggaaaaaagc acataacttta aacatgtata attttctagt tccttttttaa 3291
 tgatgattat tctgaatgta tttgccacta catttacaat aaattctttg gtattatgca 3351
 aaaaaaaaaa a 3362

<210> 470
 <211> 968
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (125) .. (736)

<400> 470
 tcgtaggttg gcgcggtttg gggtcgggggt ctgaggcttg ggcgctgcct gggccgagcg 60
 gagatcgggg tttgcctccc gtccccgctc aggaccctga cgtggctgaa gcgcccccg 120
 gagc atg agc ggg cag cgc gtg gac gtc aag gtg gtg atg ctg ggc aag 169
 Met Ser Gly Gln Arg Val Asp Val Lys Val Val Met Leu Gly Lys
 1 5 10
 gag tac gtg ggc aag act agc ctg gtg gag cgc tac gtg cac gac cgc 217
 Glu Tyr Val Gly Lys Thr Ser Leu Val Glu Arg Tyr Val His Asp Arg
 16 21 26 31
 ttt ctg gtg ggg cct tat cag aac acc atc ggg gcc gcc ttc gtg gcc 265
 Phe Leu Val Gly Pro Tyr Gln Asn Thr Ile Gly Ala Ala Phe Val Ala
 32 37 42 47
 aag gtg atg tcg gtc gga gac cgg act gtg aca tta ggt att tgg gac 313
 Lys Val Met Ser Val Gly Asp Arg Thr Val Thr Leu Gly Ile Trp Asp
 48 53 58 63
 aca gca ggc tct gag cgc tat gag gcc atg agt aga atc tac tat cgg 361
 Thr Ala Gly Ser Glu Arg Tyr Glu Ala Met Ser Arg Ile Tyr Tyr Arg
 64 69 74 79
 ggt gcc aag gct gcc atc gtc tgc tat gac ctc aca gac agc agc agc 409
 Gly Ala Lys Ala Ala Ile Val Cys Tyr Asp Leu Thr Asp Ser/Ser Ser
 80 85 90 95
 ttt gag cga gca aag ttc tgg gtg aag gaa ctg cgc agc cta gag gag 457

Phe	Glu	Arg	Ala	Lys	Phe	Trp	Val	Lys	Glu	Leu	Arg	Ser	Leu	Glu	Glu	
96					101					106					111	
ggc	tgc	caa	atc	tac	tta	tgt	ggc	acc	aag	agt	gac	ctg	ctg	gaa	gaa	505
Gly	Cys	Gln	Ile	Tyr	Leu	Cys	Gly	Thr	Lys	Ser	Asp	Leu	Leu	Glu	Glu	
112					117					122					127	
gac	cgg	agg	cgt	cga	cgt	gtg	gac	ttc	cac	gac	gtc	cag	gac	tat	gca	553
Asp	Arg	Arg	Arg	Arg	Arg	Val	Asp	Phe	His	Asp	Val	Gln	Asp	Tyr	Ala	
128					133					138					143	
gac	aat	atc	aaa	gct	cag	ctc	ttt	gaa	aca	tcc	agc	aag	aca	ggc	cag	601
Asp	Asn	Ile	Lys	Ala	Gln	Leu	Phe	Glu	Thr	Ser	Ser	Lys	Thr	Gly	Gln	
144					149					154					159	
agt	gtg	gac	gag	ctc	ttc	cag	aaa	gtg	gca	gag	gat	tac	gtc	agt	gtg	649
Ser	Val	Asp	Glu	Leu	Phe	Gln	Lys	Val	Ala	Glu	Asp	Tyr	Val	Ser	Val	
160					165					170					175	
gct	gcc	ttc	cag	gtg	atg	aca	gag	gac	aag	ggc	gtg	gat	ctg	ggc	cag	697
Ala	Ala	Phe	Gln	Val	Met	Thr	Glu	Asp	Lys	Gly	Val	Asp	Leu	Gly	Gln	
176					181					186					191	
aag	cca	aac	ccc	tac	ttc	tac	agc	tgt	tgt	cat	cac	tga	gtcagcactc			746
Lys	Pro	Asn	Pro	Tyr	Phe	Tyr	Ser	Cys	Cys	His	His	*				
192					197					202						
acctggcctg	ggggaattaa	aggaattccc	cgtaagggct	ggaccagct	cctttctggg											806
cttgggtagt	caaatgtctg	agctacccca	ggctctcatg	tcagcagagt	ggcgccctgcc											866
tgtgctggcc	catggaacgg	agacagcatt	gggctgactg	tgggcatgag	gagggataag											926
gctgatttgg	acccagggct	tctgccttgg	acagcacttg	tg												968

<210> 471
 <211> 1111
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (133)..(1032)

atttggccct	cgagcagtaa	ttcggcacga	ggggccagaa	gcaggcgccg	cttcgaggcc	60										
cgcggaatac	gcgcgccgag	acccgctcct	gcagtattag	ttcttgagc	tggtggtggc	120										
ggctgaggcg	gc	atg	gat	ctc	agc	gag	ctg	gag	aga	gac	aat	aca	ggc	168		
		Met	Asp	Leu	Ser	Glu	Leu	Glu	Arg	Asp	Asn	Thr	Gly			
		1				5						10				
cgc	tgt	cgc	ctg	agt	tcg	cct	gtg	ccc	gcg	gtg	tgc	cgc	aag	gag	cct	216

Arg	Cys	Arg	Leu	Ser	Ser	Pro	Val	Pro	Ala	Val	Cys	Arg	Lys	Glu	Pro	
13					18					23					28	
tgc	gtc	ctg	ggc	gtc	gat	gag	gcg	ggc	agg	ggc	ccc	gtg	ctg	ggc	ccc	264
Cys	Val	Leu	Gly	Val	Asp	Glu	Ala	Gly	Arg	Gly	Pro	Val	Leu	Gly	Pro	
29					34					39					44	
atg	gtc	tac	gcc	atc	tgt	tat	tgt	ccc	ctg	cct	cgc	ctg	gca	gat	ctg	312
Met	Val	Tyr	Ala	Ile	Cys	Tyr	Cys	Pro	Leu	Pro	Arg	Leu	Ala	Asp	Leu	
45					50					55					60	
gag	gcg	ctg	aaa	gtg	gca	gac	tca	aag	acc	cta	ttg	gag	agc	gag	cgg	360
Glu	Ala	Leu	Lys	Val	Ala	Asp	Ser	Lys	Thr	Leu	Leu	Glu	Ser	Glu	Arg	
61					66					71					76	
gaa	agg	ctg	ttt	gcg	aaa	atg	gag	gac	acg	gac	ttt	gtc	ggc	tgg	gcg	408
Glu	Arg	Leu	Phe	Ala	Lys	Met	Glu	Asp	Thr	Asp	Phe	Val	Gly	Trp	Ala	
77					82					87					92	
ctg	gat	gtg	ctg	tct	cca	aac	ctc	atc	tct	acc	agc	atg	ctt	ggg	cgg	456
Leu	Asp	Val	Leu	Ser	Pro	Asn	Leu	Ile	Ser	Thr	Ser	Met	Leu	Gly	Arg	
93					98					103					108	
gtc	aaa	tac	aac	ctg	aac	tcc	ctg	tca	cat	gat	aca	gcc	act	ggg	ctt	504
Val	Lys	Tyr	Asn	Leu	Asn	Ser	Leu	Ser	His	Asp	Thr	Ala	Thr	Gly	Leu	
109					114					119					124	
ata	cag	tat	gca	ttg	gac	cag	ggc	gtg	aac	gtc	acc	cag	gta	ttc	gtg	552
Ile	Gln	Tyr	Ala	Leu	Asp	Gln	Gly	Val	Asn	Val	Thr	Gln	Val	Phe	Val	
125					130					135					140	
gac	acc	gta	ggg	atg	cca	gag	aca	tac	cag	gcg	cgg	ctg	cag	caa	agt	600
Asp	Thr	Val	Gly	Met	Pro	Glu	Thr	Tyr	Gln	Ala	Arg	Leu	Gln	Gln	Ser	
141					146					151					156	
ttt	ccc	ggg	att	gag	gtg	acg	gtc	aag	gcc	aaa	gca	gat	gcc	ctc	tac	648
Phe	Pro	Gly	Ile	Glu	Val	Thr	Val	Lys	Ala	Lys	Ala	Asp	Ala	Leu	Tyr	
157					162					167					172	
ccg	gtg	gtt	agt	gct	gcc	agc	atc	tgt	gcc	aag	gtg	gcc	cgg	gac	cag	696
Pro	Val	Val	Ser	Ala	Ala	Ser	Ile	Cys	Ala	Lys	Val	Ala	Arg	Asp	Gln	
173					178					183					188	
gcc	gtg	aag	aaa	tgg	cag	ttc	gtg	gag	aaa	ctg	cag	gac	ttg	gat	act	744
Ala	Val	Lys	Lys	Trp	Gln	Phe	Val	Glu	Lys	Leu	Gln	Asp	Leu	Asp	Thr	
189					194					199					204	
gat	tat	ggc	tca	ggc	tac	ccc	aat	gat	ccc	aag	aca	aaa	gcg	tgg	ttg	792
Asp	Tyr	Gly	Ser	Gly	Tyr	Pro	Asn	Asp	Pro	Lys	Thr	Lys	Ala	Trp	Leu	
205					210					215					220	
aag	gag	cac	gtg	gag	cct	gtg	ttc	ggc	ttc	ccc	cag	ttt	gtc	cgg	ttc	840
Lys	Glu	His	Val	Glu	Pro	Val	Phe	Gly	Phe	Pro	Gln	Phe	Val	Arg	Phe	
221					226					231					236	
agc	tgg	cgc	acg	gcc	cag	acc	atc	ctg	gag	aaa	gag	gcg	gaa	gat	gtt	888
Ser	Trp	Arg	Thr	Ala	Gln	Thr	Ile	Leu	Glu	Lys	Glu	Ala	Glu	Asp	Val	

237	242	247	252	
ata tgg gag gac tca gca tcc gag aat cag gag gga ctc agg aag atc				936
Ile Trp Glu Asp Ser Ala Ser Glu Asn Gln Glu Gly Leu Arg Lys Ile				
253	258	263	268	
aca tcc tac ttc ctc aat gaa ggg tcc caa gcc cgt ccc cgt tct tcc				984
Thr Ser Tyr Phe Leu Asn Glu Gly Ser Gln Ala Arg Pro Arg Ser Ser				
269	274	279	284	
cac cga tat ttc ctg gaa cgc ggc ctg gag tca gca acc agc ctc tag				1032
His Arg Tyr Phe Leu Glu Arg Gly Leu Glu Ser Ala Thr Ser Leu *				
285	290	295	300	
cagctgcctc tacgcgctct acctgcttcc ccaaccaga cattaataatt gtttaaggag				1092
aaccataaaaa aaaaaaaa				1111

<210> 472
 <211> 1097
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (84) .. (764)

<400> 472	
tttgtagat tgcgttcgag taccggtccg gaattcccg gtcgaccac gcgtccgcgc	60
agggcggtcg agcccgcggc gcc	
atg gct cac gtc gcc tcc cgc aag cgc	110
Met Ala His Val Gly Ser Arg Lys Arg	
1 5	
tgc agg agt cgc agc cgg tcc cgg gga cgg ggg tgc gaa aag aga aag	158
Ser Arg Ser Arg Ser Arg Ser Arg Gly Arg Gly Ser Glu Lys Arg Lys	
10 15 20 25	
aag aag agc agg aaa gac acc tgc agg aac tgc tgc gcc tcc aca tcc	206
Lys Lys Ser Arg Lys Asp Thr Ser Arg Asn Cys Ser Ala Ser Thr Ser	
26 31 36 41	
caa ggt cgc aag gcc agc acg gcc cct ggg gcg gag gag aga agc aag	254
Gln Gly Arg Lys Ala Ser Thr Ala Pro Gly Ala Glu Glu Arg Ser Lys	
42 47 52 57	
cag aag gcc cgg agg aga aca aga tcc agc tcc tcc tcc tct tct tcc	302
Gln Lys Ala Arg Arg Arg Thr Arg Ser Ser Ser Ser Ser Ser Ser Ser	
58 63 68 73	
agt tct tct agc tcc tct tct tcc tcc tgc tcc tcc tcc tct tcc tcc	350
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser	
74 79 84 89	

agt gat ggc cgg aag aag cgg ggg aag tac aag gac aag agg agg aag	398
Ser Asp Gly Arg Lys Lys Arg Gly Lys Tyr Lys Asp Lys Arg Arg Lys	
90 95 100 105	
aag aag aag aag agg aag aag ctg aag aag aag ggc aag gag aag gcg	446
Lys Lys Lys Lys Arg Lys Lys Leu Lys Lys Lys Gly Lys Glu Lys Ala	
106 111 116 121	
gaa gca cag cag gtg gag gct ctg ccg ggc ccc tcg ctg gac cag tgg	494
Glu Ala Gln Gln Val Glu Ala Leu Pro Gly Pro Ser Leu Asp Gln Trp	
122 127 132 137	
cac cga tca gct ggg gag gaa gag gat ggc cca gtc ctg acg gat gag	542
His Arg Ser Ala Gly Glu Glu Glu Asp Gly Pro Val Leu Thr Asp Glu	
138 143 148 153	
cag aag tcc cga atc cag gcc atg aag ccc atg acc aag gag gag tgg	590
Gln Lys Ser Arg Ile Gln Ala Met Lys Pro Met Thr Lys Glu Glu Trp	
154 159 164 169	
gat gcc cgg cag agc atc atc cgc aag gtg gtg gac cct gag acg ggg	638
Asp Ala Arg Gln Ser Ile Ile Arg Lys Val Val Asp Pro Glu Thr Gly	
170 175 180 185	
cgc acc agg ctt att aag gga gat ggc gag gtc cta gag gaa atc gta	686
Arg Thr Arg Leu Ile Lys Gly Asp Gly Glu Val Leu Glu Glu Ile Val	
186 191 196 201	
acc aaa gaa cga cac aga gag atc aac aag gtg ggt gtg gcc cct ctg	734
Thr Lys Glu Arg His Arg Glu Ile Asn Lys Val Gly Val Ala Pro Leu	
202 207 212 217	
cct gcc atc cgc ccc cag ctc tgt ttg tga t gtacccctcc toctgtgtgc	785
Pro Ala Ile Arg Pro Gln Leu Cys Leu *	
218 223	
tttcttcccc agcaagccac ccgagggggac tgcttggcct tccagatgcg agctggggtg	845
cttccctgag ggcccccgct ggccaaggcc tgtggacgac gctggcggcc cagcctgggc	905
aggttttcagg gtgccagtgg gaagcctgat ggggtgctggt ggcctttccc cagtggattg	965
gtctctggcc cagcccagtc tcttctcagg ggcaggggggt ggagggttggg gtcacccggcc	1025
tgcttggcac ccccatctga aagagcagca cttctcagct attaaaggcc ccttggatag	1085
aaaaaaaaaa aa	1097

<210> 473
 <211> 2695
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> (256)..(2253)

<220>
 <221> misc_feature
 <222> (1)...(2695)
 <223> n = a,t,c or g

<400> 473
 tcataattgt caaaaaccag aattaggtca agttcatagt ttctgtaatt ggctttgaat 60
 caaagggggca ccagggttag ggggttacgg ggagtatgtg agtaacgcct gctttggaac 120
 ataaaccccc tcccccgccc ccattgtgcgc tgtgaccac gccctgcag tctttctct 180
 ggaatcatcc atgcgcccct ggagcaagct ggggcgtctg tgaagggtgcg gcagatccgg 240
 gctctagaca gcgac atg cag acc ctg gtc tat gag aac tac aac aag ttc 291
 Met Gln Thr Leu Val Tyr Glu Asn Tyr Asn Lys Phe
 1 5 10
 atc tca gcc aca gac acc atc cgg aag atg aag aac gat ttc cgg aag 339
 Ile Ser Ala Thr Asp Thr Ile Arg Lys Met Lys Asn Asp Phe Arg Lys
 13 18 23 28
 atg gag gat gag atg gac cgg ctg gcc acc aac atg gca gtg atc acc 387
 Met Glu Asp Glu Met Asp Arg Leu Ala Thr Asn Met Ala Val Ile Thr
 29 34 39 44
 gac ttc agc gct cgc atc agc gcc acg ctg cag gac cgc cac gag cgc 435
 Asp Phe Ser Ala Arg Ile Ser Ala Thr Leu Gln Asp Arg His Glu Arg
 45 50 55 60
 atc acc aag ctg gca ggg gtc cac gcg ctg ctg cgg aag ctg cag ttc 483
 Ile Thr Lys Leu Ala Gly Val His Ala Leu Leu Arg Lys Leu Gln Phe
 61 66 71 76
 ctc ttt gag ctg ccc tcg cgc ctc acc aag tgc gtg gaa ctg ggc gcc 531
 Leu Phe Glu Leu Pro Ser Arg Leu Thr Lys Cys Val Glu Leu Gly Ala
 77 82 87 92
 tat ggg cag gcg gtg cgc tac cag ggc cgc gcg cag gcc gtg ctg cag 579
 Tyr Gly Gln Ala Val Arg Tyr Gln Gly Arg Ala Gln Ala Val Leu Gln
 93 98 103 108
 cag tac caa cac ctg ccc tcg ttc cgc gcc atc cag gac gac tgc cag 627
 Gln Tyr Gln His Leu Pro Ser Phe Arg Ala Ile Gln Asp Asp Cys Gln
 109 114 119 124
 gtc atc acg gcc cgc ctg gcc cag cag ctg cgg cag cgc ttt agg gag 675
 Val Ile Thr Ala Arg Leu Ala Gln Gln Leu Arg Gln Arg Phe Arg Glu
 125 130 135 140
 ggc ggc tca ggc gcc ccg gag cag gca gag tgc gtg gag ctg ctg ctg 723
 Gly Gly Ser Gly Ala Pro Glu Gln Ala Glu Cys Val Glu Leu Leu Leu
 141 146 151 156

gcc ctg ggc gag cct gcg gag gag ctg tgc gag gag ttc ctg gcg cac	771
Ala Leu Gly Glu Pro Ala Glu Glu Leu Cys Glu Glu Phe Leu Ala His	
157 162 167 172	
gcc cgc ggc cgg ctg gag aag gag ctg aga aac ctg gag gcc gag ctg	819
Ala Arg Gly Arg Leu Glu Lys Glu Leu Arg Asn Leu Glu Ala Glu Leu	
173 178 183 188	
ggg ccc tca cct ccg gct ccc gac gtg tta gag ttc acc gac cat gga	867
Gly Pro Ser Pro Pro Ala Pro Asp Val Leu Glu Phe Thr Asp His Gly	
189 194 199 204	
ggc agt ggc ttc gtg ggc ggc ctc tgc cag gtg gcg gcg gcc tac cag	915
Gly Ser Gly Phe Val Gly Gly Leu Cys Gln Val Ala Ala Ala Tyr Gln	
205 210 215 220	
gag ctg ttt gcg gcc cag ggc cca gca ggt gcc gag aag ctg gcg gcc	963
Glu Leu Phe Ala Ala Gln Gly Pro Ala Gly Ala Glu Lys Leu Ala Ala	
221 226 231 236	
ttc gcc cgc cag ctg ggc agc cgc tat ttt gcg ctg gtg gag cgg cgg	1011
Phe Ala Arg Gln Leu Gly Ser Arg Tyr Phe Ala Leu Val Glu Arg Arg	
237 242 247 252	
ctg gcg cag gag cag ggt ggt ggt gac aac tca ctg ctg gtg cgg gcg	1059
Leu Ala Gln Glu Gln Gly Gly Gly Asp Asn Ser Leu Leu Val Arg Ala	
253 258 263 268	
ctg gac cgc ttc cac cgg cgc ttg cgg gct ccc ggg gcc ctg ctg gcc	1107
Leu Asp Arg Phe His Arg Arg Leu Arg Ala Pro Gly Ala Leu Leu Ala	
269 274 279 284	
gct gcc ggg ctc gca gac gct gcc acg gag atc gtg gaa cga gtg gcc	1155
Ala Ala Gly Leu Ala Asp Ala Ala Thr Glu Ile Val Glu Arg Val Ala	
285 290 295 300	
cgc gag cgc ctg ggc cac cac ctg cag ggt ctc cgg gcg gcc ttc ctg	1203
Arg Glu Arg Leu Gly His His Leu Gln Gly Leu Arg Ala Ala Phe Leu	
301 306 311 316	
ggc tgc ctg aca gac gtc cgc cag gcg ctg gca gca cct cgc gtg gct	1251
Gly Cys Leu Thr Asp Val Arg Gln Ala Leu Ala Ala Pro Arg Val Ala	
317 322 327 332	
ggg aag gag ggc cct ggc ctg gcc gag ttg ctg gcc aat gtg gcc agc	1299
Gly Lys Glu Gly Pro Gly Leu Ala Glu Leu Leu Ala Asn Val Ala Ser	
333 338 343 348	
tcc atc ctg agc cac att aag gcc tct ctg gca gca gtg cac ctt ttc	1347
Ser Ile Leu Ser His Ile Lys Ala Ser Leu Ala Ala Val His Leu Phe	
349 354 359 364	
acc gcc aaa gag gtg tcc ttc tcc aac aag ccc tac ttc cgg ggt gag	1395
Thr Ala Lys Glu Val Ser Phe Ser Asn Lys Pro Tyr Phe Arg Gly Glu	
365 370 375 380	
ttc tgc agt cag ggt gtc cgt gag ggc ctc atc gtg ggc ttc gtc cac	1443

Phe Cys Ser Gln Gly Val Arg Glu Gly Leu Ile Val Gly Phe Val His	
381 386 391 396	
tct atg tgc cag acg gct cag agc ttc tgc gac agc cct ggg gag aag	1491
Ser Met Cys Gln Thr Ala Gln Ser Phe Cys Asp Ser Pro Gly Glu Lys	
397 402 407 412	
ggg ggt gcc aca cca cct gcc ctg ctc ctg ctg ctc tcc cgc ctc tgc	1539
Gly Gly Ala Thr Pro Pro Ala Leu Leu Leu Leu Leu Ser Arg Leu Cys	
413 418 423 428	
ctg gac tac gag acg gcc acc atc tcc tac atc ctc act ctc act gat	1587
Leu Asp Tyr Glu Thr Ala Thr Ile Ser Tyr Ile Leu Thr Leu Thr Asp	
429 434 439 444	
gaa cag ttt ctg gtg cag gat cag ttc cca gtg acg ccc gtg agc acg	1635
Glu Gln Phe Leu Val Gln Asp Gln Phe Pro Val Thr Pro Val Ser Thr	
445 450 455 460	
ctg tgt gca gag gcc agg gaa acg gcg cgg cgg ctg ctg acc cac tac	1683
Leu Cys Ala Glu Ala Arg Glu Thr Ala Arg Arg Leu Leu Thr His Tyr	
461 466 471 476	
gtg aag gtg cag ggc ctg gtc ata tca cag atg ctg cgc aag agc gtg	1731
Val Lys Val Gln Gly Leu Val Ile Ser Gln Met Leu Arg Lys Ser Val	
477 482 487 492	
gag act cgc gac tgg ctc agc act ctg gag ccc cgg aat gtg cgg gcc	1779
Glu Thr Arg Asp Trp Leu Ser Thr Leu Glu Pro Arg Asn Val Arg Ala	
493 498 503 508	
gtc atg aag cgg gtg gtg gag gat acc acc gcc atc gac gtg cag gtg	1827
Val Met Lys Arg Val Val Glu Asp Thr Thr Ala Ile Asp Val Gln Val	
509 514 519 524	
ctg ccc agg ctg gcc ggg gta gcc ctg acg cag gct ggg ggt act gtc	1875
Leu Pro Arg Leu Ala Gly Val Ala Leu Thr Gln Ala Gly Gly Thr Val	
525 530 535 540	
cct tca aga ggg gct ggg gca gca gag gat cac tgg cag tcc ctg cct	1923
Pro Ser Arg Gly Ala Gly Ala Ala Glu Asp His Trp Gln Ser Leu Pro	
541 546 551 556	
gga gga ggg gac atg tgt atc tgg gct tct cac ggg gcc agt tct gta	1971
Gly Gly Gly Asp Met Cys Ile Trp Ala Ser His Gly Ala Ser Ser Val	
557 562 567 572	
gcc agg gcg tcc gtg agg gaa ccc cag ggg aac aag tct cca agg atg	2019
Ala Arg Ala Ser Val Arg Glu Pro Gln Gly Asn Lys Ser Pro Arg Met	
573 578 583 588	
aat acc aaa cgg gct ggg gag tgc cta tgt cca cgg tct tgt tcc ttc	2067
Asn Thr Lys Arg Ala Gly Glu Cys Leu Cys Pro Arg Ser Cys Ser Phe	
589 594 599 604	
tca gcc cag gat tat gac atc ttc gcc cct att tta cct gtg gag aag	2115
Ser Ala Gln Asp Tyr Asp Ile Phe Ala Pro Ile Leu Pro Val Glu Lys	

605	610	615	620	
cag agg ctc agg gtt acc cag gaa gtc agg gca ggg ttg gtg ctg gtg				2163
Gln Arg Leu Arg Val Thr Gln Glu Val Arg Ala Gly Leu Val Leu Val				
621	626	631	636	
ctg aag att aga cct cag acc aac tct tgt atc ctg cct ttg ccc cac				2211
Leu Lys Ile Arg Pro Gln Thr Asn Ser Cys Ile Leu Pro Leu Pro His				
637	642	647	652	
tcc act ggt tct ata aat agc gac cat gta cct act aaa tag cgggccc				2260
Ser Thr Gly Ser Ile Asn Ser Asp His Val Pro Thr Lys *				
653	658	663		
cgcggtgatt accctgtgat ccttgtgatg cttgagtagc tgacttaggg catcctcagc				2320
accgatgggc ttggtgggtt ccctgactc gggcctcctt gcagtacctc tttttaccac				2380
caggtggggc tcctgtacga agaggggtgt cgcaaggccc agagcagcga ctccagcaag				2440
aggactttct ccgtgtacag cagctctcgg cagcagggcc gctacgcccc cagctatacc				2500
cccaagtgcc ccgatggaca ccaacctctt gagcaatatc caagaagcta ttctcngaac				2560
gtattgatgt gttcaagccc tgtggagttc aacaagggtg cggtgctgac cggcatcatc				2620
aagatcagcc tgaagacgct gctggagtgt gtgcggctgc gcacctttgg gcgcttcggg				2680
gctgcagcag gtgca				2695

<210> 474
 <211> 3063
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (128) .. (2791)

<400> 474	
actcttcgag taccggtccg gaattcccgg gtcgaccac gcgtccggtg gggctcagct	60
ggttcattta tgttgtttt cctgtaccta agttcccgt gtaggtggta cctttgcaga	120
cggtgcg atg ggg gaa gca gag aag ttt cac tac atc tat agt tgt gac	169
Met Gly Glu Ala Glu Lys Phe His Tyr Ile Tyr Ser Cys Asp	
1 5 10	
ctg gat atc aac gtc cag ctt aag ata gga agc ttg gaa ggg aag aga	217
Leu Asp Ile Asn Val Gln Leu Lys Ile Gly Ser Leu Glu Gly Lys Arg	
15 / 20 25 30	
gaa caa aag agt tat aaa gct gtc ctg gaa gac cca atg ttg aag ttc	265
Glu Gln Lys Ser Tyr Lys Ala Val Leu Glu Asp Pro Met Leu Lys Phe	

31	36	41	46	
tca gga cta tat caa gag aca tgc tct gat ctt tat gtt act tgt caa				313
Ser Gly Leu Tyr Gln Glu Thr Cys Ser Asp Leu Tyr Val Thr Cys Gln				
47	52	57	62	
ggt ttt gca gaa ggg aag cct ttg gcc ttg cca gtg aga aca tcc tac				361
Val Phe Ala Glu Gly Lys Pro Leu Ala Leu Pro Val Arg Thr Ser Tyr				
63	68	73	78	
aaa gca ttt agt aca aga tgg aac tgg aat gaa tgg ctg aaa cta cca				409
Lys Ala Phe Ser Thr Arg Trp Asn Trp Asn Glu Trp Leu Lys Leu Pro				
79	84	89	94	
gta aaa tac cct gac ctg ccc agg aat gcc caa gtg gcc ctc acc ata				457
Val Lys Tyr Pro Asp Leu Pro Arg Asn Ala Gln Val Ala Leu Thr Ile				
95	100	105	110	
tgg gat gtg tat ggt ccc gga aaa gca gtg cct gta gga gga aca acg				505
Trp Asp Val Tyr Gly Pro Gly Lys Ala Val Pro Val Gly Gly Thr Thr				
111	116	121	126	
ggt tgc ctc ttt gga aaa tac ggc atg ttt cgc caa ggg atg cat gac				553
Val Ser Leu Phe Gly Lys Tyr Gly Met Phe Arg Gln Gly Met His Asp				
127	132	137	142	
ttg aaa gtc tgg cct aat gta gaa gca gat gga tca gaa ccc aca aaa				601
Leu Lys Val Trp Pro Asn Val Glu Ala Asp Gly Ser Glu Pro Thr Lys				
143	148	153	158	
act cct ggc aga aca agt agc act ctc tca gaa gat cag atg agc cgt				649
Thr Pro Gly Arg Thr Ser Ser Thr Leu Ser Glu Asp Gln Met Ser Arg				
159	164	169	174	
ctt gcc aag ctc acc aaa gct cat cga caa gga cac atg gtg aaa gta				697
Leu Ala Lys Leu Thr Lys Ala His Arg Gln Gly His Met Val Lys Val				
175	180	185	190	
gat tgg ctg gat aga ttg aca ttt aga gaa ata gaa atg ata aat gag				745
Asp Trp Leu Asp Arg Leu Thr Phe Arg Glu Ile Glu Met Ile Asn Glu				
191	196	201	206	
agt gtg aaa cga agt tct aat ttc atg tac ctg atg ggt gga ttt cga				793
Ser Val Lys Arg Ser Ser Asn Phe Met Tyr Leu Met Gly Gly Phe Arg				
207	212	217	222	
tgt gtc aag tgt gat gat aag gaa tat ggt att gtt tat tat gaa aag				841
Cys Val Lys Cys Asp Asp Lys Glu Tyr Gly Ile Val Tyr Tyr Glu Lys				
223	228	233	238	
gac ggt gat gaa tca tct cca att tta aca agt ttt gaa tta gtg aaa				889
Asp Gly Asp Glu Ser Ser Pro Ile Leu Thr Ser Phe Glu Leu Val Lys				
239	244	249	254	
ggt cct gac ccc cag atg tcc ctg gag aat tta gtt gag agc aaa cac				937
Val Pro Asp Pro Gln Met Ser Leu Glu Asn Leu Val Glu Ser Lys His				
255	260	265	270	

cac aac ctt ccc cgg agt tta aga agt gga cct tct gac cac gat ctg	985
His Asn Leu Pro Arg Ser Leu Arg Ser Gly Pro Ser Asp His Asp Leu	
271 276 281 286	
aaa ccc tat cct tcc ccg aga gat cag tta aat att att gtg agt tat	1033
Lys Pro Tyr Pro Ser Pro Arg Asp Gln Leu Asn Ile Ile Val Ser Tyr	
287 292 297 302	
cca cca acc aag caa ctt aca tat gaa gaa caa gat ctt gtt tgg aag	1081
Pro Pro Thr Lys Gln Leu Thr Tyr Glu Glu Gln Asp Leu Val Trp Lys	
303 308 313 318	
ttt aga tat tat ctt acg aat caa gaa aaa gcc ttg aca aaa ttc ttg	1129
Phe Arg Tyr Tyr Leu Thr Asn Gln Glu Lys Ala Leu Thr Lys Phe Leu	
319 324 329 334	
aaa tgt gtt aat tgg gat cta cct caa gag gcc aaa cag gcc ttg gaa	1177
Lys Cys Val Asn Trp Asp Leu Pro Gln Glu Ala Lys Gln Ala Leu Glu	
335 340 345 350	
ctt ctg gga aaa tgg aag ccg atg gat gta gag gac tcc ttg gag ctg	1225
Leu Leu Gly Lys Trp Lys Pro Met Asp Val Glu Asp Ser Leu Glu Leu	
351 356 361 366	
tta tcc tct cat tac acc aac cca act gtg agg cgt tat gct gtt gcc	1273
Leu Ser Ser His Tyr Thr Asn Pro Thr Val Arg Arg Tyr Ala Val Ala	
367 372 377 382	
cgg ttg cga cag gcc gat gat gag gat ttg ttg atg tac cta tta caa	1321
Arg Leu Arg Gln Ala Asp Asp Glu Asp Leu Leu Met Tyr Leu Leu Gln	
383 388 393 398	
ttg gtc cag gct ctc aaa tat gaa aat ttt gat gat ata aag aat gga	1369
Leu Val Gln Ala Leu Lys Tyr Glu Asn Phe Asp Asp Ile Lys Asn Gly	
399 404 409 414	
ttg gaa cct acc aag aag gat agt cag agt tca gtg tca gaa aat gtg	1417
Leu Glu Pro Thr Lys Lys Asp Ser Gln Ser Ser Val Ser Glu Asn Val	
415 420 425 430	
tca aat tct gga ata aat tct gca gaa ata gat agc tcc caa att ata	1465
Ser Asn Ser Gly Ile Asn Ser Ala Glu Ile Asp Ser Ser Gln Ile Ile	
431 436 441 446	
acc agc ccc ctt cct tca gtc tct tca cct cct cct gca tca aaa aca	1513
Thr Ser Pro Leu Pro Ser Val Ser Ser Pro Pro Pro Ala Ser Lys Thr	
447 452 457 462	
aaa gaa gtt cca gat ggc gaa aat ctg gaa caa gat ctc tgt acc ttc	1561
Lys Glu Val Pro Asp Gly Glu Asn Leu Glu Gln Asp Leu Cys Thr Phe	
463 468 473 478	
ttg ata tcg aga gcc tgc aaa aac tca aca ctg gct aat tat tta tac	1609
Leu Ile Ser Arg Ala Cys Lys Asn Ser Thr Leu Ala Asn Tyr Leu Tyr	
479 484 489 494	

tggtatgtgatagtggaatgtgaaatcaaatactcagcagagaat	1657
Trp Tyr Val Ile Val Glu Cys Glu Asp Gln Asp Thr Gln Gln Arg Asp	
495 500 505 510	
cca aag acc cat gag atg tac ttg aac gta atg aga aga ttc agc caa	1705
Pro Lys Thr His Glu Met Tyr Leu Asn Val Met Arg Arg Phe Ser Gln	
511 516 521 526	
gca ttg ttg aag ggt gat aag tct gtc aga gtt atg cgt tct ttg ctg	1753
Ala Leu Leu Lys Gly Asp Lys Ser Val Arg Val Met Arg Ser Leu Leu	
527 532 537 542	
gct gca caa cag aca ttt gta gat cgg ttg gtg cat cta atg aag gca	1801
Ala Ala Gln Gln Thr Phe Val Asp Arg Leu Val His Leu Met Lys Ala	
543 548 553 558	
gta caa cgc gaa agt gga aat cgt aag aaa aag aat gag aga cta cag	1849
Val Gln Arg Glu Ser Gly Asn Arg Lys Lys Lys Asn Glu Arg Leu Gln	
559 564 569 574	
gca ttg ctt gga gat aat gaa aag atg aat ttg tca gat gtg gaa ctt	1897
Ala Leu Leu Gly Asp Asn Glu Lys Met Asn Leu Ser Asp Val Glu Leu	
575 580 585 590	
atc ccg ttg cct tta gaa ccc caa gtg aaa att aga gga ata att ccg	1945
Ile Pro Leu Pro Leu Glu Pro Gln Val Lys Ile Arg Gly Ile Ile Pro	
591 596 601 606	
gaa aca gct aca ctg ttt aaa agt gcc ctt atg cct gca cag ttg ttt	1993
Glu Thr Ala Thr Leu Phe Lys Ser Ala Leu Met Pro Ala Gln Leu Phe	
607 612 617 622	
ttt aag acg gaa gat gga ggc aaa tat cca gtt ata ttt aag cat gga	2041
Phe Lys Thr Glu Asp Gly Gly Lys Tyr Pro Val Ile Phe Lys His Gly	
623 628 633 638	
gat gat tta cgt caa gat caa ctt att ctt caa atc att tca ctc atg	2089
Asp Asp Leu Arg Gln Asp Gln Leu Ile Leu Gln Ile Ile Ser Leu Met	
639 644 649 654	
gac aag ctg tta cgg aaa gaa aat ctg gac ttg aaa ttg aca cct tat	2137
Asp Lys Leu Leu Arg Lys Glu Asn Leu Asp Leu Lys Leu Thr Pro Tyr	
655 660 665 670	
aag gtg tta gcc acc agt aca aaa cat ggc ttc atg cag ttt atc cag	2185
Lys Val Leu Ala Thr Ser Thr Lys His Gly Phe Met Gln Phe Ile Gln	
671 676 681 686	
tca gtt cct gtg gct gaa gtt ctt gat aca gag gga agc att cag aac	2233
Ser Val Pro Val Ala Glu Val Leu Asp Thr Glu Gly Ser Ile Gln Asn	
687 692 697 702	
ttt ttt aga aaa tat gca cca agt gag aat ggg cca aat ggg att agt	2281
Phe Phe Arg Lys Tyr Ala Pro Ser Glu Asn Gly Pro Asn Gly Ile Ser	
703 708 713 718	
gct gag gtc atg gac act tac gtt aaa agc tgt gct gga tat tgc gtg	2329

<211> 3302
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (98)..(2563)

<400> 475

```

atttcaagtg tcatattttg catttaaatt tgccaaaaag gattgtccag tctccaacat      60
caataattct tctattcctt cagctcttcc tgaaccg atg act gct agt gaa gca      115
                               Met Thr Ala Ser Glu Ala
                               1
gct gct agg aaa agc caa ata aaa gcc aga ata aca gat acc att gga      163
Ala Ala Arg Lys Ser Gln Ile Lys Ala Arg Ile Thr Asp Thr Ile Gly
  7                               12                               17                               22
cca aca gaa acc tca att gca cca aga caa aga cca aag gcc aac tct      211
Pro Thr Glu Thr Ser Ile Ala Pro Arg Gln Arg Pro Lys Ala Asn Ser
  23                               28                               33                               38
gct act act gcc act ccc agt gtg ctg acc att caa agt tca gca aca      259
Ala Thr Thr Ala Thr Pro Ser Val Leu Thr Ile Gln Ser Ser Ala Thr
  39                               44                               49                               54
cct gtt aaa gtc ctt gct cct ggt gaa ttc ggt aac cat aga cca aaa      307
Pro Val Lys Val Leu Ala Pro Gly Glu Phe Gly Asn His Arg Pro Lys
  55                               60                               65                               70
ggg gca cta aga cct gga aat ggc cct gaa att tta ttg ggt cag gga      355
Gly Ala Leu Arg Pro Gly Asn Gly Pro Glu Ile Leu Leu Gly Gln Gly
  71                               76                               81                               86
cct cct cag cag ccg cca cag cag cat aga gta ctc cag caa cta cag      403
Pro Pro Gln Gln Pro Pro Gln Gln His Arg Val Leu Gln Gln Leu Gln
  87                               92                               97                               102
cag gga gat tgg aga tta cag caa ctc cat tta cag cat cgt cat cct      451
Gln Gly Asp Trp Arg Leu Gln Gln Leu His Leu Gln His Arg His Pro
  103                               108                               113                               118
cac cag cag cag cag cag cag cag cag caa cag caa cag cag cag cag      499
His Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
  119                               124                               129                               134
caa cag caa cag cag cag cag cag cag cag cag cag cac cac cac cac      547
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His His His His
  135                               140                               145                               150
cac cac cac cac cta ctt caa gat gct tat atg cag cag tat caa cat      595
His His His His Leu Leu Gln Asp Ala Tyr Met Gln Gln Tyr Gln His
  151                               156                               161                               166
gca aca cag cag caa cag atg ctt caa caa caa ttt tta atg cat tcg      643
Ala Thr Gln Gln Gln Gln Met Leu Gln Gln Gln Phe Leu Met His Ser

```

167	172	177	182	
gta tat caa cca caa cct tct gca tca cag tat cct aca atg atg ccg				691
Val Tyr Gln Pro Gln Pro Ser Ala Ser Gln Tyr Pro Thr Met Met Pro				
183	188	193	198	
cag tat cag cag gct ttc ttt caa cag cag atg cta gct caa cat cag				739
Gln Tyr Gln Gln Ala Phe Phe Gln Gln Gln Met Leu Ala Gln His Gln				
199	204	209	214	
ccg tct caa caa cag gca tca cct gaa tat ctt acc tcc cct caa gag				787
Pro Ser Gln Gln Gln Ala Ser Pro Glu Tyr Leu Thr Ser Pro Gln Glu				
215	220	225	230	
ttc tca cca gcc tta gtt tcc tac act tca tca ctt cca gct cag gtt				835
Phe Ser Pro Ala Leu Val Ser Tyr Thr Ser Ser Leu Pro Ala Gln Val				
231	236	241	246	
gga acc ata atg gac tcc tcc tat agt gcc aat agg tca gtt gct gat				883
Gly Thr Ile Met Asp Ser Ser Tyr Ser Ala Asn Arg Ser Val Ala Asp				
247	252	257	262	
aaa gag gcc att gca aat ttc aca aat cag aag aac atc agc aat cca				931
Lys Glu Ala Ile Ala Asn Phe Thr Asn Gln Lys Asn Ile Ser Asn Pro				
263	268	273	278	
cct gat atg tca ggg tgg aat cct ttt gga gag gat aat ttc tct aag				979
Pro Asp Met Ser Gly Trp Asn Pro Phe Gly Glu Asp Asn Phe Ser Lys				
279	284	289	294	
tta aca gaa gag gaa cta ttg gac aga gaa ttt gac ctt cta aga tca				1027
Leu Thr Glu Glu Glu Leu Leu Asp Arg Glu Phe Asp Leu Leu Arg Ser				
295	300	305	310	
aat agg ctc gag gag aga gca tcc tca gat aag aat gta gac tca ctt				1075
Asn Arg Leu Glu Glu Arg Ala Ser Ser Asp Lys Asn Val Asp Ser Leu				
311	316	321	326	
tct gct cca cat aac cat cct cca gaa gat cct ttt ggt tct gtt cct				1123
Ser Ala Pro His Asn His Pro Pro Glu Asp Pro Phe Gly Ser Val Pro				
327	332	337	342	
ttc att tct cat tca ggt tct cct gaa aag aaa gct gaa cat tca tct				1171
Phe Ile Ser His Ser Gly Ser Pro Glu Lys Lys Ala Glu His Ser Ser				
343	348	353	358	
ata aat caa gaa aat ggc act gca aac cct atc aag aac ggt aaa aca				1219
Ile Asn Gln Glu Asn Gly Thr Ala Asn Pro Ile Lys Asn Gly Lys Thr				
359	364	369	374	
agt cca gca tct aaa gat cag cgg act gga aag aaa acc tca gta cag				1267
Ser Pro Ala Ser Lys Asp Gln Arg Thr Gly Lys Lys Thr Ser Val Gln				
375	380	385	390	
ggg caa gtg caa aag ggg aat gat gaa tct gaa agt gat ttt gaa tca				1315
Gly Gln Val Gln Lys Gly Asn Asp Glu Ser Glu Ser Asp Phe Glu Ser				
391	396	401	406	

gat ccc cct tct cct aag agc agt gaa gag gaa gag caa gat gat gaa Asp Pro Pro Ser Pro Lys Ser Ser Glu Glu Glu Glu Gln Asp Asp Glu 407 412 417 422	1363
gaa gtt ctt cag ggg gaa caa gga gat ttt aat gat gat gat act gaa Glu Val Leu Gln Gly Glu Gln Gly Asp Phe Asn Asp Asp Asp Thr Glu 423 428 433 438	1411
cca gaa aat ctg ggt cat agg cct ctc ctc atg gat tct gaa gat gag Pro Glu Asn Leu Gly His Arg Pro Leu Leu Met Asp Ser Glu Asp Glu 439 444 449 454	1459
gaa gaa gag gag aaa cat agc tct gat tct gat tat gag cag gct aaa Glu Glu Glu Glu Lys His Ser Ser Asp Ser Asp Tyr Glu Gln Ala Lys 455 460 465 470	1507
gca aag tac agt gac atg agc tct gtc tac aga gac aga tct ggc agt Ala Lys Tyr Ser Asp Met Ser Ser Val Tyr Arg Asp Arg Ser Gly Ser 471 476 481 486	1555
gga cca acc caa gat ctt aat aca ata ctc ctc acc tca gcc caa tta Gly Pro Thr Gln Asp Leu Asn Thr Ile Leu Leu Thr Ser Ala Gln Leu 487 492 497 502	1603
tcc tct gat gtt gca gtg gag act ccc aaa cag gag ttt gat gta ttt Ser Ser Asp Val Ala Val Glu Thr Pro Lys Gln Glu Phe Asp Val Phe 503 508 513 518	1651
ggc gct gtc ccc ttc ttt gca gtg cgt gct caa cag ccc cag caa gaa Gly Ala Val Pro Phe Phe Ala Val Arg Ala Gln Gln Pro Gln Gln Glu 519 524 529 534	1699
aag aat gaa aag aac ctc cct caa cac agg ttt cct gct gca gga ctg Lys Asn Glu Lys Asn Leu Pro Gln His Arg Phe Pro Ala Ala Gly Leu 535 540 545 550	1747
gag cag gag gaa ttt gat gta ttc aca aag gcg cct ttt agc aag aag Glu Gln Glu Glu Phe Asp Val Phe Thr Lys Ala Pro Phe Ser Lys Lys 551 556 561 566	1795
gtg aat gta caa gaa tgc cat gca gtg ggg cct gag gca cat act atc Val Asn Val Gln Glu Cys His Ala Val Gly Pro Glu Ala His Thr Ile 567 572 577 582	1843
cct ggt tat ccc aaa agt gta gat gta ttt ggc tcc act cca ttt cag Pro Gly Tyr Pro Lys Ser Val Asp Val Phe Gly Ser Thr Pro Phe Gln 583 588 593 598	1891
ccc ttc ctc aca tca aca agt aaa agt gaa agc aat gag gac ctt ttt Pro Phe Leu Thr Ser Thr Ser Lys Ser Glu Ser Asn Glu Asp Leu Phe 599 604 609 614	1939
ggg ctt gtg ccc ttt gat gaa ata acg ggg agc cag cag caa aaa gtc Gly Leu Val Pro Phe Asp Glu Ile Thr Gly Ser Gln Gln Gln Lys Val 615 620 625 630	1987

aaa cag cgc agc tta cag aaa ctg tcc tct cgc caa agg cgc aca aag Lys Gln Arg Ser Leu Gln Lys Leu Ser Ser Arg Gln Arg Arg Thr Lys 631 636 641 646	2035
cag gat atg tcc aaa agt aat ggg aag cgg cat cat ggc acg cca act Gln Asp Met Ser Lys Ser Asn Gly Lys Arg His His Gly Thr Pro Thr 647 652 657 662	2083
agc aca aag aag act ttg aag cct acc tat cgc act cca gag agg gct Ser Thr Lys Lys Thr Leu Lys Pro Thr Tyr Arg Thr Pro Glu Arg Ala 663 668 673 678	2131
cgc agg cac aaa aaa gtg ggc cgc cga gac tct caa agt agc aat gaa Arg Arg His Lys Lys Val Gly Arg Arg Asp Ser Gln Ser Ser Asn Glu 679 684 689 694	2179
ttt tta acc atc tca gac tcc aag gag aac att agt gtt gca ctg act Phe Leu Thr Ile Ser Asp Ser Lys Glu Asn Ile Ser Val Ala Leu Thr 695 700 705 710	2227
gat ggg aaa gat agg ggg aat gtc tta caa cct gag gag agc ctg ttg Asp Gly Lys Asp Arg Gly Asn Val Leu Gln Pro Glu Glu Ser Leu Leu 711 716 721 726	2275
gac ccc ttc ggt gcc aag ccc ttc cat tct cca gac ctg tca tgg cac Asp Pro Phe Gly Ala Lys Pro Phe His Ser Pro Asp Leu Ser Trp His 727 732 737 742	2323
cct cca cat cag ggc ctg agc gac atc cgt gct gat cac aat act gtc Pro Pro His Gln Gly Leu Ser Asp Ile Arg Ala Asp His Asn Thr Val 743 748 753 758	2371
ctg cca ggg cgg cca aga caa aat tca cta cat ggg tca ttc cat agt Leu Pro Gly Arg Pro Arg Gln Asn Ser Leu His Gly Ser Phe His Ser 759 764 769 774	2419
gca gat gta ttg aaa atg gat gat ttt ggt gcc gtg ccc ttt aca gaa Ala Asp Val Leu Lys Met Asp Asp Phe Gly Ala Val Pro Phe Thr Glu 775 780 785 790	2467
ctt gtg gtg caa agc atc act cca cat cag tcc caa cag tcc caa cca Leu Val Val Gln Ser Ile Thr Pro His Gln Ser Gln Gln Ser Gln Pro 791 796 801 806	2515
gtc gaa tta gac cca ttt ggt gct gct cca ttt cct tct aaa cag tag Val Glu Leu Asp Pro Phe Gly Ala Ala Pro Phe Pro Ser Lys Gln * 807 812 817 822	2563
atacttctga tggattctcg gcattaactc ctgtttcaaaa aaagtgtgaa cagttttatg	2623
aatttgaaag aaaatttgggt agctctttat agcattcatt cttaaagatc agtcagaata	2683
ggtgatttct aaataaacca aatagaagaa tgaagtatct ctacagggta gtaacttgat	2743
tcctcttcag gagaaaaggg agctaaattg caagctctaa ctaagggttt ctgctactga	2803
catcacaaca cagaaatgca agtgtggtac ttccagttaa agcacatggc acctttctag	2863

```

gtgtgtagcc actgagaagg gacagtgaag ctgttatttt tgatatcaga atgtcatttt 2923
tatgtgcata tccctaaaat taggggttatt tctacatata ctagttacac ttgtgaattt 2983
ttttaaggt ctcttttaat ttccagacag ttaaaaacaa tctagttatc ttaaagcatt 3043
agaaagttat tatctggaga gtgcagagat ttcagtccat acacctttct ccacaaagca 3103
gagccagaag taactgacta ttgtgcctaa aactctgttt cattttttaa aacaagtgcc 3163
attaaaatgg aatatctaata gataagcata tgaaataatg tgtaattagc tcaatttaac 3223
tattccacaa cttacatatt ccaaaacaat gttatacatg ataaatatat ataatttttg 3283
tcagttaaaa aaaaaaaaaa 3302

```

```

<210> 476
<211> 776
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (405)..(755)

```

```

<220>
<221> misc_feature
<222> (1)...(776)
<223> n = a,t,c or g

```

```

<400> 476
attggagaaa ctgagcggn attgccaaac accatnngaa aataataatg gtgtggccaa 60
ttcaagcgat gcaatggatg caagctgcaa tcggaatgca tggttaagcc tgaagaaatg 120
tttcctgtaa tggaagatgg gaaatatgtc gataaatggg caatacgaac gacggcaatg 180
attgccagag aacttggtta acagaacaac aaagctgcct gatagtggcc tttatttttg 240
gcataaataa cagaataaac actgcactgt gtattcattc caacgagtga atacacggag 300
caatgtcgct cgtaactaaa caggagccga cttgttctga ttattggaaa tcttctttgc 360
cctccagtgt gagggcgatt ttttatctgt gaggatatga acag atg tca aac atc 416
Met Ser Asn Ile
1

```

```

aaa aaa tac atc att gat tac gac tgg aaa gca tca ata gaa att gaa 464
Lys Lys Tyr Ile Ile Asp Tyr Asp Trp Lys Ala Ser Ile Glu Ile Glu
5 10 / 15 20

```

```

atc gac cat gac gta atg aca gag gaa aaa ctt cac cag att aat aat 512
Ile Asp His Asp Val Met Thr Glu Glu Lys Leu His Gln Ile Asn Asn

```

21	26	31	36	
ttc tgg tca gac tct gaa tac cga ctc aat aaa cac ggc tct gta tta				560
Phe Trp Ser Asp Ser Glu Tyr Arg Leu Asn Lys His Gly Ser Val Leu				
37	42	47	52	
aat gct gta tta atc atg ctg gcg caa cat gct ctg ctt ata gca att				608
Asn Ala Val Leu Ile Met Leu Ala Gln His Ala Leu Leu Ile Ala Ile				
53	58	63	68	
tca agc gac tta aat gca tat ggt gtt gtg tgt gag ttc gac tgg aat				656
Ser Ser Asp Leu Asn Ala Tyr Gly Val Val Cys Glu Phe Asp Trp Asn				
69	74	79	84	
gat gga aat ggt cag gaa gga tgg cct cca atg gat ggt agc gaa gga				704
Asp Gly Asn Gly Gln Glu Gly Trp Pro Pro Met Asp Gly Ser Glu Gly				
85	90	95	100	
ata aga att acc gat atc gat aca tca gga ata ttt att cag atg ata				752
Ile Arg Ile Thr Asp Ile Asp Thr Ser Gly Ile Phe Ile Gln Met Ile				
101	106	111	116	
tga ctatcaagcc tgcagcgtgg t				776
*				
117				

<210> 477
 <211> 1298
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (138)..(629)

<400> 477	
gctcgagatc cagaagggaa gatttattac taccatgtga tcacaatgag acagagtctt	60
tctttgttgc ccagactgat ctgcacgaac tcctggcttc aagcgatcct cccacctaag	120
cctcccaaaa tgctggg atg aca ggc gtg agg cac cac acc cag cta caa	170
Met Thr Gly Val Arg His His Thr Gln Leu Gln	
1 5	
ctg cag act cag tgg gat cct cct act tgg gaa agc cca gga gat gat	218
Leu Gln Thr Gln Trp Asp Pro Pro Thr Trp Glu Ser Pro Gly Asp Asp	
12 17 22 27	
gcc agc ctt gag cat gaa gct gag atg gac ctg gga act cca aca tat	266
Ala Ser Leu Glu His Glu Ala Glu Met Asp Leu Gly Thr Pro Thr Tyr	
28 33 38 43	
gat gaa aac ccc atg aag gcc tcg aaa aag ccc aag aca gca gaa gca	314

Asp	Glu	Asn	Pro	Met	Lys	Ala	Ser	Lys	Lys	Pro	Lys	Thr	Ala	Glu	Ala		
44					49					54					59		
gac acc tcc agt gaa cta gca aag aaa agc aaa gaa gta ttc aga aaa 362																	
Asp	Thr	Ser	Ser	Glu	Leu	Ala	Lys	Lys	Ser	Lys	Glu	Val	Phe	Arg	Lys		
60					65					70					75		
gag atg tcc cag ttc atc gtc cag tgc ctg aac cct tac cgg aaa cct 410																	
Glu	Met	Ser	Gln	Phe	Ile	Val	Gln	Cys	Leu	Asn	Pro	Tyr	Arg	Lys	Pro		
76					81					86					91		
gac tgc aaa gtg gga aga att acc aca act gaa gac ttt aaa cat ctg 458																	
Asp	Cys	Lys	Val	Gly	Arg	Ile	Thr	Thr	Thr	Glu	Asp	Phe	Lys	His	Leu		
92					97					102					107		
gct cgc aag ctg act cac ggt gtt atg aat aag gag ctg aag tac tgt 506																	
Ala	Arg	Lys	Leu	Thr	His	Gly	Val	Met	Asn	Lys	Glu	Leu	Lys	Tyr	Cys		
108					113					118					123		
aag aat cct gag gac ctg gag tgc aat gag aat gtg aaa cac aaa acc 554																	
Lys	Asn	Pro	Glu	Asp	Leu	Glu	Cys	Asn	Glu	Asn	Val	Lys	His	Lys	Thr		
124					129					134					139		
aag gag tac att aag aag tac atg cag aag ttt ggg gct gtt tac aaa 602																	
Lys	Glu	Tyr	Ile	Lys	Lys	Tyr	Met	Gln	Lys	Phe	Gly	Ala	Val	Tyr	Lys		
140					145					150					155		
ccc aaa gag gac act gaa tta gag tga ctgtt gggccagggt gggaggatgg 654																	
Pro	Lys	Glu	Asp	Thr	Glu	Leu	Glu	*									
156					161												
gtggtcaggt aagacagact ctaggagag gaaatcctgt gggcctttct gtcccacccc 714																	
tgtcagcact gtgctactga tgatacatca ccctggggaa ttcaaccctg cagatgtcaa 774																	
ctgaaggcca caaaattgaa ctcatctaca agtgattacc tagttgtgag ctgttgcat 834																	
gtggttagaa gccatcagag gtgcaagggt ttagaaaaga ccctggccag acctgactcc 894																	
actcttaaac ctgggtcttc tccttggcgg tgctgtcagc gcacagaccc atgcgcatcc 954																	
ccaccacaaa cactttaccc tgatgatctg tattatattt taatgtatat gtgaatatat 1014																	
tgaaaataat ttgttttttc ctgggtttttg tttggttttc gttttgcttt tagcctctac 1074																	
atgctaggat cacaggaaga ctttgtaagg acagtttaag ttctcctgca aggtttaatt 1134																	
tgttatcatg taaatattcc aaagcaggct gccttggtgt tttggccagc cttgtgctat 1194																	
gttgataaga ttgatttact gcttaaaatc actttaacttt atccaatttt tactgaactt 1254																	
tttatgtaaa aaaataaaat caattaaaga aaaaaaaaaa aaaa 1298																	

<211> 1640
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (403) .. (723)

<400> 478

```

atagaaacac cttgactgtg aacacgttaa gcttggcacg aggagccaga gaaggctctc      60
tgtgttgaac actcctgtga ttccagtggc tgcacccaga tcctccgggc cgtttcccct      120
cccttaagga ttcctatgcc atgtaacagc acaggcatgg gtgtgatctc acgtgttcac      180
agcttccggg ggctaggatg agacatgctt gggggcgggg gccacttaaa aatgtgcctg      240
cactgtgggc gtgatgctct gcaactgtgga aggaaaagga gttaaagag aaatgatggg      300
gggcgctgag cctgagcagc gccgctttgt gccgcagcat caacctgtgg gaaatggcgg      360
agttcctgct gaaacaggac gtgggtcaacg ccatcaacct gg   atg ggg gtg gct      414
                                   Met Gly Val Ala
                                   1

ctg cca cct ttg tgc tca acg gga cct tgg cca gtt acc cgt cag atc      462
Leu Pro Pro Leu Cys Ser Thr Gly Pro Trp Pro Val Thr Arg Gln Ile
   5                10                15                20

act gcc agg aca aca tgt ggc gct gtc ccc gcc aag tgt cca ccg tgg      510
Thr Ala Arg Thr Thr Cys Gly Ala Val Pro Ala Lys Cys Pro Pro Trp
  21                26                31                36

tgt gtg tgc acg aac ccc gct gcc agc cgc ctg act gcc acg gcc acg      558
Cys Val Cys Thr Asn Pro Ala Ala Ser Arg Leu Thr Ala Thr Ala Thr
  37                42                47                52

gga cct gcg tgg acg ggc act gcc aat gca ccg ggc act tct ggc ggg      606
Gly Pro Ala Trp Thr Gly Thr Ala Asn Ala Pro Gly Thr Ser Gly Gly
  53                58                63                68

gtc ccg gct gtg atg agc tgg act gtg gcc cct cta act gca gcc agc      654
Val Pro Ala Val Met Ser Trp Thr Val Ala Pro Leu Thr Ala Ala Ser
  69                74                79                84

acg gac tgt gca cgg aga ccg gct gcc gct gtg atg ccg gat gga ccg      702
Thr Asp Cys Ala Arg Arg Pro Ala Ala Ala Val Met Pro Asp Gly Pro
  85                90                95                100

ggg cca act gca gtg aag taa ag cagtgtctcc agccacctgg aagccacct      755
Gly Pro Thr Ala Val Lys *
101                106

gagggcggga gaactctcct ttttcaccag gaccgcctgg ctagccctca ccctggcgct      815
ggccttctctc ctgctgatca gcattgcagc aaacctgtcc ttgctcctgt ccagagcaga      875

```

gaggaaccgg cgctgcatg gggactatgc ataccacccg ctgcaggaga tgaacgggga	935
gcctctggcc gcagagaagg agcagccagg gggcgcccac aacccttca aggactgaag	995
cctcaagctg cccgggggtg cacgtcgca aagcttggtt cccacgggtc tggcttctgc	1055
aggggaaatt tcaaggccac tggcgtggac catctgggtg tctcagccc ctgtggggca	1115
gccaagttcc tgatagcact tgtgcctcag cccctcacct ggccacctgc cagggcacct	1175
gcaaccctag caataccatg ctgcgtggag aggtcagct gcctgcttct cgctgcctg	1235
tgtctgctgc cgagaagccc gtgcccccg gagggctgcc gcactgcaa agagtctccc	1295
tcctcctggg gaaggggctg ccaacgaacc agactcagtg accacgtcat gacagaacag	1355
cacatcctgg ccagcacccc tggctggagt gggtaaagg gacgagtctg ccttcctggc	1415
tgtgacacgg gacccctttt ctacagacct catcactgga tttgccaact agaattcgat	1475
ttctgtcat aggaagctcc ttggaagaag ggatgggggg atgaaatcat gtttacagac	1535
ctgttttgtc atcctgctgc caagaagttt ttaatacact tgaataaatt gatataataa	1595
aaggagccac caggtggtgt gtggattctg aaaaaaaaaa aaaaa	1640

<210> 479
 <211> 3627
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (590) .. (3412)

<400> 479	
cctgtaggta ccggtccgga attcccgggt cgaccacgc gtccgcggac gcgtgggggc	60
gcggagcccg ggacgcgct acgcctgct gcttctctg atctgcttta acgttggaag	120
tggacttcac ttacaggtct taagcacaag aaatgaaaat aagctgcttc ctaaaccatcc	180
tcatttagtg cggcaaaagc gcgcctggat caccgcccc gtggctcttc tggagggaga	240
ggatctgtcc aagaagaatc caattgcaa gatacttct gatcttgag aagaaagagg	300
actcaaaatt acttacaat aactggaaa agggattaca gagccacctt ttggtatatt	360
tgtctttaac aaagatactg gagaactgaa tgttaccagc attcttgatc gagaagaaac	420
accatttttt ctgctaacag gttacgcttt ggatgcaaga ggaaacaatg tagagaaacc	480
cttagagcta cgcattaagg ttcttgatat caatgacaac gaaccagtgt tcacacagga	540

tgtctttgtt	gggtctgttg	aagagttgag	tcgagcacat	actcttgtg	atg aaa	595
					Met Lys	
					1	
atc aat gca aca gat gca gat gag ccc aat acc ctg aat tcg aaa att						643
Ile Asn Ala Thr Asp Ala Asp Glu Pro Asn Thr Leu Asn Ser Lys Ile						
3	8		13		18	
tcc tat aga atc gta tct ctg gag cct gct tat cct cca gtg ttc tac						691
Ser Tyr Arg Ile Val Ser Leu Glu Pro Ala Tyr Pro Pro Val Phe Tyr						
19	24		29		34	
cta aat aaa gat aca gga gag att tat aca acc agt gtt acc ttg gac						739
Leu Asn Lys Asp Thr Gly Glu Ile Tyr Thr Thr Ser Val Thr Leu Asp						
35	40		45		50	
aga gag gaa cac agc agc tac act ttg aca gta gaa gca aga gat ggc						787
Arg Glu Glu His Ser Ser Tyr Thr Leu Thr Val Glu Ala Arg Asp Gly						
51	56		61		66	
aat gga gaa gtt aca gac aaa cct gta aaa caa gct caa gtt cag att						835
Asn Gly Glu Val Thr Asp Lys Pro Val Lys Gln Ala Gln Val Gln Ile						
67	72		77		82	
cgt att ttg gat gtc aat gac aat ata cct gta gta gaa aat aaa gtg						883
Arg Ile Leu Asp Val Asn Asp Asn Ile Pro Val Val Glu Asn Lys Val						
83	88		93		98	
ctt gaa ggg atg gtt gaa gaa aat caa gtc aac gta gaa gtt acg cgc						931
Leu Glu Gly Met Val Glu Glu Asn Gln Val Asn Val Glu Val Thr Arg						
99	104		109		114	
gta aaa gtg ttc gat gca gat gaa ata ggt tct gat aat tgg ctg gca						979
Val Lys Val Phe Asp Ala Asp Glu Ile Gly Ser Asp Asn Trp Leu Ala						
115	120		125		130	
aat ttt aca ttt gca tca gga aat gaa gga ggt tat ttc cac ata gaa						1027
Asn Phe Thr Phe Ala Ser Gly Asn Glu Gly Gly Tyr Phe His Ile Glu						
131	136		141		146	
aca gat gct caa act aac gaa gga att gtg acc ctt att aag gaa gta						1075
Thr Asp Ala Gln Thr Asn Glu Gly Ile Val Thr Leu Ile Lys Glu Val						
147	152		157		162	
gat tat gaa gaa atg aag aat ctt gac ttc agt gtt att gtc gct aat						1123
Asp Tyr Glu Glu Met Lys Asn Leu Asp Phe Ser Val Ile Val Ala Asn						
163	168		173		178	
aaa gca gct ttt cac aag tcg att agg agt aaa tac aag cct aca ccc						1171
Lys Ala Ala Phe His Lys Ser Ile Arg Ser Lys Tyr Lys Pro Thr Pro						
179	184		189		194	
att ccc atc aag gtc aaa gtg aaa aat gtg aaa gaa ggc att cat ttt						1219
Ile Pro Ile Lys Val Lys Val Lys Asn Val Lys Glu Gly Ile His Phe						
195	200		205		210	
aaa agc agc gtc atc tca att tat gtt agc gag agc atg gat aga tca						1267

Lys Ser Ser Val Ile Ser Ile Tyr Val Ser Glu Ser Met Asp Arg Ser	
211 216 221 226	
agc aaa ggc caa ata att gga aat ttt caa gct ttt gat gag gac act	1315
Ser Lys Gly Gln Ile Ile Gly Asn Phe Gln Ala Phe Asp Glu Asp Thr	
227 232 237 242	
gga cta cca gcc cat gca aga tat gta aaa tta gaa gat aga gat aat	1363
Gly Leu Pro Ala His Ala Arg Tyr Val Lys Leu Glu Asp Arg Asp Asn	
243 248 253 258	
tgg atc tct gtg gat tct gtc aca tct gaa att aaa ctt gca aaa ctt	1411
Trp Ile Ser Val Asp Ser Val Thr Ser Glu Ile Lys Leu Ala Lys Leu	
259 264 269 274	
cct gat ttt gaa tct aga tat gtt caa aat ggc aca tac act gta aag	1459
Pro Asp Phe Glu Ser Arg Tyr Val Gln Asn Gly Thr Tyr Thr Val Lys	
275 280 285 290	
att gtg gcc ata tca gaa gat tat cct aga aaa acc atc act ggc aca	1507
Ile Val Ala Ile Ser Glu Asp Tyr Pro Arg Lys Thr Ile Thr Gly Thr	
291 296 301 306	
gtc ctt atc aat gtt gaa gac atc aac gac aac tgt ccc aca ctg ata	1555
Val Leu Ile Asn Val Glu Asp Ile Asn Asp Asn Cys Pro Thr Leu Ile	
307 312 317 322	
gag cct gtg cag aca atc tgt cac gat gca gag tat gtg aat gtt act	1603
Glu Pro Val Gln Thr Ile Cys His Asp Ala Glu Tyr Val Asn Val Thr	
323 328 333 338	
gca gag gac ctg gat gga cac cca aac agt ggc cct ttc agt ttc tcc	1651
Ala Glu Asp Leu Asp Gly His Pro Asn Ser Gly Pro Phe Ser Phe Ser	
339 344 349 354	
gtc att gac aaa cca cct ggc atg gca gaa aaa tgg aaa ata gca cgc	1699
Val Ile Asp Lys Pro Pro Gly Met Ala Glu Lys Trp Lys Ile Ala Arg	
355 360 365 370	
caa gaa agt acc agt gtg ctg ctg caa caa agt gag aaa aag ctt ggg	1747
Gln Glu Ser Thr Ser Val Leu Leu Gln Gln Ser Glu Lys Lys Leu Gly	
371 376 381 386	
aga agt gaa att cag ttc ctg att tca gac aat cag ggt ttt agt tgt	1795
Arg Ser Glu Ile Gln Phe Leu Ile Ser Asp Asn Gln Gly Phe Ser Cys	
387 392 397 402	
cct gaa aag cag gtc ctt aca ctc aca gtt tgt gag tgt ctg cat ggc	1843
Pro Glu Lys Gln Val Leu Thr Leu Thr Val Cys Glu Cys Leu His Gly	
403 408 413 418	
agc ggc tgc agg gaa gca cag cat gac tcc tat gtg ggc ctg gga ccc	1891
Ser Gly Cys Arg Glu Ala Gln His Asp Ser Tyr Val Gly Leu Gly Pro	
419 424 429 434	
gca gca att gcg ctc atg att ttg gcc ttt ctg ctc ctg cta ttg gta	1939
Ala Ala Ile Ala Leu Met Ile Leu Ala Phe Leu Leu Leu Leu Val	

435	440	445	450	
cca ctt tta ctg ctg atg tgc cat tgc gga aag ggc gcc aaa ggc ttt				1987
Pro Leu Leu Leu Leu Met Cys His Cys Gly Lys Gly Ala Lys Gly Phe				
451	456	461	466	
acc ccc ata cct ggc acc ata gag atg ctg cat cct tgg aat aat gaa				2035
Thr Pro Ile Pro Gly Thr Ile Glu Met Leu His Pro Trp Asn Asn Glu				
467	472	477	482	
gga gca cca cct gaa gac aag gtg gtg cca tca ttt ctg cca gtg gat				2083
Gly Ala Pro Pro Glu Asp Lys Val Val Pro Ser Phe Leu Pro Val Asp				
483	488	493	498	
caa ggg ggc agt cta gta gga aga aat gga gta gga ggt atg gcc aag				2131
Gln Gly Gly Ser Leu Val Gly Arg Asn Gly Val Gly Gly Met Ala Lys				
499	504	509	514	
gaa gcc acg atg aaa gga agt agc tct gct tcc att gtc aaa ggg caa				2179
Glu Ala Thr Met Lys Gly Ser Ser Ser Ala Ser Ile Val Lys Gly Gln				
515	520	525	530	
cat gag atg tcc gag atg gat gga agg tgg gaa gaa cac aga agc ctg				2227
His Glu Met Ser Glu Met Asp Gly Arg Trp Glu Glu His Arg Ser Leu				
531	536	541	546	
ctt tct ggt aga gct acc cag ttt aca ggg gcc aca ggc gct atc atg				2275
Leu Ser Gly Arg Ala Thr Gln Phe Thr Gly Ala Thr Gly Ala Ile Met				
547	552	557	562	
acc act gaa acc acg aag acc gca agg gcc aca ggg gct tcc aga gac				2323
Thr Thr Glu Thr Thr Lys Thr Ala Arg Ala Thr Gly Ala Ser Arg Asp				
563	568	573	578	
atg gcc gga gct cag gca gct gct gtt gca ctg aac gaa gaa ttc tta				2371
Met Ala Gly Ala Gln Ala Ala Ala Val Ala Leu Asn Glu Glu Phe Leu				
579	584	589	594	
aga aat tat ttc act gat aaa gcg gcc tct tac act gag gaa gat gaa				2419
Arg Asn Tyr Phe Thr Asp Lys Ala Ala Ser Tyr Thr Glu Glu Asp Glu				
595	600	605	610	
aat cac aca gcc aaa gat tgc ctt ctg gtt tat tct cag gaa gaa act				2467
Asn His Thr Ala Lys Asp Cys Leu Leu Val Tyr Ser Gln Glu Glu Thr				
611	616	621	626	
gaa tcg ctg aat gct tct att ggt tgt tgc agt ttt att gaa gga gag				2515
Glu Ser Leu Asn Ala Ser Ile Gly Cys Cys Ser Phe Ile Glu Gly Glu				
627	632	637	642	
cta gat gac cgc ttc tta gat gat ttg gga ctt aaa ttc aag aca cta				2563
Leu Asp Asp Arg Phe Leu Asp Asp Leu Gly Leu Lys Phe Lys Thr Leu				
643	648	653	658	
gct gaa gtt tgc ctg ggt caa aaa ata gat ata aat aag gaa att gag				2611
Ala Glu Val Cys Leu Gly Gln Lys Ile Asp Ile Asn Lys Glu Ile Glu				
659	664	669	674	

cag aga caa aaa cct gcc aca gaa aca agt atg aac aca gct tca cat	2659
Gln Arg Gln Lys Pro Ala Thr Glu Thr Ser Met Asn Thr Ala Ser His	
675 680 685 690	
tca ctc tgt gag caa act atg gtt aat tca gag aat acc tac tcc tct	2707
Ser Leu Cys Glu Gln Thr Met Val Asn Ser Glu Asn Thr Tyr Ser Ser	
691 696 701 706	
ggc agt agc ttc cca gtt cca aaa tct ttg caa gaa gcc aat gca gag	2755
Gly Ser Ser Phe Pro Val Pro Lys Ser Leu Gln Glu Ala Asn Ala Glu	
707 712 717 722	
aaa gta act cag gaa ata gtc act gaa aga tct gtg ³ tct tct agg cag	2803
Lys Val Thr Gln Glu Ile Val Thr Glu Arg Ser Val Ser Ser Arg Gln	
723 728 733 738	
gcg caa aag gta gct aca cct ctt cct gac cca atg gct tct aga aat	2851
Ala Gln Lys Val Ala Thr Pro Leu Pro Asp Pro Met Ala Ser Arg Asn	
739 744 749 754	
gtg ata gca aca gaa act tcc tat gtc aca ggg tcc act atg cca cca	2899
Val Ile Ala Thr Glu Thr Ser Tyr Val Thr Gly Ser Thr Met Pro Pro	
755 760 765 770	
acc act gtg atc ctg ggt cct agc cag cca cag agc ctt att gtg aca	2947
Thr Thr Val Ile Leu Gly Pro Ser Gln Pro Gln Ser Leu Ile Val Thr	
771 776 781 786	
gag agg gtg tat gct cca gct tct acc ttg gta gat cag cct tat gct	2995
Glu Arg Val Tyr Ala Pro Ala Ser Thr Leu Val Asp Gln Pro Tyr Ala	
787 792 797 802	
aat gaa ggt aca gtt gtg gtc act gaa aga gta ata cag cct cat ggg	3043
Asn Glu Gly Thr Val Val Val Thr Glu Arg Val Ile Gln Pro His Gly	
803 808 813 818	
ggt gga tcg aat cct ctg gaa ggc act cag cat ctt caa gat gta cct	3091
Gly Gly Ser Asn Pro Leu Glu Gly Thr Gln His Leu Gln Asp Val Pro	
819 824 829 834	
tac gtc atg gtg agg gaa aga gag agc ttc ctt gcc ccc agc tca ggt	3139
Tyr Val Met Val Arg Glu Arg Glu Ser Phe Leu Ala Pro Ser Ser Gly	
835 840 845 850	
gtg cag cct act ctg gcc atg cct aat ata gca gta gga cag aat gtg	3187
Val Gln Pro Thr Leu Ala Met Pro Asn Ile Ala Val Gly Gln Asn Val	
851 856 861 866	
aca gtg aca gaa aga gtt cta gca cct gct tcc act ctg caa tcc agt	3235
Thr Val Thr Glu Arg Val Leu Ala Pro Ala Ser Thr Leu Gln Ser Ser	
867 872 877 882	
tac cag att ccc act gaa aat tct atg acg gct agg aac acc acg gtg	3283
Tyr Gln Ile Pro Thr Glu Asn Ser Met Thr Ala Arg Asn Thr Thr Val	
883 888 893 898	

caa tgt aag gag tgt gaa aat gta aaa gaa ata aaa gtt aag gag gaa	336
Gln Cys Lys Glu Cys Glu Asn Val Lys Glu Ile Lys Val Lys Glu Glu	
97 102 107 112	
aat gaa aca gag atc caa gaa ata aag atg gag gag gag agg aat ata	384
Asn Glu Thr Glu Ile Gln Glu Ile Lys Met Glu Glu Glu Arg Asn Ile	
113 118 123 128	
ata cca aga gaa gaa aag cct att gag gat gaa att gaa aga aaa gaa	432
Ile Pro Arg Glu Glu Lys Pro Ile Glu Asp Glu Ile Glu Arg Lys Glu	
129 134 139 144	
aat att aag ccc tct ctg gga agt aaa aag aat tta tta gaa tct ata	480
Asn Ile Lys Pro Ser Leu Gly Ser Lys Lys Asn Leu Leu Glu Ser Ile	
145 150 155 160	
cct aca cat tct gat cag gaa aaa gaa gtt aac att aaa aaa cca gaa	528
Pro Thr His Ser Asp Gln Glu Lys Glu Val Asn Ile Lys Lys Pro Glu	
161 166 171 176	
gac aat gaa aat ctg gat gac aaa gat gat gac aca act agg gta gat	576
Asp Asn Glu Asn Leu Asp Asp Lys Asp Asp Asp Thr Thr Arg Val Asp	
177 182 187 192	
gaa tcc ctc aac ata aag gta gaa gct gag gaa gaa aaa gca aaa tct	624
Glu Ser Leu Asn Ile Lys Val Glu Ala Glu Glu Glu Lys Ala Lys Ser	
193 198 203 208	
gga gat gaa acg aat aaa gaa gaa gat gaa gat gat gaa gaa gca gaa	672
Gly Asp Glu Thr Asn Lys Glu Glu Asp Glu Asp Asp Glu Glu Ala Glu	
209 214 219 224	
gag gag gag gag gag gaa gaa gaa gaa gag gat gaa gat gat gat gac	720
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Asp Asp Asp	
225 230 235 240	
aac aat gag gaa gag gag ttt gag tgc tat cca cca ggc atg aaa gtc	768
Asn Asn Glu Glu Glu Glu Phe Glu Cys Tyr Pro Pro Gly Met Lys Val	
241 246 251 256	
caa gtg cgg tat gga cga ggg aaa aat caa aaa atg tat gaa gct agt	816
Gln Val Arg Tyr Gly Arg Gly Lys Asn Gln Lys Met Tyr Glu Ala Ser	
257 262 267 272	
att aaa gat tct gat gtc gaa ggt gga gag gtc ctt tac ttg gtg cat	864
Ile Lys Asp Ser Asp Val Glu Gly Gly Glu Val Leu Tyr Leu Val His	
273 278 283 288	
tac tgc gga tgg aat gtg aga tac gat gaa tgg att aaa gca gat aaa	912
Tyr Cys Gly Trp Asn Val Arg Tyr Asp Glu Trp Ile Lys Ala Asp Lys	
289 294 299 304	
ata gta aga cct gct gat aaa aat gtg cca aag ata aaa cat cgg aag	960
Ile Val Arg Pro Ala Asp Lys Asn Val Pro Lys Ile Lys His Arg Lys	
305 310 315 320	
aaa ata aag aat aaa tta gac aaa gaa aaa gac aaa gat gaa aaa tac	1008

Lys Ile Lys Asn Lys Leu Asp Lys Glu Lys Asp Lys Asp Glu Lys Tyr	
321 326 331 336	
tct cca aaa aac tgt aaa ctt cgg cgc ttg tcc aaa cca cca ttt cag	1056
Ser Pro Lys Asn Cys Lys Leu Arg Arg Leu Ser Lys Pro Pro Phe Gln	
337 342 347 352	
aca aat cca tct cct gaa atg gta tcc aaa ctg gat ctc act gat gcc	1104
Thr Asn Pro Ser Pro Glu Met Val Ser Lys Leu Asp Leu Thr Asp Ala	
353 358 363 368	
aaa aac tct gat act gct cat att aag tcc ata gaa att act tcg atc	1152
Lys Asn Ser Asp Thr Ala His Ile Lys Ser Ile Glu Ile Thr Ser Ile	
369 374 379 384	
ctt aat gga ctt caa gct tct gaa agt tct gct gaa gac agt gag cag	1200
Leu Asn Gly Leu Gln Ala Ser Glu Ser Ser Ala Glu Asp Ser Glu Gln	
385 390 395 400	
gaa gat gag aga ggt gct caa gac atg gat aat aat ggc aaa gag gaa	1248
Glu Asp Glu Arg Gly Ala Gln Asp Met Asp Asn Asn Gly Lys Glu Glu	
401 406 411 416	
tct aag att gat cat ttg acc aac aac aga aat gat ctt att tca aag	1296
Ser Lys Ile Asp His Leu Thr Asn Asn Arg Asn Asp Leu Ile Ser Lys	
417 422 427 432	
gag gaa cag aac agt tca tct ttg cta gaa gaa aac aaa gtt cat gca	1344
Glu Glu Gln Asn Ser Ser Ser Leu Leu Glu Glu Asn Lys Val His Ala	
433 438 443 448	
gat ttg gta ata tcc aaa cca gtg tca aaa tct cca gaa aga tta agg	1392
Asp Leu Val Ile Ser Lys Pro Val Ser Lys Ser Pro Glu Arg Leu Arg	
449 454 459 464	
aaa gat ata gaa gta tta tcc gaa gat act gat tat gaa gaa gat gaa	1440
Lys Asp Ile Glu Val Leu Ser Glu Asp Thr Asp Tyr Glu Glu Asp Glu	
465 470 475 480	
gtc aca aaa aag aga aag gat gtc aag aag gac aca aca gat aaa tct	1488
Val Thr Lys Lys Arg Lys Asp Val Lys Lys Asp Thr Thr Asp Lys Ser	
481 486 491 496	
tca aaa cca caa ata aaa cgt ggt aaa aga agg tat tgc aat aca gaa	1536
Ser Lys Pro Gln Ile Lys Arg Gly Lys Arg Arg Tyr Cys Asn Thr Glu	
497 502 507 512	
gag tgt cta aaa act gga tca cct ggc aaa aag gaa gag aag gcc aag	1584
Glu Cys Leu Lys Thr Gly Ser Pro Gly Lys Lys Glu Glu Lys Ala Lys	
513 518 523 528	
aac aaa gaa tca ctt tgc atg gaa aac agt agc aac agc tct tca gat	1632
Asn Lys Glu Ser Leu Cys Met Glu Asn Ser Ser Asn Ser Ser Ser Asp	
529 534 539 544	
gaa gat gaa gaa gaa aca aaa gca aag atg aca cca act aag aaa tac	1680
Glu Asp Glu Glu Glu Thr Lys Ala Lys Met Thr Pro Thr Lys Lys Tyr	

545	550	555	560	
aat ggt ttg gag gaa aaa aga aaa tct cta cgg aca act ggt ttc tat				1728
Asn Gly Leu Glu Glu Lys Arg Lys Ser Leu Arg Thr Thr Gly Phe Tyr				
561	566	571	576	
tca gga ttt tca gaa gtg gca gaa aaa agg att aaa ctt tta aat aac				1776
Ser Gly Phe Ser Glu Val Ala Glu Lys Arg Ile Lys Leu Leu Asn Asn				
577	582	587	592	
tct gat gaa aga ctt caa aac agc agg gcc aaa gat cga aaa gat gtc				1824
Ser Asp Glu Arg Leu Gln Asn Ser Arg Ala Lys Asp Arg Lys Asp Val				
593	598	603	608	
tgg tca agt att cag gga cag tgg cct aaa aaa acg ctg aaa gag ctt				1872
Trp Ser Ser Ile Gln Gly Gln Trp Pro Lys Lys Thr Leu Lys Glu Leu				
609	614	619	624	
ttt tca gac tct gat act gag gct gca gct tcc cca ccg cat cct gcc				1920
Phe Ser Asp Ser Asp Thr Glu Ala Ala Ala Ser Pro Pro His Pro Ala				
625	630	635	640	
cca gag gag ggg gtg gca gag gag tca ctg cag act gtg gct gaa gag				1968
Pro Glu Glu Gly Val Ala Glu Glu Ser Leu Gln Thr Val Ala Glu Glu				
641	646	651	656	
gag agt tgt tca ccc agt gta gaa cta gaa aaa cca cct cca gtc aat				2016
Glu Ser Cys Ser Pro Ser Val Glu Leu Glu Lys Pro Pro Pro Val Asn				
657	662	667	672	
gtc gat agt aaa ccc att gaa gaa aaa aca gta gag gtc aat gac aga				2064
Val Asp Ser Lys Pro Ile Glu Glu Lys Thr Val Glu Val Asn Asp Arg				
673	678	683	688	
aaa gca gaa ttt cca agt agt ggc agt aat tca gtg cta aat acc cct				2112
Lys Ala Glu Phe Pro Ser Ser Gly Ser Asn Ser Val Leu Asn Thr Pro				
689	694	699	704	
cct act aca cct gaa tcg cct tca tca gtc act gta aca gaa ggc agc				2160
Pro Thr Thr Pro Glu Ser Pro Ser Ser Val Thr Val Thr Glu Gly Ser				
705	710	715	720	
cgg cag cag tct tct gta aca gta tca gaa cca ctg gct cca aac caa				2208
Arg Gln Gln Ser Ser Val Thr Val Ser Glu Pro Leu Ala Pro Asn Gln				
721	726	731	736	
gaa gag gtt cga agt atc aag agt gaa act gat agc aca att gag gtg				2256
Glu Glu Val Arg Ser Ile Lys Ser Glu Thr Asp Ser Thr Ile Glu Val				
737	742	747	752	
gat agt gtt gct ggg gag ctc caa gac ctc cag tct gaa ggg aat agc				2304
Asp Ser Val Ala Gly Glu Leu Gln Asp Leu Gln Ser Glu Gly Asn Ser				
753	758	763	768	
tcg cca gca ggt ttt gat gcc agt gtg agc tca agc agt agt aat cag				2352
Ser Pro Ala Gly Phe Asp Ala Ser Val Ser Ser Ser Ser Ser Asn Gln				
769	774	779	784	

cca gaa cca gaa cat cct gaa aaa gcc tgt aca ggt cag aaa aga gtg	2400
Pro Glu Pro Glu His Pro Glu Lys Ala Cys Thr Gly Gln Lys Arg Val	
785 790 795 800	
aaa gat gct cag gga gga gga agt tca tca aaa aag cag aaa aga agc	2448
Lys Asp Ala Gln Gly Gly Gly Ser Ser Ser Lys Lys Gln Lys Arg Ser	
801 806 811 816	
cat aaa gca aca gtg gta aac aac aaa aag aag gga aaa ggc aca aat	2496
His Lys Ala Thr Val Val Asn Asn Lys Lys Lys Gly Lys Gly Thr Asn	
817 822 827 832	
agt agt gat agt gaa gaa ctt tca gct ggt gaa agt ata act aag agt	2544
Ser Ser Asp Ser Glu Glu Leu Ser Ala Gly Glu Ser Ile Thr Lys Ser	
833 838 843 848	
cag cca gtc aaa tca gtt tcc act gga atg aag tct cat agt acc aaa	2592
Gln Pro Val Lys Ser Val Ser Thr Gly Met Lys Ser His Ser Thr Lys	
849 854 859 864	
tct ccc gca agg acg cag tct cca gga aaa tgt gga aag aat ggt gat	2640
Ser Pro Ala Arg Thr Gln Ser Pro Gly Lys Cys Gly Lys Asn Gly Asp	
865 870 875 880	
aag gat cct gat ctc aag gaa ccc agt aat cga tta ccc aaa gtt tac	2688
Lys Asp Pro Asp Leu Lys Glu Pro Ser Asn Arg Leu Pro Lys Val Tyr	
881 886 891 896	
aaa tgg agt ttt cag atg tcg gac ctg gaa aat atg aca agt gcc gaa	2736
Lys Trp Ser Phe Gln Met Ser Asp Leu Glu Asn Met Thr Ser Ala Glu	
897 902 907 912	
cgc atc aca att ctt caa gaa aaa ctt caa gaa atc aga aaa cat tat	2784
Arg Ile Thr Ile Leu Gln Glu Lys Leu Gln Glu Ile Arg Lys His Tyr	
913 918 923 928	
ctg tca tta aaa tct gaa gta gct tcc att gat cgg agg aga aag cgt	2832
Leu Ser Leu Lys Ser Glu Val Ala Ser Ile Asp Arg Arg Arg Lys Arg	
929 934 939 944	
tta aag aag aaa gag aga gaa agt gct gct aca tcc tca tcc tcc tct	2880
Leu Lys Lys Lys Glu Arg Glu Ser Ala Ala Thr Ser Ser Ser Ser Ser	
945 950 955 960	
tca cct tca tcc agt tcc ata aca gct gct gtt atg tta act tta gct	2928
Ser Pro Ser Ser Ser Ser Ile Thr Ala Ala Val Met Leu Thr Leu Ala	
961 966 971 976	
gaa ccg tca atg tcc agc gca tca caa aat gga atg tca gtt gag tgc	2976
Glu Pro Ser Met Ser Ser Ala Ser Gln Asn Gly Met Ser Val Glu Cys	
977 982 987 992	
agg tga cagcaggact tgctaaagca ctttgactt aatggctgtt gagggccact	3032
Arg *	
993	

ttttttttat actgcacagt ggcacaaaaa aatatcagac aagcactatt ttatatatta	3092
aaattgtttc ttgacaagct gacttggcac ttaagtgcac ttttttatga agaaaaagta	3152
caatgaactg cttttcctca agcaataatt gtttccaact tgtctgggaa ttgtgtgtct	3212
ggtaactgga aggccttcca ctgtggcaaa tggaggcttt tcactgcctg tagagacaat	3272
acagtaagca tagttaaggg gtgggtcaga acatgttaag ataacttact gtatatgtat	3332
tcccttgat tttgttaaag ctggaacatt tgatattttt ccatttattt atgaaaaaat	3392
atgaacctat tttcatttgt acaaggtaat tgttttttaa agcaagtcac cttaggggtg	3452
ctttaattgt ataagtcaag cacatgtaat aaattcaaaa cctgcagtta acaggatatt	3512
agacatcaat cctggtaacc aaatattaaa gattctcttt aaaaaagact gaacatgttt	3572
acaggtttga attaggctaa aaggctctgc agtggccttt catggccctt caaattggaa	3632
tggaaactact gtactttgcc atttttctat aaatcagtat ttttttttaa ttttgatata	3692
cattgtgtga aaaaagaaaa tggctaataa actgtattaa atcttaaaca atgtataaag	3752
attgtactta gccagttcaa agtgtatatt tattcataat gaattataac agttatattt	3812
ttgtgttttc ttgtaaatgt ttcttttccc ttaaatacag ataattcatt tgtattgctt	3872
attttattat gagctacaac aaaaggactt caggaacaag taatgtatta gtatgggttca	3932
agattgttga taggaactgt ctcaaaagga tgggtggttat tttaaatata aatagcta	3992
gggggtggta ggctataaaa attaaatgcc ttgtataaaa tccaaaatga atgcaaaatt	4052
gttttcactt gtattgactt tatgttgtat gattccaatc tctgttctgt ttggcacttg	4112
tatttaattc ttcacctttg taagacattt gtatattgtg gatgtgttca ttcaagctat	4172
ttaatatctg gcactgttaa tacacagtac tttattgtaa aaaaaaaaaa aaaa	4226

<210> 481
 <211> 6765
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (259) .. (3105)

<400> 481	
accaattccc ttcctgggag ttggggcttc cctcgtcgg cccactccc gtttaccctt	60
tccccagctc ccgccttagc caggggcttc cccgcctgcc gctagggctc gggccgaagc	120

gccgctcagc gccagcctgc cgcctcccgg gctccacttt cactttcggt cctgggggag 180

ctaggccggc ggcagtggtg gtggcggcgg cgcaagggtg agggcggccc cagaacccca 240

ggtaggtaga gcaagaag atg gtg ttt ctg ccc ctc aaa tgg tcc ctt gca 291
Met Val Phe Leu Pro Leu Lys Trp Ser Leu Ala
1 5

acc atg tca ttt cta ctt tcc tca ctg ttg gct ctc tta act gtg tcc 339
Thr Met Ser Phe Leu Leu Ser Ser Leu Leu Ala Leu Leu Thr Val Ser
12 17 22 27

act cct tca tgg tgt cag agc act gaa gca tct cca aaa cgt agt gat 387
Thr Pro Ser Trp Cys Gln Ser Thr Glu Ala Ser Pro Lys Arg Ser Asp
28 33 38 43

ggg aca cca ttt cct tgg aat aaa ata cga ctt cct gag tac gtc atc 435
Gly Thr Pro Phe Pro Trp Asn Lys Ile Arg Leu Pro Glu Tyr Val Ile
44 49 54 59

cca gtt cat tat gat ctc ttg atc cat gca aac ctt acc acg ctg acc 483
Pro Val His Tyr Asp Leu Leu Ile His Ala Asn Leu Thr Thr Leu Thr
60 65 70 75

ttc tgg gga acc acg aaa gta gaa atc aca gcc agt cag ccc acc agc 531
Phe Trp Gly Thr Thr Lys Val Glu Ile Thr Ala Ser Gln Pro Thr Ser
76 81 86 91

acc atc atc ctg cat agt cac cac ctg cag ata tct agg gcc acc ctc 579
Thr Ile Ile Leu His Ser His His Leu Gln Ile Ser Arg Ala Thr Leu
92 97 102 107

agg aag gga gct gga gag agg cta tcg gaa gaa ccc ctg cag gtc ctg 627
Arg Lys Gly Ala Gly Glu Arg Leu Ser Glu Glu Pro Leu Gln Val Leu
108 113 118 123

gaa cac ccc cct cag gag caa att gca ctg ctg gct ccc gag ccc ctc 675
Glu His Pro Pro Gln Glu Gln Ile Ala Leu Leu Ala Pro Glu Pro Leu
124 129 134 139

ctt gtc ggg ctc ccg tac aca gtt gtc att cac tat gct ggc aat ctt 723
Leu Val Gly Leu Pro Tyr Thr Val Val Ile His Tyr Ala Gly Asn Leu
140 145 150 155

tcg gag act ttc cac gga ttt tac aaa agc acc tac aga acc aag gaa 771
Ser Glu Thr Phe His Gly Phe Tyr Lys Ser Thr Tyr Arg Thr Lys Glu
156 161 166 171

ggg gaa ctg agg ata cta gca tca aca caa ttt gaa ccc act gca gct 819
Gly Glu Leu Arg Ile Leu Ala Ser Thr Gln Phe Glu Pro Thr Ala Ala
172 177 182 187

aga atg gcc ttt ccc tgc ttt gat gaa cct gcc ttc aaa gca agt ttc 867
Arg Met Ala Phe Pro Cys Phe Asp Glu Pro Ala Phe Lys Ala Ser Phe
188 193 198 203

tca atc aaa att aga aga gag cca agg cac cta gcc atc tcc aat atg 915

Ser Ile Lys Ile Arg Arg Glu Pro Arg His Leu Ala Ile Ser Asn Met	
204 209 214 219	
cca ttg gtg aaa tct gtg act gtt gct gaa gga ctc ata gaa gac cat	963
Pro Leu Val Lys Ser Val Thr Val Ala Glu Gly Leu Ile Glu Asp His	
220 225 230 235	
ttt gat gtc act gtg aag atg agc acc tat ctg gtg gcc ttc atc att	1011
Phe Asp Val Thr Val Lys Met Ser Thr Tyr Leu Val Ala Phe Ile Ile	
236 241 246 251	
tca gat ttt gag tct gtc agc aag ata acc aag agt gga gtc aag gtt	1059
Ser Asp Phe Glu Ser Val Ser Lys Ile Thr Lys Ser Gly Val Lys Val	
252 257 262 267	
tct gtt tat gct gtg cca gac aag ata aat caa gca gat tat gca ctg	1107
Ser Val Tyr Ala Val Pro Asp Lys Ile Asn Gln Ala Asp Tyr Ala Leu	
268 273 278 283	
gat gct gcg gtg act ctt cta gaa ttt tat gag gat tat ttc agc ata	1155
Asp Ala Ala Val Thr Leu Leu Glu Phe Tyr Glu Asp Tyr Phe Ser Ile	
284 289 294 299	
ccg tat ccc cta ccc aaa caa gat ctt gct gct att ccc gac ttt cag	1203
Pro Tyr Pro Leu Pro Lys Gln Asp Leu Ala Ala Ile Pro Asp Phe Gln	
300 305 310 315	
tct ggt gct atg gaa aac tgg gga ctg aca aca tat aga gaa tct gct	1251
Ser Gly Ala Met Glu Asn Trp Gly Leu Thr Thr Tyr Arg Glu Ser Ala	
316 321 326 331	
ctg ttg ttt gat gca gaa aag tct tct gca tca agt aag ctt ggc atc	1299
Leu Leu Phe Asp Ala Glu Lys Ser Ser Ala Ser Ser Lys Leu Gly Ile	
332 337 342 347	
aca gtg act gtg gcc cat gaa ctg gcc cac cag tgg ttt ggg aac ctg	1347
Thr Val Thr Val Ala His Glu Leu Ala His Gln Trp Phe Gly Asn Leu	
348 353 358 363	
gtc act atg gaa tgg tgg aat gat ctt tgg cta aat gaa gga ttt gcc	1395
Val Thr Met Glu Trp Trp Asn Asp Leu Trp Leu Asn Glu Gly Phe Ala	
364 369 374 379	
aaa ttt atg gag ttt gtg tct gtc agt gtg acc cat cct gaa ctg aaa	1443
Lys Phe Met Glu Phe Val Ser Val Ser Val Thr His Pro Glu Leu Lys	
380 385 390 395	
gtt gga gat tat ttc ttt ggc aaa tgt ttt gac gca atg gag gta gat	1491
Val Gly Asp Tyr Phe Phe Gly Lys Cys Phe Asp Ala Met Glu Val Asp	
396 401 406 411	
gct tta aat tcc tca cac cct gtg tct aca cct gtg gaa aat cct gct	1539
Ala Leu Asn Ser Ser His Pro Val Ser Thr Pro Val Glu Asn Pro Ala	
412 417 422 / 427	
cag atc cgg gag atg ttt gat gat gtt tct tat gat aag gga gct tgt	1587
Gln Ile Arg Glu Met Phe Asp Asp Val Ser Tyr Asp Lys Gly Ala Cys	

428	433	438	443	
att ctg aat atg cta agg gag tat ctt agc gct gac gca ttt aaa agt				1635
Ile Leu Asn Met Leu Arg Glu Tyr Leu Ser Ala Asp Ala Phe Lys Ser				
444	449	454	459	
ggt att gta cag tat ctc cag aag cat agc tat aaa aat aca aaa aac				1683
Gly Ile Val Gln Tyr Leu Gln Lys His Ser Tyr Lys Asn Thr Lys Asn				
460	465	470	475	
gag gac ctg tgg gat agt atg gca agt att tgc cct aca gat ggt gta				1731
Glu Asp Leu Trp Asp Ser Met Ala Ser Ile Cys Pro Thr Asp Gly Val				
476	481	486	491	
aaa ggg atg gat ggc ttt tgc tct aga agt caa cat tca tct tca tcc				1779
Lys Gly Met Asp Gly Phe Cys Ser Arg Ser Gln His Ser Ser Ser Ser				
492	497	502	507	
tca cat tgg cat cag gaa ggg gtg gat gtg aaa acc atg atg aac act				1827
Ser His Trp His Gln Glu Gly Val Asp Val Lys Thr Met Met Asn Thr				
508	513	518	523	
tgg aca ctg cag agg ggt ttt ccc cta ata acc atc aca gtg agg ggg				1875
Trp Thr Leu Gln Arg Gly Phe Pro Leu Ile Thr Ile Thr Val Arg Gly				
524	529	534	539	
agg aat gta cac atg aag caa gag cac tac atg aag ggc tct gac ggc				1923
Arg Asn Val His Met Lys Gln Glu His Tyr Met Lys Gly Ser Asp Gly				
540	545	550	555	
gcc ccg gac act ggg tac ctg tgg cat gtt cca ttg aca ttc atc acc				1971
Ala Pro Asp Thr Gly Tyr Leu Trp His Val Pro Leu Thr Phe Ile Thr				
556	561	566	571	
agc aaa tcc gac atg gtc cat cga ttt ttg cta aaa aca aaa aca gat				2019
Ser Lys Ser Asp Met Val His Arg Phe Leu Leu Lys Thr Lys Thr Asp				
572	577	582	587	
gtg ctc atc ctc cca gaa gag gtg gaa tgg atc aaa ttt aat gtg ggc				2067
Val Leu Ile Leu Pro Glu Glu Val Glu Trp Ile Lys Phe Asn Val Gly				
588	593	598	603	
atg aat ggc tat tac att gtg cat tac gag gat gat gga tgg gac tct				2115
Met Asn Gly Tyr Tyr Ile Val His Tyr Glu Asp Asp Gly Trp Asp Ser				
604	609	614	619	
ttg act ggc ctt tta aaa gga aca cac aca gca gtc agc agt aat gat				2163
Leu Thr Gly Leu Leu Lys Gly Thr His Thr Ala Val Ser Ser Asn Asp				
620	625	630	635	
cgg gca agt ctc att aac aat gca ttt cag ctc gtc agc att ggg aag				2211
Arg Ala Ser Leu Ile Asn Asn Ala Phe Gln Leu Val Ser Ile Gly Lys				
636	641	646	651	
ctg tcc att gaa aag gcc ttg gat tta tcc ctg tac ttg aaa cat gaa				2259
Leu Ser Ile Glu Lys Ala Leu Asp Leu Ser Leu Tyr Leu Lys His Glu				
652	657	662	667	

act gaa att atg ccc gtg ttt caa ggt ttg aat gag ctg att cct atg	2307
Thr Glu Ile Met Pro Val Phe Gln Gly Leu Asn Glu Leu Ile Pro Met	
668 673 678 683	
tat aag tta atg gag aaa aga gat atg aat gaa gtg gaa act caa ttc	2355
Tyr Lys Leu Met Glu Lys Arg Asp Met Asn Glu Val Glu Thr Gln Phe	
684 689 694 699	
aag gcc ttc ctc atc agg ctg cta agg gac ctc att gat aag cag aca	2403
Lys Ala Phe Leu Ile Arg Leu Leu Arg Asp Leu Ile Asp Lys Gln Thr	
700 705 710 715	
tgg aca gac gag ggc tca gtc tca gag caa atg ctg cgg agt gaa cta	2451
Trp Thr Asp Glu Gly Ser Val Ser Glu Gln Met Leu Arg Ser Glu Leu	
716 721 726 731	
cta ctc ctc gcc tgt gtg cac aac tat cag ccg tgc gta cag agg gca	2499
Leu Leu Leu Ala Cys Val His Asn Tyr Gln Pro Cys Val Gln Arg Ala	
732 737 742 747	
gaa ggc tat ttc aga aag tgg aag gaa tcc aat gga aac ttg agc ctg	2547
Glu Gly Tyr Phe Arg Lys Trp Lys Glu Ser Asn Gly Asn Leu Ser Leu	
748 753 758 763	
cct gtc gac gtg acc ttg gca gtg ttt gct gtg ggg gcc cag agc aca	2595
Pro Val Asp Val Thr Leu Ala Val Phe Ala Val Gly Ala Gln Ser Thr	
764 769 774 779	
gaa ggc tgg gat ttt ctt tat agt aaa tat cag ttt tct ttg tcc agt	2643
Glu Gly Trp Asp Phe Leu Tyr Ser Lys Tyr Gln Phe Ser Leu Ser Ser	
780 785 790 795	
act gag aaa agc caa att gaa ttt gcc ctc tgc aga acc caa aat aag	2691
Thr Glu Lys Ser Gln Ile Glu Phe Ala Leu Cys Arg Thr Gln Asn Lys	
796 801 806 811	
gaa aag ctt caa tgg cta cta gat gaa agc ttt aag gga gat aaa ata	2739
Glu Lys Leu Gln Trp Leu Leu Asp Glu Ser Phe Lys Gly Asp Lys Ile	
812 817 822 827	
aaa act cag gag ttt cca caa att ctt aca ctc att ggc agg aac cca	2787
Lys Thr Gln Glu Phe Pro Gln Ile Leu Thr Leu Ile Gly Arg Asn Pro	
828 833 838 843	
gta gga tac cca ctg gcc tgg caa ttt ctg agg aaa aac tgg aac aaa	2835
Val Gly Tyr Pro Leu Ala Trp Gln Phe Leu Arg Lys Asn Trp Asn Lys	
844 849 854 859	
ctt gta caa aag ttt gaa ctt ggc tca tct tcc ata gcc cac atg gta	2883
Leu Val Gln Lys Phe Glu Leu Gly Ser Ser Ser Ile Ala His Met Val	
860 865 870 875	
atg ggt aca aca aat caa ttc tcc aca aga aca cgg ctt gaa gag gta	2931
Met Gly Thr Thr Asn Gln Phe Ser Thr Arg Thr Arg Leu Glu Glu Val	
876 881 886 891	

aaa gga ttc ttc agc tct ttg aaa gaa aat ggt tct cag ctc cgt tgt	2979
Lys Gly Phe Phe Ser Ser Leu Lys Glu Asn Gly Ser Gln Leu Arg Cys	
892 897 902 907	
gtc caa cag aca att gaa acc att gaa gaa aac atc ggt tgg atg gat	3027
Val Gln Gln Thr Ile Glu Thr Ile Glu Glu Asn Ile Gly Trp Met Asp	
908 913 918 923	
aag aat ttt gat aaa atc aga gtg tgg ctg caa agt gaa aag ctt gaa	3075
Lys Asn Phe Asp Lys Ile Arg Val Trp Leu Gln Ser Glu Lys Leu Glu	
924 929 934 939	
cat gat cct gaa gct gac gca aca gga tga a aatccatcag aatctcagac	3126
His Asp Pro Glu Ala Asp Ala Thr Gly *	
940 945	
tacagcacta aatatgcttt gatgctacat caaacggaat ggaagcatag ctgacttcgc	3186
taaagttact tcatctccat ctagcaaatg aggcactgtt ctcaaccaa ggagatgggg	3246
atctggttta gggcaatccc ttataattt gatgtgctgt ggtctccttg gtaatgtata	3306
atttggatt gcacaggtga ttagtcaagg aagtctggaa aagctttggt cccacagcct	3366
tgccacacag catgtaaata attaaaacaa tattgatgct gaggttcttc tactgctagt	3426
atgaaagtga caaattttta ctgggtgtgaa ttgggaagaa aacaatgcta ttccatgacg	3486
tttgtaaaat gtttgtaaaa gctcaaacat gacgattcca taaaataaac ttgagggttaa	3546
ataatgggta gtaaattata gaatgtataa gaaaaatat aaaggagaaa atcaattatc	3606
aggaaagcta aagaactttt caaatctagt aatttgaata tagacacaat gcactttatt	3666
gcactttcaa ttcttataaa gcaacaataa tattaaggct cttgactatg tgtacaatgt	3726
tttcacatat atagtttcat ttaatcattt caaagttaat ctctgccatc tcgctaaatc	3786
atcagtctcg gctctttotga aatagaagggt gcctgatctt cctaataatt ctgcctatct	3846
tcatttgctt taaacaggcg ccctattttc ttctagttg tggctgcgca aaaacattta	3906
tctcccaaat aagatgtgct gcttaccgag gtatcacggg gtggggctcc agcttgggctc	3966
gttgaagctg ggggttgagg aaccacttca gagatggcag cagcaagttt agcatcttca	4026
aatttctttt attgaaaaaa attttattag taacatgttg tatataaaat tatgagcaca	4086
atgccatcac ttaactataa ctcttaaaga tagcttaatg actgtttatt ctcttgacca	4146
aatagactca taataacata taattttaaa agaaatttaa attctttctt ctctattgta	4206
ttattttata caatttgcta ttctatttc cttctcatat tgattattct aaatactatg	4266
caataatata acttagagtt ccacggtttg ttacacatt tcctgttgta catttagggt	4326
attcaaagtt ttcagctctt taaaattgc totgaataag ttctagttag tgagttatgg	4386

tgctggctat attttgctaa actgccctct caaatgttgc taggaattca tactgcgaaa	4446
agcaatgaat aagcatgcct gttttcccat ggcccttgctt gccagaattt gactttttatt	4506
atgataatca gtgtaaaatg atatactact attgcttgta tattgtggta tacgggtgtca	4566
ggtttcaggg ttttttttca acgttaaata ttctagaaac tttctgaaat aatttctggt	4626
taaaaatatt gaatatttgc ttcatttcaa atactccctt ttgacaaaaa aacttaggta	4686
taactgttga tgaaaaacca gaaaaaagtc cagaactctt tgggtgactcc aactatggat	4746
agcttatttt gaaaaaggag aattgcaaat tttacccaaa gatggagaaa agcacattaa	4806
aaagatacca acattcagaa attcatttca gcatgttatt attggaaatt atttaacta	4866
atthagataa ctataagata cttattgtcc atttataccc tgtaaagccg ttttagaatg	4926
taatatttta ggtaatccaa aatgtactaa attaaattca ttttttagtta tgagaaatct	4986
ttgcttatat gacaaatgaa aagaataaca agttgtcaaa tgaaaagaat gacattgaaa	5046
catttgtatt gtctcttctt aaactatctt attgacttat tatttaagcc ttttaatact	5106
aagtatgaaa caacctatgg tctggaaatt tgtatcgcaa agctatatgt gcatatgtta	5166
tttaattcat ctaacgctac acaaaagcat aaaataatga tttttcactc tctttaaaaa	5226
tactaaatca tttatgtcca tttctcaatt ttttcattga tctatgcttt gagtttgctt	5286
tctcaacatt attgtatttt ccacttatta ttactgtata acatatgcta gtgttttagtt	5346
ggattaatct tacctaaaag tactgaaaaa tgcttttttag tactttttca tatttttatac	5406
atttattttc cgaatgtatc attgaataat tttattgagt tataaaaagta tcttattgct	5466
atttaataaa aaattaacac ataaaatgac ttgaattgtc atcattcttt ttaagatatt	5526
tagttaaact gacttaatgt atggccttca atttttttgt gtccttattt ttctgatcat	5586
ttctcctttt atagtttaca ttaagtctga tctcatatta attacatttt ctcatctggt	5646
gttactaata aacatggcat aatgttactt acaaatgtat tatctacaag tagtgctatc	5706
cacaaatata ttcaaatggt cccttttaat gtttgtcatt tttttcatgt gttgttaatg	5766
attcttccat gtgataataa gcagaaatga caataaactt ttcatagttt ctgattttaa	5826
ggaaaatgcc tccagcatga tattgaatat ttgattctga aaactaaaga ctctttaaca	5886
gattagggga ttgcctactt tttaaaaagt ttttatttat aatatgagta tatgtaaaat	5946
tttaaataga tctttttacat ggacatgatt atttgtttct atttgatata ccactacaat	6006
atattgacag ttttctgct actgaatcaa tacttataat ggcaaataat ttaactgttt	6066

gttatattct atgtatgctg tatgtaattt ttacatctac acatttaagt aacttttagct 6126
 gataccgtta tttttgtcag attttaagat tagcaccata attactcata gaagcaacta 6186
 tgtgacccca tctttttcat gacatattta tgccacataa gaactgagtg ttcaacagtt 6246
 agagtcatct ttaaaccctc agtagaagga cagtttgaaa atcattgcaa tttttcttc 6306
 agtctttttt taggttttgt gaattacgca gtttaatat tttgtttaat cttagaaaat 6366
 tgttgtacat agtgtttcct aataatttat ttgtgctctg tactgattat tgtattttct 6426
 cacatttatg ttaaatttta ttagtaagat tttttctct atttatcagt tttgtaaaat 6486
 gttaaaaatt cataaaagcc aactgactat tggctttaaa ctaccaataa tttagttgat 6546
 ctctatatta ttatattact ctgttaaaat ttaattgtat tttttgtaag gtttttttc 6606
 ctcttttata tttgctagta ttttataaag tttttgttat ttcaaaagaa acaactattg 6666
 gccagttaac tttcatgccg ctattttcat ttcttggtat gcttattgct actttgtttt 6726
 tgggtggtac cttattaaaa cttttagaaa tttcagttt 6765

<210> 482
 <211> 866
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (42)..(749)

<400> 482
 ggcacttact cctgagcta agggggaaga gctggatcac c atg aaa tat gtc 53
 Met Lys Tyr Val
 1

ttc tat ttg ggt gtc ctc gct ggg aca ttt ttc ttt gct gac tca tct 101
 Phe Tyr Leu Gly Val Leu Ala Gly Thr Phe Phe Phe Ala Asp Ser Ser
 5 10 15 20

gtt cag aaa gaa gac cct gct ccc tat ttg gtg tac ctc aag tct cac 149
 Val Gln Lys Glu Asp Pro Ala Pro Tyr Leu Val Tyr Leu Lys Ser His
 21 26 31 36

ttc aac ccc tgt gtg ggc gtc ctc atc aaa ccc agc tgg gtg ctg gcc 197
 Phe Asn Pro Cys Val Gly Val Leu Ile Lys Pro Ser Trp Val Leu Ala
 37 42 47 52

cca gct cac tgc tat tta cca aat ctg aaa gtg atg ctg gga aat ttc 245
 Pro Ala His Cys Tyr Leu Pro Asn Leu Lys Val Met Leu Gly Asn Phe
 53 58 63 68

aag agc aga gtc aga gac ggt act gaa cag aca att aac ccc att cag	293
Lys Ser Arg Val Arg Asp Gly Thr Glu Gln Thr Ile Asn Pro Ile Gln	
69 74 79 84	
atc gtc cgc tac tgg aac tac agt cat agc gcc cca cag gat gac ctc	341
Ile Val Arg Tyr Trp Asn Tyr Ser His Ser Ala Pro Gln Asp Asp Leu	
85 90 95 100	
atg ctc atc aag ctg gct aag cct gcc atg ctc aat ccc aaa gtc cag	389
Met Leu Ile Lys Leu Ala Lys Pro Ala Met Leu Asn Pro Lys Val Gln	
101 106 111 116	
ccc ctt ccc ctc gcc acc acc aat gtc agg cca ggc act gtc tgt cta	437
Pro Leu Pro Leu Ala Thr Thr Asn Val Arg Pro Gly Thr Val Cys Leu	
117 122 127 132	
ctc tca ggt ttg gac tgg agc caa gaa aac agt ggc cga cac cct gac	485
Leu Ser Gly Leu Asp Trp Ser Gln Glu Asn Ser Gly Arg His Pro Asp	
133 138 143 148	
ttg cgg cag aac ctg gag gcc ccc gtg atg tct gat cga gaa tgc caa	533
Leu Arg Gln Asn Leu Glu Ala Pro Val Met Ser Asp Arg Glu Cys Gln	
149 154 159 164	
aaa aca gaa caa gga aaa agc cac agg aat tcc tta tgt gtg aaa ttt	581
Lys Thr Glu Gln Gly Lys Ser His Arg Asn Ser Leu Cys Val Lys Phe	
165 170 175 180	
gtg aaa gta ttc agc cga att ttt ggg gag gtg gcc gtt gct act gtc	629
Val Lys Val Phe Ser Arg Ile Phe Gly Glu Val Ala Val Ala Thr Val	
181 186 191 196	
atc tgc aaa gac aag ctc cag gga atc gag gtg ggg cac ttc atg gga	677
Ile Cys Lys Asp Lys Leu Gln Gly Ile Glu Val Gly His Phe Met Gly	
197 202 207 212	
ggg gac gtc ggc atc tac acc aat gtt tac aaa tat gta tcc tgg att	725
Gly Asp Val Gly Ile Tyr Thr Asn Val Tyr Lys Tyr Val Ser Trp Ile	
213 218 223 228	
gag aac act gct aag gac aag tga gaccctactt ctccctctgc attccactgg	779
Glu Asn Thr Ala Lys Asp Lys *	
229 234	
ctctgccatg gactatacaa gcagataatt ttccctctat tcaaaataaa atctccaaat	839
gaaaatttgg gaatgtagca tactagt	866

<210> 483

<211> 2472

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (44) ..(1771)

<400> 483

atttggccct cgaggccaag aattcggcac gagcactgta act atg gcc aca aag 55
Met Ala Thr Lys

1

aaa cat ttc tca att ata tta aat ctt ctg gga atg tta ctt aag aaa 103
Lys His Phe Ser Ile Ile Leu Asn Leu Leu Gly Met Leu Leu Lys Lys
5 10 15 20

gat aac cag gac acg agg aaa ctg tta atg act tgg gct ttg gaa gta 151
Asp Asn Gln Asp Thr Arg Lys Leu Leu Met Thr Trp Ala Leu Glu Val
21 26 31 36

gct gtt gta atg aag aag tcc gaa aca tat gca cct tta ttc tgt ctt 199
Ala Val Val Met Lys Lys Ser Glu Thr Tyr Ala Pro Leu Phe Cys Leu
37 42 47 52

ccg tct ttc cat aaa ttt tgc aaa ggc ctt tta gcc gac act ctc gtt 247
Pro Ser Phe His Lys Phe Cys Lys Gly Leu Leu Ala Asp Thr Leu Val
53 58 63 68

gaa gat gtg aat atc tgt ctg cag gca tgc agc agt cta cat gct cta 295
Glu Asp Val Asn Ile Cys Leu Gln Ala Cys Ser Ser Leu His Ala Leu
69 74 79 84

tcc tct tcc ttg cca gat gat ctt tta cag aga tgt gtt gat gtt tgc 343
Ser Ser Ser Leu Pro Asp Asp Leu Leu Gln Arg Cys Val Asp Val Cys
85 90 95 100

cgt gtc caa cta gtg cac cgt gga act tgt att cga caa gca ttt gga 391
Arg Val Gln Leu Val His Arg Gly Thr Cys Ile Arg Gln Ala Phe Gly
101 106 111 116

aaa ctg ttg aaa tca att cct tta ggt gtt ttc cta agc gat aac aat 439
Lys Leu Leu Lys Ser Ile Pro Leu Gly Val Phe Leu Ser Asp Asn Asn
117 122 127 132

cac aca gaa att caa gaa att tct tta gca tta aga agt cac atg agt 487
His Thr Glu Ile Gln Glu Ile Ser Leu Ala Leu Arg Ser His Met Ser
133 138 143 148

aaa gca cca agt aat aca ttc cac ccc caa gat ttc tct gat gtt att 535
Lys Ala Pro Ser Asn Thr Phe His Pro Gln Asp Phe Ser Asp Val Ile
149 154 159 164

agt ttt att ttg tat ggg aac tct cat aga aca ggg aag gac aat tgg 583
Ser Phe Ile Leu Tyr Gly Asn Ser His Arg Thr Gly Lys Asp Asn Trp
165 170 175 180

ttg gaa aga ctg ttc tat agc tgc cag aga ctg gat aag cgt gac cag 631
Leu Glu Arg Leu Phe Tyr Ser Cys Gln Arg Leu Asp Lys Arg Asp Gln
181 186 191 196

tca aca att cca cgc aat ctc ctg aag aca gat gct atc ctt tgg cag 679

Ser Thr Ile Pro Arg Asn Leu Leu Lys Thr Asp Ala Ile Leu Trp Gln	
197 202 207 212	
tgg gcc ata tgg gaa gct gca caa ttc act gtt ctt tct aag ctg aga	727
Trp Ala Ile Trp Glu Ala Ala Gln Phe Thr Val Leu Ser Lys Leu Arg	
213 218 223 228	
acc cca ctg ggc aga gct caa gac acc ttc cag aca att gaa ggt atc	775
Thr Pro Leu Gly Arg Ala Gln Asp Thr Phe Gln Thr Ile Glu Gly Ile	
229 234 239 244	
att cga agt ctc gca gct cac aca tta aac cct gat cag gat gtt agt	823
Ile Arg Ser Leu Ala Ala His Thr Leu Asn Pro Asp Gln Asp Val Ser	
245 250 255 260	
cag tgg aca act gca gac agt gat gaa ggc cat ggt aac aac caa ctt	871
Gln Trp Thr Thr Ala Asp Ser Asp Glu Gly His Gly Asn Asn Gln Leu	
261 266 271 276	
aga ctt gtt ctt ctt ctg cag tat ctg gaa tat ctg gag aaa tta atg	919
Arg Leu Val Leu Leu Leu Gln Tyr Leu Glu Tyr Leu Glu Lys Leu Met	
277 282 287 292	
tat aat gca tac gag gga tgt gct aat gcc tta act tca cct ccc aag	967
Tyr Asn Ala Tyr Glu Gly Cys Ala Asn Ala Leu Thr Ser Pro Pro Lys	
293 298 303 308	
gtc att aga act ttt ttg tat acc aat cgc caa act tgt cag gac tgg	1015
Val Ile Arg Thr Phe Leu Tyr Thr Asn Arg Gln Thr Cys Gln Asp Trp	
309 314 319 324	
cta acg cgg att cga ctc tcc atc atg agg gta gga ttg ttg gca ggc	1063
Leu Thr Arg Ile Arg Leu Ser Ile Met Arg Val Gly Leu Leu Ala Gly	
325 330 335 340	
cag cct gca gtg aca gtg aga cat ggc ttt gac ttg ctt aca gag atg	1111
Gln Pro Ala Val Thr Val Arg His Gly Phe Asp Leu Leu Thr Glu Met	
341 346 351 356	
aaa aca acc agc cta tct cag ggg aat gaa ttg gaa gta agc att atg	1159
Lys Thr Thr Ser Leu Ser Gln Gly Asn Glu Leu Glu Val Ser Ile Met	
357 362 367 372	
atg gtg gta gaa gca cta tgt gaa ctt cat tgt cct gaa gct ata cag	1207
Met Val Val Glu Ala Leu Cys Glu Leu His Cys Pro Glu Ala Ile Gln	
373 378 383 388	
gga att gct gtc tgg tca tca tct att gtt gga aaa cat ctt ctg tgg	1255
Gly Ile Ala Val Trp Ser Ser Ser Ile Val Gly Lys His Leu Leu Trp	
389 394 399 404	
att aac tca gtg gct caa cag gct gaa ggg agg ttt gaa aag gcc tct	1303
Ile Asn Ser Val Ala Gln Gln Ala Glu Gly Arg Phe Glu Lys Ala Ser	
405 410 415 420	
gtg gag tac cag gaa cac ctg tgt gcc atg aca ggt gtt gat tgc tgc	1351
Val Glu Tyr Gln Glu His Leu Cys Ala Met Thr Gly Val Asp Cys Cys	

421	426	431	436	
atc tcc agc ttt gac aaa tcg gtg ctc acc tta gcc agt gct ggg tgt				1399
Ile Ser Ser Phe Asp Lys Ser Val Leu Thr Leu Ala Ser Ala Gly Cys				
437	442	447	452	
aag agt gcc agc ctg aaa cat tgt ctg aat ggt gaa tcc aga aaa agt				1447
Lys Ser Ala Ser Leu Lys His Cys Leu Asn Gly Glu Ser Arg Lys Ser				
453	458	463	468	
gtg ctg tcc aaa ccg act gac tct tcc cct gag gtt ata aat tat tta				1495
Val Leu Ser Lys Pro Thr Asp Ser Ser Pro Glu Val Ile Asn Tyr Leu				
469	474	479	484	
gga aac aaa gca tgt gag tgc tac atc tca act gcc gat tgg gct gct				1543
Gly Asn Lys Ala Cys Glu Cys Tyr Ile Ser Thr Ala Asp Trp Ala Ala				
485	490	495	500	
gtg cag gaa tgg cag aac gct atc cat gac ttg aaa aag agt acc agt				1591
Val Gln Glu Trp Gln Asn Ala Ile His Asp Leu Lys Lys Ser Thr Ser				
501	506	511	516	
agc act tcc ctc aac ctg aaa gct gac ttc aac tat ata aaa tca tta				1639
Ser Thr Ser Leu Asn Leu Lys Ala Asp Phe Asn Tyr Ile Lys Ser Leu				
517	522	527	532	
agc agc ttt gag tct gga aaa ttt gtc gaa tgt acc gag caa tta gaa				1687
Ser Ser Phe Glu Ser Gly Lys Phe Val Glu Cys Thr Glu Gln Leu Glu				
533	538	543	548	
ttg tta cca gga gaa aat atc aat cta ctt gct gga gga tca aaa gaa				1735
Leu Leu Pro Gly Glu Asn Ile Asn Leu Leu Ala Gly Gly Ser Lys Glu				
549	554	559	564	
aaa ata gac atg aaa aaa ctg ctt cgt aac atg tga agtc cagatccaag				1785
Lys Ile Asp Met Lys Lys Leu Leu Arg Asn Met *				
565	570	575		
ggaacctcag aaatccattg aagttccatt gttaagaagt totgtttgtt tggcaactgc				1845
tttaaaccog atagaacaag atcagaagtg gcagtctata actgaaaatg tggtaaagta				1905
cttgaagcaa acatcccgca tcgctattgg acctctgaga ctttctactt taacagtttc				1965
acagtctttg ccagtttctaa gtaccttgca gctgtattgc tcgtctgctt tggagaccac				2025
agtttctaac agactttcaa cagaggactg tcttattcca ctcttcggcg aagctttacg				2085
ttcatgtaaa cagcatgacg tgaggccgtg gatgcaggca ttaaggtata ctgtgtacca				2145
gaatcagttg ttggagaaaa ttaaagttaa gtggttttcc tttttttttt ttgtaagaga				2205
aaattaaagg tggttttttt tttttaattt tgctttattg aggtttatat tacacattct				2265
aagtgtatgg tttgatgagt tctaacatgt cttcacttgt gtgaccacca atacgatcga				2325
gatacagaac agcgtcttac ccagaagggt tcccttgaga tcatctcttc atttgcccct				2385

gtcagcagtt actgatttgc tttctgtcac tatggattag acttgtcttt actaaagttt 2445

catgtacgtg aaatcattac caccaaaa 2472

<210> 484

<211> 1276

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (331)..(930)

<400> 484

acggactcct cggtcgacga tttcgtgtcc gtgttatatc atctggtctc attgataggc 60

gggatatgga gggggattcc agccccctg gaccggccgg aggtttattc tagagttact 120

ggcgggtagc tgtgcttttc tttcccgttt gtaggtgaaa cccattggc ttcattggct 180

ccttgattta aaccacgccc ggctttctgc cctctttgct gctgctgggc caggttgccc 240

agccatatcc cagccccgtc tgcagggagc cggaggetgc tgctgctgct atttgttgga 300

tgccgcgcgt gtcttctctt ctttccagag atg gct aac agg ggc ccg agc 351
Met Ala Asn Arg Gly Pro Ser
1 5

tat ggc tta agc cga gag gtg cag gag aag atc gag cag aag tat gat 399
Tyr Gly Leu Ser Arg Glu Val Gln Glu Lys Ile Glu Gln Lys Tyr Asp
8 13 18 23

gcg gac ctg gag aac aag ctg gtg gac tgg atc atc ctg cag tgc gcc 447
Ala Asp Leu Glu Asn Lys Leu Val Asp Trp Ile Ile Leu Gln Cys Ala
24 29 34 39

gag gac ata gag cac ccg ccc ccc ggc agg gcc cat ttt cag aaa tgg 495
Glu Asp Ile Glu His Pro Pro Pro Gly Arg Ala His Phe Gln Lys Trp
40 45 50 55

tta atg gac ggg acg gtc ctg tgc aag ctg ata aat agt tta tac cca 543
Leu Met Asp Gly Thr Val Leu Cys Lys Leu Ile Asn Ser Leu Tyr Pro
56 61 66 71

cca gga caa gag ccc ata ccc aag atc tca gag tca aag atg gct ttt 591
Pro Gly Gln Glu Pro Ile Pro Lys Ile Ser Glu Ser Lys Met Ala Phe
72 77 82 87

aag cag atg gag caa atc tcc cag ttc cta aaa gct gcg gag acc tat 639
Lys Gln Met Glu Gln Ile Ser Gln Phe Leu Lys Ala Ala Glu Thr Tyr
88 93 98 103

ggg gtc aga acc acc gac atc ttt cag acg gtg gat cta tgg gaa ggg 687

Gly Val Arg Thr Thr Asp Ile Phe Gln Thr Val Asp Leu Trp Glu Gly	
104 109 114 119	
aag gac atg gca gct gtg cag agg acc ctg atg gct tta ggc agc gtt	735
Lys Asp Met Ala Ala Val Gln Arg Thr Leu Met Ala Leu Gly Ser Val	
120 125 130 135	
gca gtc acc aag gat gat ggc tgc tat cgg gga gag cca tcc tgg ttt	783
Ala Val Thr Lys Asp Asp Gly Cys Tyr Arg Gly Glu Pro Ser Trp Phe	
136 141 146 151	
cac agg aaa gcc cag cag aat cgg aga ggc ttt tcc gag gag cag ctt	831
His Arg Lys Ala Gln Gln Asn Arg Arg Gly Phe Ser Glu Glu Gln Leu	
152 157 162 167	
cgc cag gga cag aac gta ata ggc ctg cag atg ggc agc aac aag gga	879
Arg Gln Gly Gln Asn Val Ile Gly Leu Gln Met Gly Ser Asn Lys Gly	
168 173 178 183	
gcc tcc cag gcg ggc atg aca ggg tac ggg atg ccc agg cag atc atg	927
Ala Ser Gln Ala Gly Met Thr Gly Tyr Gly Met Pro Arg Gln Ile Met	
184 189 194 199	
tag gacg cggcatcctg cccctggtag agaggacgaa tgttccacac catggtctct	984
* 200	
acgaaaaaga aatagttagt caccttctga ccttctcctc tttctcaaag ccttctgtcc	1044
ctgggtttttg caagtgtctgc atttccgccg agaatccgcg ttgcctactg ctgccacctc	1104
ctgttcattt agaactatgc aaagactccg cttccgtttt cctgagctcc tcgggccccca	1164
gagtctctgt ttgattattt atttatttat ttatttat ttgcaaaaatt ctctctttca	1224
acttatagaa tgcacctaat aaagtaatta gtcttgtgtc aaaaaaaaaa aa	1276

<210> 485
 <211> 1826
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (755)..(1726)

<400> 485	
ccggtcagga attctcgggg cgaccacgc gtccgctgat gcttgggtgca ggattgcttc	60
caataccgac cccaaatcct ttgactactc ttgggtgtttc acttagcagt ttgggagcta	120
taccagcagc agcactagac cccaacattg caacacttgg agagatacca cagccaccac	180
ttatgggaaa cgtggatcct tccaaaatag atgaaattag gagaacgggtt tatgttggaa	240

atctgaattc ccagacaacg acagctgac	aactacttga attttttaaa caagttggag	300
aagtgaagtt tgtgcggatg gcaggtgatg	agactcagcc aactcggttt gcttttgtgg	360
aatttgcaga ccaaaattct gtaccaagg	cccttgcttt taatggagtt atgtttggag	420
acaggccact gaaaataaat cactccaaca	atgcaatagt aaaaccccct gagatgacac	480
ctcaggctgc agctaaggag ttagaagaag	taatgaagcg agtacgagaa gctcagtcac	540
ttatctcagc agctattgaa ccagggtggc	tgcactcaac gagtttatgc aatgactttc	600
ttggatgttt ctgaaggagg aggatgtaca	gagagtaggc cccttgactc atatgtggta	660
cattccactt gtgcctgatt attaaactggg	atctttaatt gttctgagct tacactgcaa	720
agtgattttt tctcccaga gtctggaaag	agca atg aaa gaa aag gcg gtc	772
	Met Lys Glu Lys Ala Val	
	1	
gat ctc gtt ccc ata ctc gct caa aat	cca ggt cta gct caa aat ccc	820
Asp Leu Val Pro Ile Leu Ala Gln Asn	Pro Gly Leu Ala Gln Asn Pro	
7	12 17 22	
att cta gaa gga aaa gat cac aat caa	aac aca gga gta gat ccc ata	868
Ile Leu Glu Gly Lys Asp His Asn Gln	Asn Thr Gly Val Asp Pro Ile	
23	28 33 38	
ata gat cac gtt caa gac aga aag aca	gac gta gat cta aga gcc cac	916
Ile Asp His Val Gln Asp Arg Lys Thr	Asp Val Asp Leu Arg Ala His	
39	44 49 54	
ata aaa aac gct cta aat caa ggg gag	aga cgg aag tca agg agt cgt	964
Ile Lys Asn Ala Leu Asn Gln Gly Glu	Arg Arg Lys Ser Arg Ser Arg	
55	60 65 70	
tcg cat tca cgg gac aag aga aaa gac	act cga gaa aag atc aag gaa	1012
Ser His Ser Arg Asp Lys Arg Lys Asp	Thr Arg Glu Lys Ile Lys Glu	
71	76 81 86	
aag gaa aga gtg aaa gag aaa gac agg	gaa aag gag aga gag agg gaa	1060
Lys Glu Arg Val Lys Glu Lys Asp Arg	Glu Lys Glu Arg Glu Arg Glu	
87	92 97 102	
aag gaa cgt gaa aaa gaa aag gaa cgg	ggt aaa aac aaa gac cgg gac	1108
Lys Glu Arg Glu Lys Glu Lys Glu Arg	Gly Lys Asn Lys Asp Arg Asp	
103	108 113 118	
aag gaa cgg gaa aag gac cgg gaa aaa	gac aag gaa aag gac aga gag	1156
Lys Glu Arg Glu Lys Asp Arg Glu Lys	Asp Lys Glu Lys Asp Arg Glu	
119	124 129 134	
aga gaa cgg gaa aaa gag cat gag aag	gat cga gac aaa gag aag gaa	1204
Arg Glu Arg Glu Lys Glu His Glu Lys	Asp Arg Asp Lys Glu Lys Glu	
135	140 145 150	

aag gaa cag gac aaa gaa aag gaa cga gaa aaa gac aga tcc aaa gag	1252
Lys Glu Gln Asp Lys Glu Lys Glu Arg Glu Lys Asp Arg Ser Lys Glu	
151 156 161 166	
ata gat gaa aaa aga aag aag gat aaa aaa tcc aga aca cca ccc agg	1300
Ile Asp Glu Lys Arg Lys Lys Asp Lys Lys Ser Arg Thr Pro Pro Arg	
167 172 177 182	
agt tac aat gca tcg cga aga tct cgt agt tcc agc agg gaa agg cgt	1348
Ser Tyr Asn Ala Ser Arg Arg Ser Arg Ser Ser Arg Glu Arg Arg	
183 188 193 198	
agg agg agg agc agg agt tct tcc aga tcg cca aga aca tca aaa acc	1396
Arg Arg Arg Ser Arg Ser Ser Ser Arg Ser Pro Arg Thr Ser Lys Thr	
199 204 209 214	
ata aaa agg aaa tct tct aga tct ccg tcc ccc agg aga aat aag aag	1444
Ile Lys Arg Lys Ser Ser Arg Ser Pro Ser Pro Arg Arg Asn Lys Lys	
215 220 225 230	
gat aaa aag aga gaa aaa gaa agg gac cac atc agt gaa aga aga gag	1492
Asp Lys Lys Arg Glu Lys Glu Arg Asp His Ile Ser Glu Arg Arg Glu	
231 236 241 246	
aga gaa cgt tca acg tct atg aga aag agt tct aat gat aga gat ggg	1540
Arg Glu Arg Ser Thr Ser Met Arg Lys Ser Ser Asn Asp Arg Asp Gly	
247 252 257 262	
aag gag aag ttg gag aag aac agt act tca ctt aaa gag aaa gag cac	1588
Lys Glu Lys Leu Glu Lys Asn Ser Thr Ser Leu Lys Glu Lys Glu His	
263 268 273 278	
aat aaa gaa cca gat tca agt gtg agc aaa gaa gta gat gac aag gat	1636
Asn Lys Glu Pro Asp Ser Ser Val Ser Lys Glu Val Asp Asp Lys Asp	
279 284 289 294	
gca cca agg act gag gaa aac aaa ata cag cac aat ggg aat tgt cag	1684
Ala Pro Arg Thr Glu Glu Asn Lys Ile Gln His Asn Gly Asn Cys Gln	
295 300 305 310	
ctg aat gaa gaa aac ctc tct acc aaa aca gaa gca gta tag gaccgac	1733
Leu Asn Glu Glu Asn Leu Ser Thr Lys Thr Glu Ala Val *	
311 316 321	
aagtgtacct ctgcactcaa tgctggaatc aaatccaaag cttttaattc totcaacaag	1793
atgtaaacag gaaagaaatc tagttgagca tga	1826

<210> 486
 <211> 632
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (67)..(486)

<400> 486

```
atttggccct cgaggccaag aattcggcac gagcaattcc gaagagctgc ccagaaggag      60
agaaca  atg tca tca cta ccc gta cca tac aca ctg cct gtt tcc ttg      108
      Met Ser Ser Leu Pro Val Pro Tyr Thr Leu Pro Val Ser Leu
      1          5          10
cct gtt ggt tgc tgc gtg ata atc aca ggg aca ccg atc ctc act ttt      156
Pro Val Gly Ser Cys Val Ile Ile Thr Gly Thr Pro Ile Leu Thr Phe
15          20          25          30
gtc aag gac cca cag ctg gag gtg aat ttc tac act ggg atg gat gag      204
Val Lys Asp Pro Gln Leu Glu Val Asn Phe Tyr Thr Gly Met Asp Glu
31          36          41          46
gac tca gat att gct ttc caa ttc cga ctg cac ttt ggt cat cct gca      252
Asp Ser Asp Ile Ala Phe Gln Phe Arg Leu His Phe Gly His Pro Ala
47          52          57          62
atc atg aac agt tgt gtg ttt ggc ata tgg aga tat gag gag aaa tgc      300
Ile Met Asn Ser Cys Val Phe Gly Ile Trp Arg Tyr Glu Glu Lys Cys
63          68          73          78
tac tat tta ccc ttt gaa gat ggc aaa cca ttt gag ctg tgc atc tat      348
Tyr Tyr Leu Pro Phe Glu Asp Gly Lys Pro Phe Glu Leu Cys Ile Tyr
79          84          89          94
gtg cgt cac aag gaa tac aag gta atg gta aat ggc caa cgc att tac      396
Val Arg His Lys Glu Tyr Lys Val Met Val Asn Gly Gln Arg Ile Tyr
95          100          105          110
aac ttt gcc cat cga ttc ccg cca gca tct gtg aag atg ctg caa gtc      444
Asn Phe Ala His Arg Phe Pro Pro Ala Ser Val Lys Met Leu Gln Val
111          116          121          126
ttg aga gat atc tcc ctg acc aga gtg ctt atc agc gat tga gggagat      493
Leu Arg Asp Ile Ser Leu Thr Arg Val Leu Ile Ser Asp *
127          132          137
gatcagactc ctcatgttg aggaatccct ctttctacct gaccatggga ttcccagagc      553
ctactaacag aataatccct cctcaccctt tcccctacac ttgatcatta aaacagcacc      613
aaacctcaaa aaaaaaaaaa      632
```

<210> 487

<211> 2102

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (309)..(1283)

<400> 487

attgaacgcc tgatgtaccg gtccggaatt cccgggtcga cccacgcgtc cggggggagg	60
cgcgtcgcga ggcgagcgtc ctccttttgt gcgagcgccg gcggctcggc ttctcgaagg	120
agaagaaact gaggcctgga atttgattaa ctcattcaag gttaccagtg tggttaattca	180
tttgcacacc tgttagcaag aaacagaagt tgaaggactg gaacaagtga actaggaaag	240
agggaaacgcc aatccaagga tagaaggaca aggacagaat caccagcact ggctgaaggt	300
acottaac atg ggg aat ctt ctt aaa gtt ttg aca tgc aca gac ctt gag	350
Met Gly Asn Leu Leu Lys Val Leu Thr Cys Thr Asp Leu Glu	
1 5 10	
cag ggg cca aat ttt ttc ctt gat ttt gaa aat gcc cag cct aca gag	398
Gln Gly Pro Asn Phe Phe Leu Asp Phe Glu Asn Ala Gln Pro Thr Glu	
15 20 25 30	
tct gag aag gaa att tat aat cag gtg aat gta gta tta aaa gat gca	446
Ser Glu Lys Glu Ile Tyr Asn Gln Val Asn Val Val Leu Lys Asp Ala	
31 36 41 46	
gaa ggc atc ttg gag gac ttg cag tca tac aga gga gct ggc cac gaa	494
Glu Gly Ile Leu Glu Asp Leu Gln Ser Tyr Arg Gly Ala Gly His Glu	
47 52 57 62	
ata cga gag gca atc cag cat cca gca gat gag aag ttg caa gag aag	542
Ile Arg Glu Ala Ile Gln His Pro Ala Asp Glu Lys Leu Gln Glu Lys	
63 68 73 78	
gca tgg ggt gca gtt gtt cca cta gta ggc aaa tta aag aaa ttt tac	590
Ala Trp Gly Ala Val Val Pro Leu Val Gly Lys Leu Lys Lys Phe Tyr	
79 84 89 94	
gaa ttt tct cag agg tta gaa gca gca tta aga ggt ctt ctg gga gcc	638
Glu Phe Ser Gln Arg Leu Glu Ala Ala Leu Arg Gly Leu Leu Gly Ala	
95 100 105 110	
tta aca agt acc cca tat tct ccc acc cag cat cta gag cga gag cag	686
Leu Thr Ser Thr Pro Tyr Ser Pro Thr Gln His Leu Glu Arg Glu Gln	
111 116 121 126	
gct ctt gct aaa cag ttt gca gaa att ctt cat ttc aca ctc cgg ttt	734
Ala Leu Ala Lys Gln Phe Ala Glu Ile Leu His Phe Thr Leu Arg Phe	
127 132 137 142	
gat gaa ctc aag atg aca aat cct gcc ata cag aat gat ttc agc tat	782
Asp Glu Leu Lys Met Thr Asn Pro Ala Ile Gln Asn Asp Phe Ser Tyr	
143 148 153 158	
tat aga aga aca ttg agt cgt atg agg att aac aat gta ccg gca gaa	830
Tyr Arg Arg Thr Leu Ser Arg Met Arg Ile Asn Asn Val Pro Ala Glu	
159 164 169 174	

gga gaa aat gaa gta aat aat gaa ttg gca aat cga atg tct ttg ttt	878
Gly Glu Asn Glu Val Asn Asn Glu Leu Ala Asn Arg Met Ser Leu Phe	
175 180 185 190	
tat gct gag gca act cca atg ctg aaa acc ttg agt gat gcc aca aca	926
Tyr Ala Glu Ala Thr Pro Met Leu Lys Thr Leu Ser Asp Ala Thr Thr	
191 196 201 206	
aaa ttt gta tca gag aat aaa aat tta cca ata gaa aat acc aca gat	974
Lys Phe Val Ser Glu Asn Lys Asn Leu Pro Ile Glu Asn Thr Thr Asp	
207 212 217 222	
tgt tta agc aca atg gct agt gta tgc aga gtc atg ctg gaa aca ccg	1022
Cys Leu Ser Thr Met Ala Ser Val Cys Arg Val Met Leu Glu Thr Pro	
223 228 233 238	
gaa tac aga agc aga ttt aca aat gaa gag aca gtg tca ttc tgc ttg	1070
Glu Tyr Arg Ser Arg Phe Thr Asn Glu Glu Thr Val Ser Phe Cys Leu	
239 244 249 254	
agg gta atg gtg ggt gtc ata ata ctc tat gac cac gta cat cca gtg	1118
Arg Val Met Val Gly Val Ile Ile Leu Tyr Asp His Val His Pro Val	
255 260 265 270	
gga gca ttt gct aaa act tcc aaa att gat atg aaa ggt tgt atc aaa	1166
Gly Ala Phe Ala Lys Thr Ser Lys Ile Asp Met Lys Gly Cys Ile Lys	
271 276 281 286	
gtt ctt aag gac caa cct cct aat agt gtg gaa ggt ctt cta aat gct	1214
Val Leu Lys Asp Gln Pro Pro Asn Ser Val Glu Gly Leu Leu Asn Ala	
287 292 297 302	
ctc agg tac aca aca aaa cat ttg aat gat gag act acc tcc aag caa	1262
Leu Arg Tyr Thr Thr Lys His Leu Asn Asp Glu Thr Thr Ser Lys Gln	
303 308 313 318	
att aaa tcc atg ctg caa taa ca attctggaat aagcacctgc tgtagacaga	1315
Ile Lys Ser Met Leu Gln *	
319 324	
agacagtatt ctgcaatgac tgagaatgca gtttttttagt gattgcaatt actatctcat	1375
ttattcttgc ttttatttct ttctctgtt cctcttccct cttttttaat catgttctta	1435
agacttcttt tctgtgccaa aatcagtaaa gttacactct gaagggatat catcctttca	1495
aacggggccat ctaaggcagc taattatgca ttgcattggg gtctctactg agaaaaattc	1555
tgtgacttga actaaatatt tttaaagtgt gattttttttt gaaactaata tttaatatgt	1615
cttctctgc atggcaaaac tgcctattct gctattttaa aacctcaat gactttattt	1675
tctactgccg cttttttcat gtgcaaccaa aatgaaaatg tttaaattaa ctgtgttgta	1735
caaatggtac ccaacacaaa ctttttttaa attagtaata cttttgttta aagttttaag	1795

ttgcatTTTT gactTTTTTT gtaaggatgt atgttgtgtg tttAACCTTT attaactaac 1855
 gttaaaagct gtgatgtgtg cgtagaatat tacgtatgca tgttcATGTC taaagaatgg 1915
 ctgttgatga taaaataaaa atcagctttc atttttctaa aaaagtcaaa atgcaaaactt 1975
 aaaactttta acaaaaagtat tactaattta aaaaaagttt gtgttgggta ccgtcgacgc 2035
 ggccgcaagt ttagtagtag tagtcgaccc ggaattccg gaccggtacc tgcaggcgta 2095
 ccagctt 2102

<210> 488
 <211> 1925
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (755)..(1585)

<400> 488
 aattgaacgt gtgaggcacc ggtccggaat tcccggtcg acccagcgt ccgccacttc 60
 ctgttgtgtc acacttgctt gcagtaacat gctgtaaggt ttgtggcata ggagcagtgg 120
 gccataccat ataatcaagg tgtcacatcc cgggtgctgg acatgccctc ttgggcttgg 180
 cagatgccag tggatccata caactgctcc gcttgggtga atctgaggtc agtgacttgc 240
 acttgttctg tggggcagaa gggacctgaa tagagagggg tggggaggag gctgtgctga 300
 tacagacatt tttctaaaac gatctctctt caatggtgag ctatatataa acgttctaag 360
 ataatgtgga gtctatTTTT aagttgtatt gcgttctaca tccaactcca agaggaagtc 420
 acctcatgtg tcaccagcag aagggtgaa gtgacaggat gttcattgac ctgtcagtgg 480
 atctgaaagt tctctaagga gagcctgggc aagcattctt aggttgatgc tggggcccag 540
 agtagcagtg agcatcctgt gtgaagatgg catttctcac tgattattgg aaaagcacta 600
 gaagagccac gtgctggagc cattgtccag ccttgccctg gaggagcagt gtctggcttt 660
 gtccttagat tgggtccactg ggaaaactgg aagggccggg gaccagccct tgaagatcat 720
 cagcagtgac tccacagggc agtccacct cctg atg gtg aat gag acg agg 772
 Met Val Asn Glu Thr Arg
 1
 ccc agg ctg cag aaa gtg gcc tca tgg cag gca cat caa ttc gag gcc 820
 Pro Arg Leu Gln Lys Val Ala Ser Trp Gln Ala His Gln Phe Glu Ala
 7 12 17 22

tgg att gct gct ttc aat tac tgg cat cca gaa att gtg tat tca ggg	868
Trp Ile Ala Ala Phe Asn Tyr Trp His Pro Glu Ile Val Tyr Ser Gly	
23 28 33 38	
ggc gac gat ggc ctt ctg agg ggc tgg gac acc agg gta ccc ggc aaa	916
Gly Asp Asp Gly Leu Leu Arg Gly Trp Asp Thr Arg Val Pro Gly Lys	
39 44 49 54	
ttt ctc ttc acc agc aaa aga cac acc atg ggt gtg tgc agc atc cag	964
Phe Leu Phe Thr Ser Lys Arg His Thr Met Gly Val Cys Ser Ile Gln	
55 60 65 70	
agc agc cct cat cgg gag cac atc ctg gcc acg gga agc tat gat gaa	1012
Ser Ser Pro His Arg Glu His Ile Leu Ala Thr Gly Ser Tyr Asp Glu	
71 76 81 86	
cac atc cta ctg tgg gac aca cga aac atg aag cag ccg ttg gca gat	1060
His Ile Leu Leu Trp Asp Thr Arg Asn Met Lys Gln Pro Leu Ala Asp	
87 92 97 102	
acg cct gtg cag ggt ggg gta tgg aga atc aag tgg cac cct ttc cac	1108
Thr Pro Val Gln Gly Gly Val Trp Arg Ile Lys Trp His Pro Phe His	
103 108 113 118	
cac cac ctg ctc ctg gcc gcc tgc atg cac agt ggc ttt aag atc ctc	1156
His His Leu Leu Leu Ala Ala Cys Met His Ser Gly Phe Lys Ile Leu	
119 124 129 134	
aac tgc caa aag gca atg gag gag agg cag gag gcg acg gtc ctg aca	1204
Asn Cys Gln Lys Ala Met Glu Glu Arg Gln Glu Ala Thr Val Leu Thr	
135 140 145 150	
tct cac aca ttg ccc gac tcg ctg gtg tat gga gcc gac tgg tcc tgg	1252
Ser His Thr Leu Pro Asp Ser Leu Val Tyr Gly Ala Asp Trp Ser Trp	
151 156 161 166	
ctg ctc ttc cgt tct ctg cag cgg gcc ccc tcg tgg tcc ttt cct agc	1300
Leu Leu Phe Arg Ser Leu Gln Arg Ala Pro Ser Trp Ser Phe Pro Ser	
167 172 177 182	
aac cta gga acc aag acg gca gac ctg aag ggt gca agc gag ttg cca	1348
Asn Leu Gly Thr Lys Thr Ala Asp Leu Lys Gly Ala Ser Glu Leu Pro	
183 188 193 198	
aca ccc tgt cat gaa tgc aga gag gat aac gat ggg gag ggc cat gcc	1396
Thr Pro Cys His Glu Cys Arg Glu Asp Asn Asp Gly Glu Gly His Ala	
199 204 209 214	
aga ccc cag agt gga atg aag cca ctc aca gag ggc atg agg aag aat	1444
Arg Pro Gln Ser Gly Met Lys Pro Leu Thr Glu Gly Met Arg Lys Asn	
215 220 225 230	
ggc acc tgg ctg cag gct aca gca gcc acc aca cgt gac tgt ggc gtg	1492
Gly Thr Trp Leu Gln Ala Thr Ala Ala Thr Thr Arg Asp Cys Gly Val	
231 236 241 246	
aac cca gaa gaa gca gac tca gcc ttc agc ctc ctg gcc acc tgc tcc	1540

Asn	Pro	Glu	Glu	Ala	Asp	Ser	Ala	Phe	Ser	Leu	Leu	Ala	Thr	Cys	Ser	
247					252					257					262	
ttc tat gac cat gcg ctc cac ctc tgg gag tgg gag ggg aac tga gct																1588
Phe Tyr Asp His Ala Leu His Leu Trp Glu Trp Glu Gly Asn *																
263					268					273						
tgaaatcatg aagcccccttc ccacaaggaa accaggaggg agactgcgag tgagtgcccg																1648
ggaccacctc atcagagatg cttactgcag cctgcaggt gcctgtgcac tgatggaatc																1708
cacagtgtag tcagaaaagc tgttgacttc tcttaaatca gcttccctgc tgggccctg																1768
aaagtggact ggggtgattct gtctggcaga gagtggggaa aagacgcggt ttccagcttg																1828
cagatttggt aagtttctca ggcagatttt gactttcagc ctttcatact tgtttaagca																1888
actatttgta ttaaatgaag ttttttgaaa aaaaaaa																1925

<210> 489
 <211> 1596
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (42)..(542)

 <220>
 <221> misc_feature
 <222> (1)...(1596)
 <223> n = a,t,c or g

<400> 489																
atttggccct cgaggccaag aattcggcac gagcgactcc c																
														atg cat cgg cta	53	
														Met His Arg Leu		
1																
ata gcc cgg aga caa gct gaa gca aat aag caa cat gta aga tgt cag																101
Ile Ala Arg Arg Gln Ala Glu Ala Asn Lys Gln His Val Arg Cys Gln																
5					10					15					20	
aaa tgc ttg gaa ttt gga cat tgg act tat gaa tgc aca gga aaa aga																149
Lys Cys Leu Glu Phe Gly His Trp Thr Tyr Glu Cys Thr Gly Lys Arg																
21					26					31					36	
aaa tac cta cat agg ccc tca agg aca gca gaa cta aag aaa gct tta																197
Lys Tyr Leu His Arg Pro Ser Arg Thr Ala Glu Leu Lys Lys Ala Leu																
37					42					47					52	
aaa gaa aaa gaa aac aga tta tta ttg caa caa agc att gga gaa acc																245
Lys Glu Lys Glu Asn Arg Leu Leu Leu Gln Gln Ser Ile Gly Glu Thr																
53					58					63					68	

aat gta gaa aga aag gcc aag aaa aaa agg tct aag agt gta acc agt	293
Asn Val Glu Arg Lys Ala Lys Lys Lys Arg Ser Lys Ser Val Thr Ser	
69 74 79 84	
tcc agt agc agt agc agt gac agt tct gcc agt gat tct tca tca gag	341
Ser Ser Ser Ser Ser Ser Asp Ser Ser Ala Ser Asp Ser Ser Ser Glu	
85 90 95 100	
agt gaa gaa aca tct acc tct tcc tcc tca gag gac agt gac act gat	389
Ser Glu Glu Thr Ser Thr Ser Ser Ser Ser Glu Asp Ser Asp Thr Asp	
101 106 111 116	
gaa agc tcc tct agt tcc tca tcc tca gcc tcc tcc aca acc tct tcc	437
Glu Ser Ser Ser Ser Ser Ser Ser Ser Ala Ser Ser Thr Thr Ser Ser	
117 122 127 132	
tcc tcc tct gat tca gac tca gat tcc agc tct tcc agt agc agt agc	485
Ser Ser Ser Asp Ser Asp Ser Asp Ser Ser Ser Ser Ser Ser Ser	
133 138 143 148	
acc agc aca gat agc agc tct gac gat gaa cca cca aag aag aag aaa	533
Thr Ser Thr Asp Ser Ser Ser Asp Asp Glu Pro Pro Lys Lys Lys Lys	
149 154 159 164	
aag aaa tag agttgct ccattcatat tggaccgatg gactgaaaac attgatgtga	589
Lys Lys *	
165	
ttcttgaaag ggaatttaga atatgttaag gccaaagtagg ttaactgggtg aacatttcta	649
gaattcaaaa gtttctaaat gttttacatt gtaagagcat agagaatatt aataatggct	709
tatagagaga gacttttatt tgaagggtga atcttgtttt ttttatcttt aaaatatatc	769
tctagaactt aaagctgaaa tctgcaaatac tgtttggtgtg atgaaactat cttttctctc	829
tgtgaaataa atgccatact ttgttatata tgtagtggt atgtatcaga catattttca	889
ggatgggtgcg tcaggatatc tggcagtgga tttctaatagc ttttggtgt atgttatgta	949
agatttaata tggtgttact gtaagcttag gagttttcct actattaata aatgtgctct	1009
atttttacat ttatgttcag aaagttatct gactttttgt cctaagtggt atgttcaagg	1069
agcctattaa tatatttata gtttttgaat gctgtaagtt tcaaattgct gtgttacgtc	1129
attcattttc ttctgggttcc ttaagttttt caagttatcc ttttctgagg aaaattatc	1189
tagaggaacc taaaaagggg caaaaaaatt gaaacttctt aggagtctaa tcttggtgcc	1249
ttctgttaaa agtcagtgtg tcagaaaaga aagcagccat gtaagaggct aacttaagta	1309
gaagtgctag aaatatcttt gtgtattaac atgcaataaa aggtaccatt caaagacagg	1369
gggaaaggta ggaagaagag gtaattttta cttgaaaatt agggcatggt ggctgccatt	1429
ttattaaaag ctttttttta agcttttcat aaagattgcc tttttgctat tttntgaaa	1489

tttgggtatt nataggtttg gtagggtnac ccggtccaat natgacagtn ctactgnctt 1549
aatataggag actaggggtg aaccaggtgt gttttacata ggggttg 1596

<210> 490
<211> 1553
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (135)..(821)

<400> 490
aattgctgct cgcgtacgtc agcttggatc ctctagagcg gccgccacct ctccccagcc 60
caggagagggc tgcggagccg cagccgcca gaccgcgcag cgcgggagggc aggttccgca 120
cgaaataaat caga atg agt tat gca gaa aaa ccc gat gaa atc acg aaa 170
Met Ser Tyr Ala Glu Lys Pro Asp Glu Ile Thr Lys
1 5 10
gat gag tgg atg gaa aag ctc aat aac ttg cat gtc cag aga gca gac 218
Asp Glu Trp Met Glu Lys Leu Asn Asn Leu His Val Gln Arg Ala Asp
13 18 23 28
atg aac cgc ctc atc atg aac tac ctg gtc aca gag ggc ttt aag gaa 266
Met Asn Arg Leu Ile Met Asn Tyr Leu Val Thr Glu Gly Phe Lys Glu
29 34 39 44
gca gcg gag aag ttt cga atg gaa tct gga atc gaa cct agt gtg gat 314
Ala Ala Glu Lys Phe Arg Met Glu Ser Gly Ile Glu Pro Ser Val Asp
45 50 55 60
ctg gaa aca ctt gat gaa cga atc aag atc cgg gag atg ata ctg aaa 362
Leu Glu Thr Leu Asp Glu Arg Ile Lys Ile Arg Glu Met Ile Leu Lys
61 66 71 76
ggg cag att cag gag gcc atc gcc ttg atc aac agc ctc cac cca gag 410
Gly Gln Ile Gln Glu Ala Ile Ala Leu Ile Asn Ser Leu His Pro Glu
77 82 87 92
ctc ttg gac aca aac cgg tat ctt tac ttc cat ttg cag caa cag cat 458
Leu Leu Asp Thr Asn Arg Tyr Leu Tyr Phe His Leu Gln Gln Gln His
93 98 103 108
ttg atc gag ctg atc cgc cag cgg gag aca gag gcg gcg ctg gag ttt 506
Leu Ile Glu Leu Ile Arg Gln Arg Glu Thr Glu Ala Ala Leu Glu Phe
109 114 119 124
gca cag act cag ctg gcg gag cag ggc gag gag agc cga gag tgc ctc 554
Ala Gln Thr Gln Leu Ala Glu Gln Gly Glu Glu Ser Arg Glu Cys Leu
125 130 135 140

aca gag atg gag cgt acc ctg gca ctg ctg gcc ttt gac agt ccc gag	602
Thr Glu Met Glu Arg Thr Leu Ala Leu Leu Ala Phe Asp Ser Pro Glu	
141 146 151 156	
gag tcg ccc ttc gga gac ctc ctc cac acc atg cag agg cag aag gtg	650
Glu Ser Pro Phe Gly Asp Leu Leu His Thr Met Gln Arg Gln Lys Val	
157 162 167 172	
tgg agt gaa gtt aac caa gct gtg cta gat tat gaa aat cgc gag tca	698
Trp Ser Glu Val Asn Gln Ala Val Leu Asp Tyr Glu Asn Arg Glu Ser	
173 178 183 188	
aca ccc aaa ctg gca aaa tta ctg aaa cta cta ctt tgg gct cag aac	746
Thr Pro Lys Leu Ala Lys Leu Leu Lys Leu Leu Leu Trp Ala Gln Asn	
189 194 199 204	
gag ctg gac cag aag aaa gta aaa tat ccc aaa atg aca gac ctc agc	794
Glu Leu Asp Gln Lys Lys Val Lys Tyr Pro Lys Met Thr Asp Leu Ser	
205 210 215 220	
aag ggt gtg att gag gag ccc aag tag cgcct gcgcttgctt ggtggatcca	846
Lys Gly Val Ile Glu Glu Pro Lys *	
221 226	
acaccagccc tgcgtcgtgg gacttgccctc agatcagcct gcgactgcaa gattccttact	906
gcagtagaga actctttttc tcccttggtac ttttttttga cctggcatct ttttataggg	966
aaaaatggcc tttgtaggca gtggaaaact tgcaaggaaa gctgccgtct cttttggcag	1026
tcttgatgca gagcctgcac tctggcactc gctgaagaat ctggaagggtt gcggtttgct	1086
cttccagtgt tcgggggcct ctggctgctg aaggattcgg tctaccacgg agggctgtgc	1146
tgttaggctg catccactc aaaatacagg aaaagcacga atcatgattc tgctttctgt	1206
tagcttaggc agacattggg ccttcaccta caagtttttc cttaccocctg tggtttttgt	1266
gttttttttt ttttcttttt ccataggaaa gaatatataa atttgtaaat cctaattcaa	1326
agatggctca tgtgtgaggg cattgagttt gatttgtttt ccctttgggc tgggttggtg	1386
ggcttttggg ggatgcgtgt gagggggcta tgtgtttttt aattttttta atatatattt	1446
tggtgctgtg tgtggaaga gacttgttcc tagtggatca atgaaccatc tcttctgggc	1506
agttttgttg aaaataaagg tttctctttg atttcaaaaa aaaaaaa	1553

<210> 491
 <211> 4964
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (167)..(2452)

<400> 491
 tttgatagcc tgtcgcatgc gctaccggtc cggaattccc gggtcgacga tttcgtgccg 60
 gtcagccgca gacactcacc cagctccgcg agctcagccg ctcagcgagt ggggtagcgg 120
 ggaccgagac ggacggtagc cgtgccagag cccggggcgc tctcgg atg cgg cag 175
 Met Arg Gln
 1
 gac aag ctg acc ggg tct ctg agg cgc ggg ggg aga tgc ctg aag cgg 223
 Asp Lys Leu Thr Gly Ser Leu Arg Arg Gly Gly Arg Cys Leu Lys Arg
 4 9 14 19
 cag ggc ggc ggc gtg ggc acc atc ctg agc aat gtg ctc aag aag cgc 271
 Gln Gly Gly Gly Val Gly Thr Ile Leu Ser Asn Val Leu Lys Lys Arg
 20 25 30 35
 agc tgc att tcc cgg acc gcg ccc cgg ctg ctg tgc acc ctg gag ccg 319
 Ser Cys Ile Ser Arg Thr Ala Pro Arg Leu Leu Cys Thr Leu Glu Pro
 36 41 46 51
 gga gtt gat acc aag ttg aaa ttc act ctt gag cca tct tta ggt caa 367
 Gly Val Asp Thr Lys Leu Lys Phe Thr Leu Glu Pro Ser Leu Gly Gln
 52 57 62 67
 aat ggt ttt cag cag tgg tac gat gct ctc aag gca gtt gcc agg cta 415
 Asn Gly Phe Gln Gln Trp Tyr Asp Ala Leu Lys Ala Val Ala Arg Leu
 68 73 78 83
 tcc aca gga ata cca aag gaa tgg agg aga aag gtt tgg ttg acc ttg 463
 Ser Thr Gly Ile Pro Lys Glu Trp Arg Arg Lys Val Trp Leu Thr Leu
 84 89 94 99
 gca gat cat tat ttg cac agt ata gcc att gac tgg gac aaa acc atg 511
 Ala Asp His Tyr Leu His Ser Ile Ala Ile Asp Trp Asp Lys Thr Met
 100 105 110 115
 cgc ttc act ttc aat gaa agg agt aat cct gat gat gac tcc atg gga 559
 Arg Phe Thr Phe Asn Glu Arg Ser Asn Pro Asp Asp Asp Ser Met Gly
 116 121 126 131
 att cag ata gtc aag gac ctt cac cgc aca ggc tgt agt tct tac tgt 607
 Ile Gln Ile Val Lys Asp Leu His Arg Thr Gly Cys Ser Ser Tyr Cys
 132 137 142 147
 ggc cag gag gct gag cag gac agg gtt gtg ttg aag cgg gtg ctg ctg 655
 Gly Gln Glu Ala Glu Gln Asp Arg Val Val Leu Lys Arg Val Leu Leu
 148 153 158 163
 gcc tat gcc cga tgg aac aaa act gtt ggg tac tgc caa ggc ttt aac 703
 Ala Tyr Ala Arg Trp Asn Lys Thr Val Gly Tyr Cys Gln Gly Phe Asn
 164 169 174 179

atc ctg gct gca cta att ctg gaa gtg atg gaa ggc aat gaa ggg gat	751
Ile Leu Ala Ala Leu Ile Leu Glu Val Met Glu Gly Asn Glu Gly Asp	
180 185 190 195	
gcc ctg aaa att atg att tac ctt att gat aag gta ctt ccc gaa agc	799
Ala Leu Lys Ile Met Ile Tyr Leu Ile Asp Lys Val Leu Pro Glu Ser	
196 201 206 211	
tat ttc gtc aat aat ctc cgg gca ttg tct gtg gat atg gct gtc ttc	847
Tyr Phe Val Asn Asn Leu Arg Ala Leu Ser Val Asp Met Ala Val Phe	
212 217 222 227	
aga gac ctt tta aga atg aag ctg ccg gaa tta tct cag cac ctg gat	895
Arg Asp Leu Leu Arg Met Lys Leu Pro Glu Leu Ser Gln His Leu Asp	
228 233 238 243	
act ctt cag aga act gca aac aaa gaa agt gga ggt gga tat gag ccc	943
Thr Leu Gln Arg Thr Ala Asn Lys Glu Ser Gly Gly Gly Tyr Glu Pro	
244 249 254 259	
cca ctt aca aat gtc ttc acg atg cag tgg ttt ctg act ctc ttt gcc	991
Pro Leu Thr Asn Val Phe Thr Met Gln Trp Phe Leu Thr Leu Phe Ala	
260 265 270 275	
aca tgc ctc cct aat cag acc gtt tta aag atc tgg gat tca gtc ttc	1039
Thr Cys Leu Pro Asn Gln Thr Val Leu Lys Ile Trp Asp Ser Val Phe	
276 281 286 291	
ttt gaa ggt tca gaa atc atc cta agg gtg tgc ctg gct atc tgg gca	1087
Phe Glu Gly Ser Glu Ile Ile Leu Arg Val Ser Leu Ala Ile Trp Ala	
292 297 302 307	
aaa tta gga gag cag ata gaa tgt tgt gaa aca gca gat gaa ttc tac	1135
Lys Leu Gly Glu Gln Ile Glu Cys Cys Glu Thr Ala Asp Glu Phe Tyr	
308 313 318 323	
agc acc atg ggg cgc ctt acc cag gag atg cta gag aat gat ctt ctg	1183
Ser Thr Met Gly Arg Leu Thr Gln Glu Met Leu Glu Asn Asp Leu Leu	
324 329 334 339	
caa agc cat gaa ctc atg cag act gtt tat tcc atg gct ccg ttc cct	1231
Gln Ser His Glu Leu Met Gln Thr Val Tyr Ser Met Ala Pro Phe Pro	
340 345 350 355	
ttc cca caa ttg gca gag ttg agg gaa aaa tac acc tac aac att aca	1279
Phe Pro Gln Leu Ala Glu Leu Arg Glu Lys Tyr Thr Tyr Asn Ile Thr	
356 361 366 371	
ccg ttc cca gcc aca gtt aaa ccc acc tca gtt tct gga cga cat agt	1327
Pro Phe Pro Ala Thr Val Lys Pro Thr Ser Val Ser Gly Arg His Ser	
372 377 382 387	
aag gcc aga gac agt gat gaa gag aat gac cca gac gat gag gat gct	1375
Lys Ala Arg Asp Ser Asp Glu Glu Asn Asp Pro Asp/Asp Glu Asp Ala	
388 393 398 403	
gtc gtt aat gca gtg ggg tgt ctt gga cct ttt agt ggg ttc ctg gct	1423

Val Val Asn Ala Val Gly Cys Leu Gly Pro Phe Ser Gly Phe Leu Ala	
404 409 414 419	
cct gaa ctg cag aag tac caa aaa caa att aaa gag cca aat gag gag	1471
Pro Glu Leu Gln Lys Tyr Gln Lys Gln Ile Lys Glu Pro Asn Glu Glu	
420 425 430 435	
cag agt ctg aga tct aat aac att gca gag ctg agt cca gga gca atc	1519
Gln Ser Leu Arg Ser Asn Asn Ile Ala Glu Leu Ser Pro Gly Ala Ile	
436 441 446 451	
aat tcc tgt cga agt gaa tac cat gca gct ttt aac agt atg atg atg	1567
Asn Ser Cys Arg Ser Glu Tyr His Ala Ala Phe Asn Ser Met Met Met	
452 457 462 467	
gaa cgc atg acc aca gat atc aat gca ctg aag cgg cag tac tct cga	1615
Glu Arg Met Thr Thr Asp Ile Asn Ala Leu Lys Arg Gln Tyr Ser Arg	
468 473 478 483	
att aaa aag aag caa cag cag cag gtt cat cag gtg tac atc agg gca	1663
Ile Lys Lys Lys Gln Gln Gln Gln Val His Gln Val Tyr Ile Arg Ala	
484 489 494 499	
gac aaa ggg cca gtg acc agc att ctc ccg tct cag gta aac agt tct	1711
Asp Lys Gly Pro Val Thr Ser Ile Leu Pro Ser Gln Val Asn Ser Ser	
500 505 510 515	
cca gtt ata aac cac ctt ctt tta gga aag aag atg aaa atg act aac	1759
Pro Val Ile Asn His Leu Leu Leu Gly Lys Lys Met Lys Met Thr Asn	
516 521 526 531	
aga gct gcc aag aat gct gtc atc cac atc cct ggt cac aca gga ggg	1807
Arg Ala Ala Lys Asn Ala Val Ile His Ile Pro Gly His Thr Gly Gly	
532 537 542 547	
aaa ata tct cct gtc ccc tac gaa gac ctt aag acg aag ctc aac tcc	1855
Lys Ile Ser Pro Val Pro Tyr Glu Asp Leu Lys Thr Lys Leu Asn Ser	
548 553 558 563	
ccg tgg cga act cac atc cga gtc cac aaa aag aac atg cca agg acc	1903
Pro Trp Arg Thr His Ile Arg Val His Lys Lys Asn Met Pro Arg Thr	
564 569 574 579	
aag agt cat ccg ggc tgt ggg gac acc gta ggg ctg ata gat gag cag	1951
Lys Ser His Pro Gly Cys Gly Asp Thr Val Gly Leu Ile Asp Glu Gln	
580 585 590 595	
aac gag gcc agc aag acc aat ggg ctg ggg gca gca gag gca ttc ccc	1999
Asn Glu Ala Ser Lys Thr Asn Gly Leu Gly Ala Ala Glu Ala Phe Pro	
596 601 606 611	
tct ggt tgt aca gcg aca gct ggg aga gaa ggc agc agc cct gaa ggc	2047
Ser Gly Cys Thr Ala Thr Ala Gly Arg Glu Gly Ser Ser Pro Glu Gly	
612 617 622 627	
agt acc agg agg acg atc gag ggg cag tct ccg gag ccg gtg ttc gga	2095
Ser Thr Arg Arg Thr Ile Glu Gly Gln Ser Pro Glu Pro Val Phe Gly	

628	633	638	643	
gat gct gat gtg gat	gtg tct gca gtt cag	gcg aag ttg gga gcc ctg		2143
Asp Ala Asp Val Asp	Val Ser Ala Val Gln	Ala Lys Leu Gly Ala Leu		
644	649	654	659	
gaa ctg aac cag agg	gat gct gca gct gaa	act gag ctg agg gtg cac		2191
Glu Leu Asn Gln Arg	Asp Ala Ala Ala Glu	Thr Glu Leu Arg Val His		
660	665	670	675	
cca ccc tgc cag cgg	cac tgc cca gag ccg	ccg agt gca ccc gaa gaa		2239
Pro Pro Cys Gln Arg	His Cys Pro Glu Pro	Pro Ser Ala Pro Glu Glu		
676	681	686	691	
aac aaa gcc acc agc	aaa gct ccc caa ggc	agc aac tca aaa acc ccc		2287
Asn Lys Ala Thr Ser	Lys Ala Pro Gln Gly	Ser Asn Ser Lys Thr Pro		
692	697	702	707	
atc ttt agc cct ttt	ccc agc gtc aag ccc	ctg cgg aaa tct gct act		2335
Ile Phe Ser Pro Phe	Pro Ser Val Lys Pro	Leu Arg Lys Ser Ala Thr		
708	713	718	723	
gcc agg aac ttg gga	tta tat ggc cct aca	gaa aga acc cca act gtg		2383
Ala Arg Asn Leu Gly	Leu Tyr Gly Pro Thr	Glu Arg Thr Pro Thr Val		
724	729	734	739	
cac ttt cct caa atg	agt agg agc ttc agc	aaa ccc ggc ggt gga aac		2431
His Phe Pro Gln Met	Ser Arg Ser Phe Ser	Lys Pro Gly Gly Gly Asn		
740	745	750	755	
agt ggc act aaa aa	cga tga tg tctccccgaa	actttgtatc tggactcacc		2484
Ser Gly Thr Lys Lys	Arg *			
756	761			
ttttcacagt agtataaggg	ttgcagctga atggctctaa	aagagtttta tttgtccagt		2544
gaaaatgaat aggttcaggg	atgagcaaca gcccataaaa	aatgggaact ggaagtttta		2604
taataggagt tagaacaggg	ctgttttccc agctacttgc	taactgacga agtggattct		2664
tgtggcaaaa taaatattgt	ggtttttatag tgtgaagttt	tcccaatttt tcattgtgag		2724
ctgttttaaaa aagactatat	ctagattgtt aactctcgtc	catccttctg ttctgggggc		2784
cttcagagtc cctgtgacag	cacccccaaa cttccagtt	ctctgggtgt tactaatact		2844
caagcatgca cataccagct	tgctaggaca gaaactgtaa	aaagaaagta agtttcttcg		2904
ttacaaaaaa cttcctgatt	ttccttttca tgctttacgg	aggggattgt gtcgtgtgag		2964
atttcccaca gtaccagttt	caaatttttt tttattctta	tgctaaatca taggagaaaa		3024
atctagatgg cttttcttta	actgtctatt tctacctgca	aatgaagaa aacotttcat		3084
ctgttgaaat ttcaatcgat	aaccagctg aagatcttat	gcacaggaca caettggcat		3144
atgctttacg cagttgctcc	ggacagcttg ctgcgccac	tgagcttttc ctgaggtttg		3204

agtaatcaca atgtgaattg gtcaatttat gagccttgcc tacttttagaa aataaagaaa 4944
cctgcagtag cctctaccac 4964

<210> 492
<211> 4892
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (167)..(2380)

<400> 492
tttgatagcc tgtcgcacgc gctaccgggc cggaattccc gggtcgacga tttcgtgccg 60
gtcagccgca gacactcacc cagctccgag agctcagccg ctcagcgagt ggggtagcgg 120
ggaccgagac ggacggtagc cgtgccagag cccggggcgc tctcgg atg cgg cag 175
Met Arg Gln
1
gac aag ctg acc ggg tct ctg agg cgc ggg ggg aga tgc ctg aag cgg 223
Asp Lys Leu Thr Gly Ser Leu Arg Arg Gly Gly Arg Cys Leu Lys Arg
4 9 14 19
cag ggc ggc ggc gtg ggc acc atc ctg agc aat gtg ctc aag aag cgc 271
Gln Gly Gly Gly Val Gly Thr Ile Leu Ser Asn Val Leu Lys Lys Arg
20 25 30 35
agc tgc att tcc cgg acc gcg ccc cgg ctg ctg tgc acc ctg gag ccg 319
Ser Cys Ile Ser Arg Thr Ala Pro Arg Leu Leu Cys Thr Leu Glu Pro
36 41 46 51
gga gtt gat acc aag ttg aaa ttc act ctt gag cca tct tta ggt caa 367
Gly Val Asp Thr Lys Leu Lys Phe Thr Leu Glu Pro Ser Leu Gly Gln
52 57 62 67
aat ggt ttt cag cag tgg tac gat gct ctc aag gca gtt gcc agg cta 415
Asn Gly Phe Gln Gln Trp Tyr Asp Ala Leu Lys Ala Val Ala Arg Leu
68 73 78 83
tcc aca gga ata cca aag gaa tgg agg aga aag gtt tgg ttg acc ttg 463
Ser Thr Gly Ile Pro Lys Glu Trp Arg Arg Lys Val Trp Leu Thr Leu
84 89 94 99
gca gat cat tat ttg cac agt ata gcc att gac tgg gac aaa acc atg 511
Ala Asp His Tyr Leu His Ser Ile Ala Ile Asp Trp Asp Lys Thr Met
100 105 110 115
cgc ttc act ttc aat gaa agg agt aat cct gat gat gac tcc atg gga 559
Arg Phe Thr Phe Asn Glu Arg Ser Asn Pro Asp Asp Asp Ser Met Gly
116 121 126 131

att cag ata gtc aag gac ctt cac cgc aca ggc tgt agt tct tac tgt	607
Ile Gln Ile Val Lys Asp Leu His Arg Thr Gly Cys Ser Ser Tyr Cys	
132 137 142 147	
ggc cag gag gct gag cag gac agg gtt gtg ttg aag cgg gtg ctg ctg	655
Gly Gln Glu Ala Glu Gln Asp Arg Val Val Leu Lys Arg Val Leu Leu	
148 153 158 163	
gcc tat gcc cga tgg aac aaa act gtt ggg tac tgc caa ggc ttt aac	703
Ala Tyr Ala Arg Trp Asn Lys Thr Val Gly Tyr Cys Gln Gly Phe Asn	
164 169 174 179	
atc ctg gct gca cta att ctg gaa gtg atg gaa ggc aat gaa ggg gat	751
Ile Leu Ala Ala Leu Ile Leu Glu Val Met Glu Gly Asn Glu Gly Asp	
180 185 190 195	
gcc ctg aaa att atg att tac ctt att gat aag gta ctt ccc gaa agc	799
Ala Leu Lys Ile Met Ile Tyr Leu Ile Asp Lys Val Leu Pro Glu Ser	
196 201 206 211	
tat ttc gtc aat aat ctc cgg gca ttg tct gtg gat atg gct gtc ttc	847
Tyr Phe Val Asn Asn Leu Arg Ala Leu Ser Val Asp Met Ala Val Phe	
212 217 222 227	
aga gac ctt tta aga atg aag ctg cgg gaa tta tct cag cac ctg gat	895
Arg Asp Leu Leu Arg Met Lys Leu Pro Glu Leu Ser Gln His Leu Asp	
228 233 238 243	
act ctt cag aga act gca aac aaa gaa agt gga ggt gga tat gag ccc	943
Thr Leu Gln Arg Thr Ala Asn Lys Glu Ser Gly Gly Gly Tyr Glu Pro	
244 249 254 259	
cca ctt aca aat gtc ttc acg atg cag tgg ttt ctg act ctc ttt gcc	991
Pro Leu Thr Asn Val Phe Thr Met Gln Trp Phe Leu Thr Leu Phe Ala	
260 265 270 275	
aca tgc ctc cct aat cag acc gtt tta aag atc tgg gat tca gtc ttc	1039
Thr Cys Leu Pro Asn Gln Thr Val Leu Lys Ile Trp Asp Ser Val Phe	
276 281 286 291	
ttt gaa ggt tca gaa atc atc cta agg gtg tgc ctg gct atc tgg gca	1087
Phe Glu Gly Ser Glu Ile Ile Leu Arg Val Ser Leu Ala Ile Trp Ala	
292 297 302 307	
aaa tta gga gag cag ata gaa tgt tgt gaa aca gca gat gaa ttc tac	1135
Lys Leu Gly Glu Gln Ile Glu Cys Cys Glu Thr Ala Asp Glu Phe Tyr	
308 313 318 323	
agc acc atg ggg cgc ctt acc cag gag atg cta gag aat gat ctt ctg	1183
Ser Thr Met Gly Arg Leu Thr Gln Glu Met Leu Glu Asn Asp Leu Leu	
324 329 334 339	
caa agc cat gaa ctc atg cag act gtt tat tcc atg gct ccg ttc cct	1231
Gln Ser His Glu Leu Met Gln Thr Val Tyr Ser Met Ala Pro Phe Pro	
340 345 350 355	
ttc cca caa ttg gca gag ttg agg gaa aaa tac acc tac aac att aca	1279

Phe	Pro	Gln	Leu	Ala	Glu	Leu	Arg	Glu	Lys	Tyr	Thr	Tyr	Asn	Ile	Thr	
356					361					366					371	
ccg	ttc	cca	gcc	aca	gtt	aaa	ccc	acc	tca	gtt	tct	gga	cga	cat	agt	1327
Pro	Phe	Pro	Ala	Thr	Val	Lys	Pro	Thr	Ser	Val	Ser	Gly	Arg	His	Ser	
372					377					382					387	
aag	gcc	aga	gac	agt	gat	gaa	gag	aat	gac	cca	gac	gat	gag	gat	gct	1375
Lys	Ala	Arg	Asp	Ser	Asp	Glu	Glu	Asn	Asp	Pro	Asp	Asp	Glu	Asp	Ala	
388					393					398					403	
gtc	gtt	aat	gca	gtg	ggg	tgt	ctt	gga	cct	ttt	agt	ggg	ttc	ctg	gct	1423
Val	Val	Asn	Ala	Val	Gly	Cys	Leu	Gly	Pro	Phe	Ser	Gly	Phe	Leu	Ala	
404					409					414					419	
cct	gaa	ctg	cag	aag	tac	caa	aaa	caa	att	aaa	gag	cca	aat	gag	gag	1471
Pro	Glu	Leu	Gln	Lys	Tyr	Gln	Lys	Gln	Ile	Lys	Glu	Pro	Asn	Glu	Glu	
420					425					430					435	
cag	agt	ctg	aga	tct	aat	aac	att	gca	gag	ctg	agt	cca	gga	gca	atc	1519
Gln	Ser	Leu	Arg	Ser	Asn	Asn	Ile	Ala	Glu	Leu	Ser	Pro	Gly	Ala	Ile	
436					441					446					451	
aat	tcc	tgt	cga	agt	gaa	tac	cat	gca	gct	ttt	aac	agt	atg	atg	atg	1567
Asn	Ser	Cys	Arg	Ser	Glu	Tyr	His	Ala	Ala	Phe	Asn	Ser	Met	Met	Met	
452					457					462					467	
gaa	cgc	atg	acc	aca	gat	atc	aat	gca	ctg	aag	cgg	cag	tac	tct	cga	1615
Glu	Arg	Met	Thr	Thr	Asp	Ile	Asn	Ala	Leu	Lys	Arg	Gln	Tyr	Ser	Arg	
468					473					478					483	
att	aaa	aag	aag	caa	cag	cag	cag	gtt	cat	cag	gtg	tac	atc	agg	gca	1663
Ile	Lys	Lys	Lys	Gln	Gln	Gln	Gln	Val	His	Gln	Val	Tyr	Ile	Arg	Ala	
484					489					494					499	
gga	aag	aag	atg	aaa	atg	act	aac	aga	gct	gcc	aag	aat	gct	gtc	atc	1711
Gly	Lys	Lys	Met	Lys	Met	Thr	Asn	Arg	Ala	Ala	Lys	Asn	Ala	Val	Ile	
500					505					510					515	
cac	atc	cct	ggt	cac	aca	gga	ggg	aaa	ata	tct	cct	gtc	ccc	tac	gaa	1759
His	Ile	Pro	Gly	His	Thr	Gly	Gly	Lys	Ile	Ser	Pro	Val	Pro	Tyr	Glu	
516					521					526					531	
gac	ctt	aag	acg	aag	ctc	aac	tcc	ccg	tgg	cga	act	cac	atc	cga	gtc	1807
Asp	Leu	Lys	Thr	Lys	Leu	Asn	Ser	Pro	Trp	Arg	Thr	His	Ile	Arg	Val	
532					537					542					547	
cac	aaa	aag	aac	atg	cca	agg	acc	aag	agt	cat	ccg	ggc	tgt	ggg	gac	1855
His	Lys	Lys	Asn	Met	Pro	Arg	Thr	Lys	Ser	His	Pro	Gly	Cys	Gly	Asp	
548					553					558					563	
acc	gta	ggg	ctg	ata	gat	gag	cag	aac	gag	gcc	agc	aag	acc	aat	ggg	1903
Thr	Val	Gly	Leu	Ile	Asp	Glu	Gln	Asn	Glu	Ala	Ser	Lys	Thr	Asn	Gly	
564					569					574					579	
ctg	ggg	gca	gca	gag	gca	ttc	ccc	tct	ggt	tgt	aca	gcg	aca	gct	ggg	1951
Leu	Gly	Ala	Ala	Glu	Ala	Phe	Pro	Ser	Gly	Cys	Thr	Ala	Thr	Ala	Gly	

580	585	590	595	
aga gaa ggc agc agc cct gaa ggc agt acc agg agg acg atc gag ggg	Arg Glu Gly Ser Ser Pro Glu Gly Ser Thr Arg Arg Thr Ile Glu Gly			1999
596	601	606	611	
cag tct ccg gag ccg gtg ttc gga gat gct gat gtg gat gtg tct gca	Gln Ser Pro Glu Pro Val Phe Gly Asp Ala Asp Val Asp Val Ser Ala			2047
612	617	622	627	
gtt cag gcg aag ttg gga gcc ctg gaa ctg aac cag agg gat gct gca	Val Gln Ala Lys Leu Gly Ala Leu Glu Leu Asn Gln Arg Asp Ala Ala			2095
628	633	638	643	
gct gaa act gag ctg agg gtg cac cca ccc tgc cag cgg cac tgc cca	Ala Glu Thr Glu Leu Arg Val His Pro Pro Cys Gln Arg His Cys Pro			2143
644	649	654	659	
gag ccg ccg agt gca ccc gaa gaa aac aaa gcc acc agc aaa gct ccc	Glu Pro Pro Ser Ala Pro Glu Glu Asn Lys Ala Thr Ser Lys Ala Pro			2191
660	665	670	675	
caa ggc agc aac tca aaa acc ccc atc ttt agc cct ttt ccc agc gtc	Gln Gly Ser Asn Ser Lys Thr Pro Ile Phe Ser Pro Phe Pro Ser Val			2239
676	681	686	691	
aag ccc ctg cgg aaa tct gct act gcc agg aac ttg gga tta tat ggc	Lys Pro Leu Arg Lys Ser Ala Thr Ala Arg Asn Leu Gly Leu Tyr Gly			2287
692	697	702	707	
cct aca gaa aga acc cca act gtg cac ttt cct caa atg agt agg agc	Pro Thr Glu Arg Thr Pro Thr Val His Phe Pro Gln Met Ser Arg Ser			2335
708	713	718	723	
ttc agc aaa ccc ggc ggt gga aac agt ggc act aaa aaa cga tga tgt	Phe Ser Lys Pro Gly Gly Gly Asn Ser Gly Thr Lys Lys Arg *			2383
724	729	734		
ctccccgaaa ctttgtatct ggactcacct ttccacagta gtataagggt tgcagctgaa				2443
tggtctctaaa agagttttat ttgtccagtg aaaatgaata gggttcaggga tgagcaacag				2503
cccataaaaa atgggaactg gaagttttat aataggagtt agaacagggc tgttttccca				2563
gctacttgct aactgacgaa gtggattcct gtggcaaaat aaatattgtg gttttatagt				2623
gtgaagtgtt cccaattttt cattgtgagc tggttaaaaa agactatatc tagattgtta				2683
actctcgtcc atcctttctgt tctggggggc ttcagagtcc ctgtgacagc acccccaaac				2743
cttccagttc tctgggtgtt actaatactc aagcatgcac ataccagctt gctaggacag				2803
aaactgtaaa aagaaagtaa gtttcttcgt tacaaaaaac ttcctgattt tccttttcat				2863
gctttacgga ggggattgtg tcgtgtgaga tttccacag taccagtttc aaattttttt				2923
ttattcttat gctaaatcat aggagaaaaa tctagatggc ctttctttta ctgtctattt				2983

ctacctgcaa aatgaagaaa acctttcatc tggtgaaatt tcaatcgata acccagctga	3043
agatcttatg cacaggacac acttggcata tgctttacgc agttgctccg gacagcttgc	3103
tcgcgccact gagcttttcc tgagggttgt gttcgctct caaggagagc tttgatcctc	3163
agtggtagcg atgacttgat gggctccatg cggagcctgg cctgcatccc ccaccacaca	3223
gctcactcac ccaccagctc tagactgcag acgcacaagg cctctgctca gaagccagaa	3283
cacagcacct gtgactctgt tacttgaatt ttgtgctttt tgattggagt cctttgttga	3343
gtactttgtt aattgaacac tgcctttctc tggagaaggc ccdagtgtt tctagctccc	3403
tctcactcct gccctttcta gctctctctc acccagcggg tcagggatag cacctcttgt	3463
ctccactatg cagatgggaa ctctgagcca cacagagggtg aagtagcact tcagttactc	3523
aaggtcagta ctctcggtat tccaagtgc ttagccacat ttccttcagt gcaatagggtg	3583
ggtttaatgc tctttgtaca cagatgtatt ggctacatag cgtgtaaaaa ccaagactgg	3643
gaagccattc actaaaatcc ctctgactc aaaggacctg tctccagatg gtacagagtc	3703
ccttgatggc attttacaaa accagctctg acttccttat cctgaacagg gagtttattt	3763
taaaaatgct tcatgcacct gttatttggc tgaacagaag gctcactcct caatcccctt	3823
ctcctcgcca tcattagagg aatagactca gccttcatgt ttgtctctgg aagacgattg	3883
gcgatacttg caggaatatt gttgatgcag ccaatattaa tttgagctaa tggattgtta	3943
attctgaaac gaaaactgta actgtagagc aggccttttac tatgagaggt actacttttt	4003
ataatagaga atgtggttgt gtgggctttt tttgaacaga aaacacaaca atgacctata	4063
ccgtgagaaa agccatttta tcttcttctg ggtattttta ccccaaagg aactgaagat	4123
ggaaaatatg actaataagt tattgcagtt ttggtcttga attctgtgcc atctgaagtt	4183
agcatccagc ttcttaaaaa gcagccacgc ctacagcctg ttttttggga aggctgtagg	4243
tggagagatg ggcttatttt gcataccacc ctcagggcc agagaccac tgcattttcc	4303
aaagttaagc atgacaccat tttcttccat cagctaaact ttacagataa tagtgtttcc	4363
acctcatatc cttttctttg ccccttctca aatgagtcag aatagtcag tttcccttga	4423
gggatgtctg acttgaatgg agaattgttc tttctctct tgaatcagct cactagctcc	4483
ctgatggctt gggttcaagg aaatgggtta tgaggtagag gccacttata caagtccttg	4543
ggattgtacc attgctgtcc acaaacttag tatcaacaac acatgctgtg ccctgtgaac	4603
actctctctt cacctatttc cagggttgggt ctctctgaga aggggatgga tgaggtaaca	4663

cacagtttgg gatacgtatc tgttgaatga atgaataagt gaaaggataa tagtcctctg 4723
 aggtaaaaat ggccttgtca gaattttgaa aatccaacag attcctatta aagcactctg 4783
 tgtaccaata acatgcatgc attgtaccaa gtaatcaciaa tgtgaattgg tcaatttatg 4843
 agccttgcct acttttagaaa ataaagaaac ctgcagtagc ctctaccac 4892

<210> 493
 <211> 1233
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (85) .. (915)

<400> 493
 atttggccct cgaggccaag aattcggcac gagcaggtct ctgcccttca tagacgcata 60
 aaggctatcg tagagggtggc tgca atg tgt gga gtc aac atc atc tgt ttc 111
 Met Cys Gly Val Asn Ile Ile Cys Phe
 1 5
 cag gaa gca tgg act atg ccc ttt gcc ttc tgt acg aga gag aag ctt 159
 Gln Glu Ala Trp Thr Met Pro Phe Ala Phe Cys Thr Arg Glu Lys Leu
 10 15 20 25
 cct tgg aca gaa ttt gct gag tca gca gag gat ggg ccc acc acc aga 207
 Pro Trp Thr Glu Phe Ala Glu Ser Ala Glu Asp Gly Pro Thr Thr Arg
 26 31 36 41
 ttc tgt cag aag ctg gcg aag aac cat gac atg gtg gtg gtg tct ccc 255
 Phe Cys Gln Lys Leu Ala Lys Asn His Asp Met Val Val Val Ser Pro
 42 47 52 57
 atc ctg gaa cga gac agc gag cat ggg gat gtt ttg tgg aat aca gcc 303
 Ile Leu Glu Arg Asp Ser Glu His Gly Asp Val Leu Trp Asn Thr Ala
 58 63 68 73
 gtg gtg atc tcc aat tcc gga gca gtc ctg gga aag acc agg aaa aac 351
 Val Val Ile Ser Asn Ser Gly Ala Val Leu Gly Lys Thr Arg Lys Asn
 74 79 84 89
 cac atc ccc aga gtg ggt gat ttc aac gag tca act tac tac atg gag 399
 His Ile Pro Arg Val Gly Asp Phe Asn Glu Ser Thr Tyr Tyr Met Glu
 90 95 100 105
 gga aac ctg ggc cac ccc gtg ttc cag acg cag ttc gga agg atc gcg 447
 Gly Asn Leu Gly His Pro Val Phe Gln Thr Gln Phe Gly Arg Ile Ala
 106 111 116 121
 gtg aac att tgc tac ggg cgg cac cac ccc ctc aac tgg ctt atg tac 495
 Val Asn Ile Cys Tyr Gly Arg His His Pro Leu Asn Trp Leu Met Tyr

122	127	132	137	
agc atc aac ggg gct gag atc atc ttc aac ccc tcg gcc acg ata gga				543
Ser Ile Asn Gly Ala Glu Ile Ile Phe Asn Pro Ser Ala Thr Ile Gly				
138	143	148	153	
gca ctc agc gag tcc ctg tgg ccc atc gag gcc aga aac gca gcc att				591
Ala Leu Ser Glu Ser Leu Trp Pro Ile Glu Ala Arg Asn Ala Ala Ile				
154	159	164	169	
gcc aat cac tgc ttc acc tgc gcc atc aat cga gtg ggc acc gag cac				639
Ala Asn His Cys Phe Thr Cys Ala Ile Asn Arg Val Gly Thr Glu His				
170	175	180	185	
ttc ccg aac gag ttt acc tcg gga gat gga aag aaa gct cac cag gac				687
Phe Pro Asn Glu Phe Thr Ser Gly Asp Gly Lys Lys Ala His Gln Asp				
186	191	196	201	
ttt ggc tac ttt tat ggc tcg agc tat gtg gca gcc cct gac agc agc				735
Phe Gly Tyr Phe Tyr Gly Ser Ser Tyr Val Ala Ala Pro Asp Ser Ser				
202	207	212	217	
cgg act cct ggg ctg tcc cgt agc cgg gat gga ctg cta gtt gct aag				783
Arg Thr Pro Gly Leu Ser Arg Ser Arg Asp Gly Leu Leu Val Ala Lys				
218	223	228	233	
ctc gac cta aac ctc tgc cag cag gtg aat gat gtc tgg aac ttc aag				831
Leu Asp Leu Asn Leu Cys Gln Gln Val Asn Asp Val Trp Asn Phe Lys				
234	239	244	249	
atg acg ggc agg tat gag atg tac gca cgg gag ctc gcc gaa gct gtc				879
Met Thr Gly Arg Tyr Glu Met Tyr Ala Arg Glu Leu Ala Glu Ala Val				
250	255	260	265	
aag tcc aac tac agc ccc acc atc gtg aaa gag tag ccgg cttcagtgcc				929
Lys Ser Asn Tyr Ser Pro Thr Ile Val Lys Glu *				
266	271	276		
tgcccttgggg tgaggaagac acctctgccc cagtggatta gcaagtgtgg caggcttaac				989
atgtccaggt tctcccacat aacattgtcc aggttggttt taaaattccc aggcaggggg				1049
agagtggcat ggggagtgac ttcttaatgg gtaaggggct gcttacttct ggggtattgg				1109
aaatgttttg ggactaggta gaggtgaatg tactaaatgc cactgaattt gtatacttca				1169
gaatgtttgt tatgtaaatt ttacctcaac taaaaaaaaa aatgcccagg taaaaaaaaa				1229
aaaa				1233

<210> 494
 <211> 3001
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1361)..(2419)

<400> 494

ctgctattcc attotcccat ctactaccta tctgttcttc aggccatcca ctcatccatt	60
cttctgtccc aggtacctag acacttgtct tcccatccgt ttgttagttg atccactcct	120
cattcagccc tcccatgggc ctggcatgta gccgagcacc ctggagaggg cagactaaga	180
agacatggtc cgtccctgcc tgtgaggagt tcaggtctct gaggaggagg aagcagtga	240
actgggcttt acacatggcc tgagaacagc ttaggcctga acataaggaa cagcttggag	300
tggaggggac acagaggaac cctcactatc atgcattgcca acccaaccac tgccctgccct	360
ttcccttctg gatttagctc gtgtctccag gctcctagtc ctgtaatcca gggacccatc	420
agcgagggat tcagggaagc agaggcagct ctccaggaag gaggaaaatc cctgcctctt	480
ccagagagac tccccattg ctgtctcttg tgtgtgtcat gcacaaggaa ggcttggttg	540
tgtgccagga taagggggcac aagggcctcg ggtgtggcca gagaccccat gcttaagctt	600
ttatggtata ggtcaggctg caggggcttg agggcctcag ttgtatatca gaatcttcag	660
agcactgcca tgttcagggg tgagtcaggt ctgtagatgt gcacggggtc ttctgaaggg	720
tcagtttctg taatcacttt caggtgtgtc agggccttgt gcagtaacag tgcacacaga	780
agttagtgtt tctgtgggct aagggttgta gctctgtatc aggattctgg gagtgggtct	840
ggatttctgg tgtgtggact taagaagctg tgtcagactt gggggagggg cgttcatgta	900
taactggggt cecataggcc aagactccca ggtgcatttt aggcagagcc tcaggtgtgt	960
tagagggtccc aggggcagag aggcctatagg tgctgtcaga ggccttgggg acatttaggg	1020
cagagcctcg agtgacaggt cctgggacag tgggagccaa gggcaagtgc tagagttgca	1080
gtgaatttag agcaaagcct cagctaagtg acacatccca gggcagtagg ggatctatct	1140
aggttcgtgc tgggcctcag gtaagtgaca ggccttagga caatgggggc tgtggcatgc	1200
gtcaggttac ctgccttgat atgggatcgt gacaggcccc tccctatgtg caggagacaa	1260
gcagcccaag aaacaggaga aaaaccagc gttgggtgtcc ccagagtttg tggatgaagc	1320
tctgtgtgcg tgcgaggagt acctagcaa cttggccac atg gac atc gac aag	1375
	Met Asp Ile Asp Lys
	1
gac ctg gag gcc ccg ctg tac ctc acc ccc gag ggc tgg tcc ctc ttc	1423
Asp Leu Glu Ala Pro Leu Tyr Leu Thr Pro Glu Gly Trp Ser Leu Phe	
6 11 16 21	

ctc cag cgc tac tac caa gtg gtc cac gaa ggg gca gaa ctc agg cac	1471
Leu Gln Arg Tyr Tyr Gln Val Val His Glu Gly Ala Glu Leu Arg His	
22 27 32 37	
ctc gac act cag gtc cag cgc tgt gag gac atc ctg cag cag ctg cag	1519
Leu Asp Thr Gln Val Gln Arg Cys Glu Asp Ile Leu Gln Gln Leu Gln	
38 43 48 53	
gcc gtg gta ccc cag ata gac atg gaa ggg gat cgc aac atc tgg atc	1567
Ala Val Val Pro Gln Ile Asp Met Glu Gly Asp Arg Asn Ile Trp Ile	
54 59 64 69	
gtg aag cca gga gcc aag tcc cgc gga cga ggc atc atg tgc atg gac	1615
Val Lys Pro Gly Ala Lys Ser Arg Gly Arg Gly Ile Met Cys Met Asp	
70 75 80 85	
cac ctg gag gag atg ctg aag ctg gtg aac ggc aac ccc gtg gtg atg	1663
His Leu Glu Glu Met Leu Lys Leu Val Asn Gly Asn Pro Val Val Met	
86 91 96 101	
aag gac ggc aag tgg gtg gtg cag aag tat att gag cgg ccc ctc ctc	1711
Lys Asp Gly Lys Trp Val Val Gln Lys Tyr Ile Glu Arg Pro Leu Leu	
102 107 112 117	
atc ttt ggc acc aag ttt gac ctc aga cag tgg ttc ctg gta act gac	1759
Ile Phe Gly Thr Lys Phe Asp Leu Arg Gln Trp Phe Leu Val Thr Asp	
118 123 128 133	
tgg aac cca ctt acc gtg tgg ttc tac cgc gac agc tat atc cgc ttt	1807
Trp Asn Pro Leu Thr Val Trp Phe Tyr Arg Asp Ser Tyr Ile Arg Phe	
134 139 144 149	
tcc acg cag ccc ttc tcc ctg aag aac ctg gac aac tca gtg cac ctg	1855
Ser Thr Gln Pro Phe Ser Leu Lys Asn Leu Asp Asn Ser Val His Leu	
150 155 160 165	
tgc aac aac tcc atc cag aag cac ctg gag aac tca tgc cat cgg cat	1903
Cys Asn Asn Ser Ile Gln Lys His Leu Glu Asn Ser Cys His Arg His	
166 171 176 181	
cca ctg ctt ccg cca gac aac atg tgg tct agc cag agg ttc cag gcc	1951
Pro Leu Leu Pro Pro Asp Asn Met Trp Ser Ser Gln Arg Phe Gln Ala	
182 187 192 197	
cac ctg cag gag atg ggt gcc cca aat gct tgg tcc acc atc atc gtg	1999
His Leu Gln Glu Met Gly Ala Pro Asn Ala Trp Ser Thr Ile Ile Val	
198 203 208 213	
cct ggc atg aag gat gct gtg atc cac gca ctt cag acc tcc cag gac	2047
Pro Gly Met Lys Asp Ala Val Ile His Ala Leu Gln Thr Ser Gln Asp	
214 219 224 229	
acc gtg cag tgt cgg aag gcc agc ttt gag ctc tat ggc gct gac ttc	2095
Thr Val Gln Cys Arg Lys Ala Ser Phe Glu Leu Tyr Gly Ala Asp Phe	
230 235 240 245	

gtg ttc ggg gag gac ttc cag ccc tgg ctg att gag atc aac gcc agc	2143
Val Phe Gly Glu Asp Phe Gln Pro Trp Leu Ile Glu Ile Asn Ala Ser	
246 251 256 261	
ccc acg atg gca ccc tcc aca gca gtc act gcc cgg ctc tgt gct ggc	2191
Pro Thr Met Ala Pro Ser Thr Ala Val Thr Ala Arg Leu Cys Ala Gly	
262 267 272 277	
gtg caa gct gac acc ctg cgc gtg gtc att gac cgg atg ctg gac cgc	2239
Val Gln Ala Asp Thr Leu Arg Val Val Ile Asp Arg Met Leu Asp Arg	
278 283 288 293	
aac tgt gac aca gga gcc ttt gag ctc atc tat aag cag ccc gtc acc	2287
Asn Cys Asp Thr Gly Ala Phe Glu Leu Ile Tyr Lys Gln Pro Val Thr	
294 299 304 309	
act tcc cca gcc tcc aca cca agg ccc agc tgc ctt ctc ccc atg tac	2335
Thr Ser Pro Ala Ser Thr Pro Arg Pro Ser Cys Leu Leu Pro Met Tyr	
310 315 320 325	
tcc gac acc agg gcc agg tcc tca gac gac agc aca gca agc tgg tgg	2383
Ser Asp Thr Arg Ala Arg Ser Ser Asp Asp Ser Thr Ala Ser Trp Trp	
326 331 336 341	
gca cta agg ccc tgt cga cca cag gca agg cct tga ggac tctaccacg	2433
Ala Leu Arg Pro Cys Arg Pro Gln Ala Arg Pro *	
342 347 352	
gctaaggtct tcatttccct cccaccgaac cttgatttca aggtggcacc cagcatcctg	2493
aagccaagaa aggtgggcct cgacctgtga ctcacaccca gtggacagtg ctgagcacgg	2553
ggtcagggct ggagggcaca ggcagagggc agctcccagg ctggctggca cccaagggga	2613
agagctggtc tccctcagaa gcccttcct ccacagactt ctgatcatct cctctttctc	2673
cctcctttc acaccgaggc tctgtctctc ctgtgcctcc gaggcccca gctggaagtg	2733
ccttgttgcc tctgcccttt gaagtcggaa caattcctag cacctgtcgg aaggtcaagg	2793
ccaaaggcaa attcaaggcc agactgtgac aaaccaggg ctgaggcctg ccccatgaag	2853
aggctgagcc cctgaaacc cctgcccctt gttggtacat tccagaggcg caggggcctg	2913
ggggatatga agctagggaa gccctgctt cgattcccca ctgcccttgt cctggatcca	2973
acaccaaata aaaagaaaca agtgaagt	3001

<210> 495
 <211> 1434
 <212> DNA
 <213> Homo sapiens
 <220>

<221> CDS

<222> (138)..(1418)

<400> 495

acccgtccgg aattccccggg tcgacccacg cgtgcggcga gtgaggcccc ggtcttctc	60
ctcgtctctgc cgcagggccga gaacccctga cggtattcag ctgcgcgtaa gtctggccgg	120
tgccatctgt ctccgca atg ccc ccc aag aaa cag gct cag gcc ggg ggc	170
Met Pro Pro Lys Lys Lys Gln Ala Gln Ala Gly Gly	
1 5	
agc aaa aag gcg gag caa aaa aag aag gag aag att atc gaa gac aaa	218
Ser Lys Lys Ala Glu Gln Lys Lys Lys Glu Lys Ile Ile Glu Asp Lys	
12 17 22 27	
act ttc ggt ttg aag aat aag aaa gga gca aag caa cag aag ttt atc	266
Thr Phe Gly Leu Lys Asn Lys Lys Gly Ala Lys Gln Gln Lys Phe Ile	
28 33 38 43	
aag gct gtc aca cat caa gtt aaa ttt ggt caa caa aat cca cgt cag	314
Lys Ala Val Thr His Gln Val Lys Phe Gly Gln Gln Asn Pro Arg Gln	
44 49 54 59	
gta gca cag agt gaa gct gaa aag aaa ttg aag aag gat gac aag aag	362
Val Ala Gln Ser Glu Ala Glu Lys Lys Leu Lys Lys Asp Asp Lys Lys	
60 65 70 75	
aaa gaa ttg cag gag cta aat gag ctg ttc aaa cct gta gtt gct gct	410
Lys Glu Leu Gln Glu Leu Asn Glu Leu Phe Lys Pro Val Val Ala Ala	
76 81 86 91	
caa aaa ata agt aaa ggt gca gat ccc aag tct gta gta tgt gca ttc	458
Gln Lys Ile Ser Lys Gly Ala Asp Pro Lys Ser Val Val Cys Ala Phe	
92 97 102 107	
ttc aag caa gga cag tgt act aaa gga gat aag tgt aag ttc tcc cat	506
Phe Lys Gln Gly Gln Cys Thr Lys Gly Asp Lys Cys Lys Phe Ser His	
108 113 118 123	
gac ttg act ctg gag aga aaa tgt gaa aag cga agt gtt tac att gat	554
Asp Leu Thr Leu Glu Arg Lys Cys Glu Lys Arg Ser Val Tyr Ile Asp	
124 129 134 139	
gca aga gat gaa gaa ctt gaa aaa gat act atg gat aat tgg gat gag	602
Ala Arg Asp Glu Glu Leu Glu Lys Asp Thr Met Asp Asn Trp Asp Glu	
140 145 150 155	
aaa aag ctg gaa gaa gta gtg aac aag aag cac ggt gag gcg gaa aag	650
Lys Lys Leu Glu Glu Val Val Asn Lys Lys His Gly Glu Ala Glu Lys	
156 161 166 171	
aaa aaa cca aaa act caa ata gtg tgc aag cat ttc ctg gaa gct att	698
Lys Lys Pro Lys Thr Gln Ile Val Cys Lys His Phe Leu Glu Ala Ile	
172 177 182 187	
gaa aac aac aag tat ggc tgg ttt tgg gta tgc cct gga ggg ggt gat	746

Glu Asn Asn Lys Tyr Gly Trp Phe Trp Val Cys Pro Gly Gly Gly Asp	
188 193 198 203	
att tgc atg tat cgt cat gca ctt cct cct gga ttt gtg ttg aaa aaa	794
Ile Cys Met Tyr Arg His Ala Leu Pro Pro Gly Phe Val Leu Lys Lys	
204 209 214 219	
gat aaa aag aaa gaa gag aaa gaa gat gaa att tca tta gaa gat cta	842
Asp Lys Lys Lys Glu Glu Lys Glu Asp Glu Ile Ser Leu Glu Asp Leu	
220 225 230 235	
att gag aga gag cgt tct gcc cta ggt cca aat gtt acc aaa atc act	890
Ile Glu Arg Glu Arg Ser Ala Leu Gly Pro Asn Val Thr Lys Ile Thr	
236 241 246 251	
cta gaa tct ttt ctt gcc tgg aag aaa agg aaa aga caa gaa aag att	938
Leu Glu Ser Phe Leu Ala Trp Lys Lys Arg Lys Arg Gln Glu Lys Ile	
252 257 262 267	
gat aaa ctt gaa caa gat atg gaa aga agg aaa gct gac ttc aaa gca	986
Asp Lys Leu Glu Gln Asp Met Glu Arg Arg Lys Ala Asp Phe Lys Ala	
268 273 278 283	
ggg aaa gca cta gtg atc agt ggt cgt gaa gtg ttt gaa ttt cgt cct	1034
Gly Lys Ala Leu Val Ile Ser Gly Arg Glu Val Phe Glu Phe Arg Pro	
284 289 294 299	
gaa ctg gtc aat gat gat gat gag gaa gca gat gat acc cgc tac acc	1082
Glu Leu Val Asn Asp Asp Asp Glu Glu Ala Asp Asp Thr Arg Tyr Thr	
300 305 310 315	
cag gga aca ggt ggt gat gag gtt gat gat tca gtg agt gta aat gac	1130
Gln Gly Thr Gly Gly Asp Glu Val Asp Asp Ser Val Ser Val Asn Asp	
316 321 326 331	
ata gat tta agc ctg tac atc cca aga gat gta gat gaa aca ggt att	1178
Ile Asp Leu Ser Leu Tyr Ile Pro Arg Asp Val Asp Glu Thr Gly Ile	
332 337 342 347	
act gta gcc agt ctt gaa aga ttc agc aca tat act tca gat aaa gat	1226
Thr Val Ala Ser Leu Glu Arg Phe Ser Thr Tyr Thr Ser Asp Lys Asp	
348 353 358 363	
gaa aac aaa tta agt gaa gct tct gga ggt agg gct gaa aat ggt gaa	1274
Glu Asn Lys Leu Ser Glu Ala Ser Gly Gly Arg Ala Glu Asn Gly Glu	
364 369 374 379	
aga agt gac ttg gaa gag gac aac gag agg gag gga acg gaa aat gga	1322
Arg Ser Asp Leu Glu Glu Asp Asn Glu Arg Glu Gly Thr Glu Asn Gly	
380 385 390 395	
gcc att gat gct gtt cct gtt gat gaa aat ctt ttc act gga gag gat	1370
Ala Ile Asp Ala Val Pro Val Asp Glu Asn Leu Phe Thr Gly Glu Asp	
396 401 406 411	
ttg gat gaa cta gaa gaa gaa tta aat aca ctt gat tta gaa gaa tga	1418
Leu Asp Glu Leu Glu Glu Glu Leu Asn Thr Leu Asp Leu Glu Glu *	

412

417

422

427

caccaaacac atcgcg

1434

<210> 496

<211> 2106

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81)..(524)

<400> 496

gcacgaggcg acgcgggaag tccggacgca gtagctccct gaagcggagg cgaaggggag 60

ttaaagcccc agcggcgggca atg gcg gag agg ccc gag gac cta aac ctg 110

Met Ala Glu Arg Pro Glu Asp Leu Asn Leu

1

5

ccc aat gcc gtg atc acc agg atc atc aag gag gcg ctc ccg gac ggt 158

Pro Asn Ala Val Ile Thr Arg Ile Ile Lys Glu Ala Leu Pro Asp Gly

11

16

21

26

gtc aac atc tcc aag gag gcc cgg agc gcc atc tcc cgc gcc gcc agc 206

Val Asn Ile Ser Lys Glu Ala Arg Ser Ala Ile Ser Arg Ala Ala Ser

27

32

37

42

gtc ttc gtg ctg tac gcc aca tcc tgt gct aac aac ttt gca atg aaa 254

Val Phe Val Leu Tyr Ala Thr Ser Cys Ala Asn Asn Phe Ala Met Lys

43

48

53

58

gga aag cgg aag acg ctg aat gcc agt gat gtg ctc tca gcc atg gaa 302

Gly Lys Arg Lys Thr Leu Asn Ala Ser Asp Val Leu Ser Ala Met Glu

59

64

69

74

gag atg gag ttc cag cgg ttc gtt acc cca ttg aaa gaa gct ctg gaa 350

Glu Met Glu Phe Gln Arg Phe Val Thr Pro Leu Lys Glu Ala Leu Glu

75

80

85

90

gca tat agg cgg gag cag aaa ggc aag aag gag gcc tca gag caa aag 398

Ala Tyr Arg Arg Glu Gln Lys Gly Lys Lys Glu Ala Ser Glu Gln Lys

91

96

101

106

aag aag gac aaa gac aaa aaa aca gac tcg gaa gag caa gac aag agc 446

Lys Lys Asp Lys Asp Lys Lys Thr Asp Ser Glu Glu Gln Asp Lys Ser

107

112

117

122

agg gat gag gac aat gat gaa gac gaa gaa agg ctg gaa gaa gaa gaa 494

Arg Asp Glu Asp Asn Asp Glu Asp Glu Glu Arg Leu Glu Glu Glu Glu

123

128

133

138

cag aat gaa gag gaa gaa gta tac aac tga a aagggcggga gactgtggca 545

Gln Asn Glu Glu Glu Glu Val Tyr Asn *

139

144

ccttgaagg taccacttga aatgagacgt gctacgtgtt tctgtgaagc ttttccatgc 605
 tgggcagagt agtctcaggc aaaagtgcct gaaaagatca gaataaaaac tgactagaaa 665
 taccgtcaaa accagcactt accaaaactca gagcatctga gtagcagaat cctgttttgc 725
 ttcacatcaatc tgaaggttat ggcccttttga caagagggat tctgaacgac taaattagtc 785
 agtttgetcg cttttgttta cttaaagtga tggtagatg gtttttgatc tgcagtcttc 845
 cctagtcccc caaataagta ataataactt ccatgotgcc tgctgtgttc cagatcacag 905
 aggcagccaa ggctcaggaa aaactggggc tttgcttatg gtcagcctat gtttgattgc 965
 acagtctttg acaatagtag cttactaaga ctgctcagaa tgagtaagct ttaggaaact 1025
 actaaaatgc tgtgggagaa taacaaaatc cggtctctct cttcacttga cagaagcatt 1085
 aactgaattt tgtttttcat agaccactt ggcccaaac ctttctatat tgcctgtaga 1145
 tgatcggcct gctggtgtgg tagtaatctg atcacagata ttcttaaactc agcagtgtgg 1205
 aatggtatta gtcaaacatg gtgccagtgt cttttacaaa aacagatggc atagtgtcag 1265
 atgtacctta ctctctgcta ctgtacagct ttaggatttg tcatcacctc ccggaagggtg 1325
 taaaacccca ggcttctctt tcttgtagtc catctcccag acttgtgact atggcttttc 1385
 attcttcaat tcatgacgag tgccaaactt gattttctct aggcacagct ttctccctct 1445
 gtgcctcctg cttcctttct ctctcctgcc tctcctctgc tccccatccc actttctcat 1505
 ctgcctcctt ttctcacttc tgtcagctcg taagctttga taacctgctt aatactccaa 1565
 agtgtgagtt cctctgatct cttgattcct tagttctaat ctcacgtttt gtttttaaga 1625
 gatggagtct ctcactctgt ggcccaggct ggagtgcagt ggcagatca tagctcattg 1685
 catccttgaa atcctgggct caggatgatcc tcccgctga gcctcctgag tatctgggac 1745
 tacagatgag tgccaccaag cctggctaata tttgtctcat gtcttctaaa aattattttg 1805
 tgaagcccct tcacaaaaaa ccttaaggga aatctgatgg tgctcaggaa tctaactctc 1865
 cctaaaccat cctctttaac tgcttctaaa atatctctgt tggcctttct tagccttttt 1925
 ctgtttccat tcagtgtctc aagcgctttt tgtttctaaag ttgagtgtct ggggtttgac 1985
 aggtagtgtgac gtgtagtgtt acactgttaa cttgttaaat acagtgaaaa gtttgtgagt 2045
 gaagaatgct gagaagattg taatgctttg taaaaataaa agtcttgta aaaaaaaaaa 2105
 a 2106

<210> 497
 <211> 1140
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (97)..(606)

```

<400> 497
gggtcgaccc acgcgtccgg cggagggagc gaccagcttt aactctctgc tcgccgcgcg      60
cgctgtcgcc gccacctcct ctgatctacg aaagtc  atg tta ccc aac acc ggg      114
                                         Met Leu Pro Asn Thr Gly
                                         1

agg ctg gca gga tgt aca gtt ttt atc aca ggt gca agc cgt ggc att      162
Arg Leu Ala Gly Cys Thr Val Phe Ile Thr Gly Ala Ser Arg Gly Ile
   7                12                17                22

ggc aaa gct att gca ttg aaa gca gca aag gat gga gca aat att gtt      210
Gly Lys Ala Ile Ala Leu Lys Ala Ala Lys Asp Gly Ala Asn Ile Val
  23                28                33                38

att gct gca aag acc gcc cag cca cat cca aaa ctt cta ggc aca atc      258
Ile Ala Ala Lys Thr Ala Gln Pro His Pro Lys Leu Leu Gly Thr Ile
  39                44                49                54

tat act gct gct gaa gaa att gaa gca gtt gga gga aag gcc ttg cca      306
Tyr Thr Ala Ala Glu Glu Ile Glu Ala Val Gly Gly Lys Ala Leu Pro
  55                60                65                70

tgt att gtt gat gtg aga gat gaa cag cag atc agt gct gca gtg gag      354
Cys Ile Val Asp Val Arg Asp Glu Gln Gln Ile Ser Ala Ala Val Glu
  71                76                81                86

aaa gcc atc aag aaa ttt gga gga att gat att ctg gta aat aat gcc      402
Lys Ala Ile Lys Lys Phe Gly Gly Ile Asp Ile Leu Val Asn Asn Ala
  87                92                97                102

agt gcc att agt ttg acc aat aca ttg gac aca cct acc aag aga ttg      450
Ser Ala Ile Ser Leu Thr Asn Thr Leu Asp Thr Pro Thr Lys Arg Leu
 103                108                113                118

gat ctg atg atg aac gtg aac acc aga ggc acc tac ctt gca tct aaa      498
Asp Leu Met Met Asn Val Asn Thr Arg Gly Thr Tyr Leu Ala Ser Lys
 119                124                129                134

gca tgt att cct tat ttg aaa aag agc aaa gtt gct cat atc ctc aat      546
Ala Cys Ile Pro Tyr Leu Lys Lys Ser Lys Val Ala His Ile Leu Asn
 135                140                145                150

atc agt cca cca ctg aac cta aat cca gtt tgg ttc aaa cag cac tgt      594
Ile Ser Pro Pro Leu Asn Leu Asn Pro Val Trp Phe Lys Gln His Cys
 151                156                161                166

```

ggt agg tgg tag gtg gtaggggtgag gggatggttt gtgcttaatt tgttttgaat 649
 Gly Arg Trp *
 167

taaatctgtg tatgtctgat gtaatcacia tctgcacata acattcatca ttgaattttc 709
 tatgccaagt cattaagtgg catttggaag gtagattctt catcttttat ctgtaattta 769
 aaaaattgag gcataattga cattcaataa aatgcacagc tcttaatggg tcagtttgat 829
 gagttttgag aaatgtatat aaccaacacc caaatcaaga tacagatttt taccatttca 889
 gaaagctctt tcatctccca atgagtgtgt tttactgtgt gtaatttatt catctataaa 949
 gttgggttaa aactatctat gagatacttt atttttctta gacaggtatg cacctgtagt 1009
 cctagctact tgaaaggctg aggtgggagg atcgcttgag cccaggagtt tgaggctgca 1069
 gtgagctagg atcatggcac tgcactcctg cctgggtgac agagcgagac cctgactcta 1129
 aaaaaaaaaa a 1140

<210> 498
 <211> 1279
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (762)..(956)

<400> 498
 ttttgcacga gggcgggggtg tgcttagcgt tgataacaga agattctgag atgggtgaga 60
 agtgggtccac acgtggccac tgtcattcct ctggcataat ggacttgggc tcaggaggtc 120
 aagccctctt caaggagcat gagctgaaat tgctaaactt tgggagtttt ccgtgacacc 180
 cttcaaagtg ctacagggtg ggcattggatc agctggggag ggttgatgtg gttttgccct 240
 gtgggggtatc tatctgtgta cttttgtctg agggaggcaa ctggggccac ttaggccggc 300
 aggtgcccac tgtgattggg tgacatgata ccaagcaaca ggatcatcca gtcaccttca 360
 atgcaggag gatggctgac aggtccctg ggtgacactt catgcaatca gatgtcgagt 420
 tggactgtga catagagcca tgtggccaca ctaaattccc cccaccctt cccctgtcca 480
 caaccgtcat tgtctgttct tgccatccag tggccactgc ctccaccatg gctgaggett 540
 tctotaagac aacctctgag gaagaccaga gcattccagga gcccaaagag gccaaactca 600
 tgacggccca gaagcagaag aagtgagggc ttccagggtc ccgtaggcgc catgccaaca 660

[illegible]

```
<220>  
<221> CDS  
<222> {710}..(1585)
```

1718

acg ctg tgc aat gtg gtc atg cgg cat gac atc cca gac ctg ggc acc	1243
Thr Leu Cys Asn Val Val Met Arg His Asp Ile Pro Asp Leu Gly Thr	
163 168 173 178	
atg tgc gag gcc aag ccc cac ctc atc aca cac ggc ttc tcc tcc cgc	1291
Met Ser Glu Ala Lys Pro His Leu Ile Thr His Gly Phe Ser Ser Arg	
179 184 189 194	
ctg ggc aag cgg gtc tct gac atc ctc cga tac cta ttt ccc gtg ccc	1339
Leu Gly Lys Arg Val Ser Asp Ile Leu Arg Tyr Leu Phe Pro Val Pro	
195 200 205 210	
aaa gat gac agc cac cgg gtc atc acc ttc gca aac cag gac gac tac	1387
Lys Asp Asp Ser His Arg Val Ile Thr Phe Ala Asn Gln Asp Asp Tyr	
211 216 221 226	
ata tca ttc cgg cac cat gtg tat aag aag aca gac cac cgc aac gtg	1435
Ile Ser Phe Arg His His Val Tyr Lys Lys Thr Asp His Arg Asn Val	
227 232 237 242	
gag ctc act gag gtc ggg ccc cgc ttt gag ctg aag ctg tac atg atc	1483
Glu Leu Thr Glu Val Gly Pro Arg Phe Glu Leu Lys Leu Tyr Met Ile	
243 248 253 258	
cgt ctg ggc acg ctg gag cag gag gcc aca gca gac gtg gag tgg cgc	1531
Arg Leu Gly Thr Leu Glu Gln Glu Ala Thr Ala Asp Val Glu Trp Arg	
259 264 269 274	
tgg cac cct tac acc aat acc gca cgc aag aga gtc ttc ctg agc acc	1579
Trp His Pro Tyr Thr Asn Thr Ala Arg Lys Arg Val Phe Leu Ser Thr	
275 280 285 290	
gag tga gcacactcac cactcagtca ggacatggac ttggaactca ggatggggct	1635
Glu *	
291	
gtcatagaca gacccaccag taggaactgt cacagaatgg cctgctgaac tgggatgtgg	1695
aactgtggcg ggtggagagg tctgaataaa ccgtctgtgt catggcaaaa aaaaaa	1751

<210> 500
 <211> 1033
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (156)..(905)

<220>
 <221> misc_feature
 <222> (1)...(1033)
 <223> n = a,t,c or g

<400> 500
aaacaccctt ggggaggatt gatcaagaaa ataatgaaac caagccaagc ttctgnctga 60
gnccaaactc tgttgaccac cgtgaagttc aggtcttaag ccaaagcatg ccactcactc 120
cgaccaggc agtncctagt ggagagaggc cctac atg tgt gtt gag tgt ggg 173
Met Cys Val Glu Cys Gly
1
aag tgc ttt ggc cgg agt tcc cac ctc ctt cag cat cag cgt atc cac 221
Lys Cys Phe Gly Arg Ser Ser His Leu Leu Gln His Gln Arg Ile His
7 12 17 22
act gga gag aag ccc tat gtg tgc agt gta tgt ggg aag gcc ttc agc 269
Thr Gly Glu Lys Pro Tyr Val Cys Ser Val Cys Gly Lys Ala Phe Ser
23 28 33 38
cag agc tca gtc ctt agt aaa cac agg aga att cac aca ggt gag aag 317
Gln Ser Ser Val Leu Ser Lys His Arg Arg Ile His Thr Gly Glu Lys
39 44 49 54
ccc tat gag tgt aat gag tgt gga aaa gcc ttt aga gtg agc tca gat 365
Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ala Phe Arg Val Ser Ser Asp
55 60 65 70
ctt gct cag cat cac aag ata cat aca gga gag aag cct cac gaa tgt 413
Leu Ala Gln His His Lys Ile His Thr Gly Glu Lys Pro His Glu Cys
71 76 81 86
ctt gag tgt cgg aaa gcc ttc act caa ctc tca cat ctc att cag cac 461
Leu Glu Cys Arg Lys Ala Phe Thr Gln Leu Ser His Leu Ile Gln His
87 92 97 102
cag cgg atc cac acg gga gaa agg cca tat gtg tgt ccg ttg tgt ggg 509
Gln Arg Ile His Thr Gly Glu Arg Pro Tyr Val Cys Pro Leu Cys Gly
103 108 113 118
aaa gcc ttc aac cat agc act gtt ctg cgg agc cac cag agg gta cac 557
Lys Ala Phe Asn His Ser Thr Val Leu Arg Ser His Gln Arg Val His
119 124 129 134
act ggg gag aag cct cac agg tgc aat gag tgt ggg aaa acc ttc agt 605
Thr Gly Glu Lys Pro His Arg Cys Asn Glu Cys Gly Lys Thr Phe Ser
135 140 145 150
gtg aag agg aca ctg ctg cag cac cag agg atc cac acc ggg gag aag 653
Val Lys Arg Thr Leu Leu Gln His Gln Arg Ile His Thr Gly Glu Lys
151 156 161 166
ccc tac acg tgc agc gag tgt ggg aag gcc ttc agc gac cgc tca gtc 701
Pro Tyr Thr Cys Ser Glu Cys Gly Lys Ala Phe Ser Asp Arg Ser Val
167 172 177 182
ctc att cag cac cac aac gtg cac acc ggg gag aag ccc tat gag tgc 749
Leu Ile Gln His His Asn Val His Thr Gly Glu Lys Pro Tyr Glu Cys
183 188 193 198

agt gag tgt ggg aag acc ttc agc cac cgc tcc aca ctg atg aat cac 797
 Ser Glu Cys Gly Lys Thr Phe Ser His Arg Ser Thr Leu Met Asn His
 199 204 209 214

gag cgg atc cac acc gag gaa aag ccc tat gca tgc tac gaa tgt ggg 845
 Glu Arg Ile His Thr Glu Glu Lys Pro Tyr Ala Cys Tyr Glu Cys Gly
 215 220 225 230

aag gcc ttc gtt cag cac tca cac ctg atc cag cac cag aaa gtg cac 893
 Lys Ala Phe Val Gln His Ser His Leu Ile Gln His Gln Lys Val His
 231 236 241 246

aga aag ttg tga ccc atggctgaca caagaatcca ttctgacaga aactgcatgt 948
 Arg Lys Leu *
 247

ggaaccacaa gcagccttca gcccaagaga agtctctgtt aactctatag gaagcttttc 1008

tttggcgatt cagtgtcaca aaata 1033

<210> 501
 <211> 1204
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (445)..(1041)

<400> 501
 taagctggac cgcatttttt tttttttttt ttttgaggta gaaaactttt attagctgga 60

gaggttgagg cctacagcgg ggaaaggact tgccagattt tcgccgcaag tcagggccat 120

agcggggggc ataacaaggc ctcccaaccg aacgtcaagc aagagctccg agcgtccac 180

acaagtcccg aacgactcgt tgacgcgcgc ctactgaagg cgcttgggtt cccggactcg 240

gccaccgcct cgccgcttcc gccoctcaga agcatggccg ccacgtagcc cggcccgat 300

tggacgttgg cgggtggacgc aaaccagttg gcaacacgat tggctgctgc ggggtgatga 360

cgctcaggggg cgggtgtcga gtgaatgggg gcagcatgag gccgggcggc ttttttgggc 420

gccggacagc ggctgagtag agcc atg agc cga tgt gtt ttg gag cct cgc 471
 Met Ser Arg Cys Val Leu Glu Pro Arg
 1 5

ccc ccg ggg aag cgg tgg atg gtg gct ggc ctg ggg aat ccc gga ctg 519
 Pro Pro Gly Lys Arg Trp Met Val Ala Gly Leu Gly Asn Pro Gly Leu
 10 15 20 25

ccc ggc acg cga cac agc gtg ggc atg gcg gtg ctg ggg cag ctg gcg 567
 Pro Gly Thr Arg His Ser Val Gly Met Ala Val Leu Gly Gln Leu Ala

26	31	36	41	
cgg cgg ctg ggt gtg gcg gag agt tgg acg cgc gac cgg cac tgt gcc				615
Arg Arg Leu Gly Val Ala Glu Ser Trp Thr Arg Asp Arg His Cys Ala				
42	47	52	57	
gcc gac ctc gcc ctg gcc ccg ctg ggg gat gcc caa ctg gtc ctg ctc				663
Ala Asp Leu Ala Leu Ala Pro Leu Gly Asp Ala Gln Leu Val Leu Leu				
58	63	68	73	
cgg cca cgg cgg ctt atg aac gcc aac ggg cgc agc gtg gcc cgg gct				711
Arg Pro Arg Arg Leu Met Asn Ala Asn Gly Arg Ser Val Ala Arg Ala				
74	79	84	89	
gcg gag ctg ttt ggg ctg act gcc gag gaa gtc tac ctg gtg cat gat				759
Ala Glu Leu Phe Gly Leu Thr Ala Glu Glu Val Tyr Leu Val His Asp				
90	95	100	105	
gag ctg gac aag ccc ctg ggg aga ctg gct ctg aag ctg ggg ggc agt				807
Glu Leu Asp Lys Pro Leu Gly Arg Leu Ala Leu Lys Leu Gly Gly Ser				
106	111	116	121	
gcc agg ggc cac aat gga gtc cgt tcc tgc att agc tgc ctc aac tcc				855
Ala Arg Gly His Asn Gly Val Arg Ser Cys Ile Ser Cys Leu Asn Ser				
122	127	132	137	
aat gca atg cca agg ctg cgg gtg ggt atc ggg cgc ccg gcg cac cct				903
Asn Ala Met Pro Arg Leu Arg Val Gly Ile Gly Arg Pro Ala His Pro				
138	143	148	153	
gag gcg gtt cag gcc cat gtg ctg ggc tgc ttc tcc cct gct gag cag				951
Glu Ala Val Gln Ala His Val Leu Gly Cys Phe Ser Pro Ala Glu Gln				
154	159	164	169	
gag ctg ctg cct ctg ttg ctg gat cga gcc acc gac ctg atc ttg gac				999
Glu Leu Leu Pro Leu Leu Leu Asp Arg Ala Thr Asp Leu Ile Leu Asp				
170	175	180	185	
cac atc cgt gag cga agc cag ggg ccc tca ctg ggg ccg tga cactagt				1048
His Ile Arg Glu Arg Ser Gln Gly Pro Ser Leu Gly Pro *				
186	191	196		
ggccatggct gcctgcctga ctgtagtgcc caccaaccga gccactgcca cagagctgcc				1108
acgccagcct tggatatctac tttttatata aatctcctct agactgttcc aggctgcctg				1168
cggattaaag tgggggtgac tgtgaaaaaa aaaaaa				1204

<210> 502
 <211> 2208
 <212> DNA
 <213> Homo sapiens
 <220>

<221> CDS

<222> (88)..(1956)

<400> 502

cgatattttcc gggcagaccc acgcagccgg tccggacagc cgcgcgctga ggggtctcggg 60

gcggggcgccg cgggacctct ccggggcc atg gca gcc cct gtc aaa ggg aac 111
Met Ala Ala Pro Val Lys Gly Asn
1 5

agg aag cag tcc acg gag ggt gac gcc cta gac cca cct gca tcc ccc 159
Arg Lys Gln Ser Thr Glu Gly Asp Ala Leu Asp Pro Pro Ala Ser Pro
9 14 19 24

aaa cct gct ggc aag cag aac gga atc cag aac ccc atc tcg ctg gag 207
Lys Pro Ala Gly Lys Gln Asn Gly Ile Gln Asn Pro Ile Ser Leu Glu
25 30 35 40

gac tcc ccc gag gca ggc ggg gag cgg gag gag gag cag gag cgg gag 255
Asp Ser Pro Glu Ala Gly Gly Glu Arg Glu Glu Glu Gln Glu Arg Glu
41 46 51 56

gag gag cag gcc ttc ctg gtc agc ctc tac aag ttc atg aag gag cga 303
Glu Glu Gln Ala Phe Leu Val Ser Leu Tyr Lys Phe Met Lys Glu Arg
57 62 67 72

cac acg ccc atc gag agg gtg ccc cat ctc ggc ttc aag cag att aac 351
His Thr Pro Ile Glu Arg Val Pro His Leu Gly Phe Lys Gln Ile Asn
73 78 83 88

ctg tgg aag atc tac aaa gca gtg gag aag ctg ggg gcc tat gag ctg 399
Leu Trp Lys Ile Tyr Lys Ala Val Glu Lys Leu Gly Ala Tyr Glu Leu
89 94 99 104

gtg acc ggg cgc cgc ctc tgg aag aac gtg tac gac gag ctg ggg ggc 447
Val Thr Gly Arg Arg Leu Trp Lys Asn Val Tyr Asp Glu Leu Gly Gly
105 110 115 120

agc cca ggc agc acc agc gcg gcc acg tgc acg cgc cgc cac tac gag 495
Ser Pro Gly Ser Thr Ser Ala Ala Thr Cys Thr Arg Arg His Tyr Glu
121 126 131 136

agg ctg gtc ctg cca tac gtg cgg cac ctg aag ggg gag gat gac aag 543
Arg Leu Val Leu Pro Tyr Val Arg His Leu Lys Gly Glu Asp Asp Lys
137 142 147 152

ccg ctg ccc acc tcc aag ccc agg aaa cag tac aag atg gct aag gag 591
Pro Leu Pro Thr Ser Lys Pro Arg Lys Gln Tyr Lys Met Ala Lys Glu
153 158 163 168

aac agg ggg gat gat ggg gcc acc gag agg ccg aag aag gcc aag gag 639
Asn Arg Gly Asp Asp Gly Ala Thr Glu Arg Pro Lys Lys Ala Lys Glu
169 174 179 184

gag cgg cgc atg gac cag atg atg cca gga aag acc aaa gca gat gct 687
Glu Arg Arg Met Asp Gln Met Met Pro Gly Lys Thr Lys Ala Asp Ala
185 190 195 200

gct gac cca gca cca ctt ccc agc cag gag ccc ccc agg aac agc aca	735
Ala Asp Pro Ala Pro Leu Pro Ser Gln Glu Pro Pro Arg Asn Ser Thr	
201 206 211 216	
gaa cag cag ggc ctg gcc tct ggg tct tct gtg tcc ttt gtg ggt gcc	783
Glu Gln Gln Gly Leu Ala Ser Gly Ser Ser Val Ser Phe Val Gly Ala	
217 222 227 232	
agc ggc tgt cct gag gcc tac aag cgg ctc cta tcc agc ttc tac tgc	831
Ser Gly Cys Pro Glu Ala Tyr Lys Arg Leu Leu Ser Ser Phe Tyr Cys	
233 238 243 248	
aag ggg aca cac ggc atc atg tca cca ctg gcc aaa aag aag ctc ctg	879
Lys Gly Thr His Gly Ile Met Ser Pro Leu Ala Lys Lys Lys Leu Leu	
249 254 259 264	
gcc cag gtg agc aag gtg gag gcc ttg cag tgc cag gag gag ggc tgc	927
Ala Gln Val Ser Lys Val Glu Ala Leu Gln Cys Gln Glu Glu Gly Cys	
265 270 275 280	
cgc cat ggg gca gag ccc cag gcg tcc cca gct gtt cac ctc cca gag	975
Arg His Gly Ala Glu Pro Gln Ala Ser Pro Ala Val His Leu Pro Glu	
281 286 291 296	
agt ccc cag agc ccc aaa ggg ctg act gag aac tcc agg cac cgg ctg	1023
Ser Pro Gln Ser Pro Lys Gly Leu Thr Glu Asn Ser Arg His Arg Leu	
297 302 307 312	
acc cct cag gag gga ttg cag gcc cca ggt ggc agc ctc aga gag gag	1071
Thr Pro Gln Glu Gly Leu Gln Ala Pro Gly Gly Ser Leu Arg Glu Glu	
313 318 323 328	
gcg cag gca ggc ccc tgc ccg gca gcc ccc atc ttc aag ggc tgc ttc	1119
Ala Gln Ala Gly Pro Cys Pro Ala Ala Pro Ile Phe Lys Gly Cys Phe	
329 334 339 344	
tac acc cac ccc acc gag gtg ctg aag cct gtc agc cag cac ccc agg	1167
Tyr Thr His Pro Thr Glu Val Leu Lys Pro Val Ser Gln His Pro Arg	
345 350 355 360	
gac ttc ttc tct aga ctt aaa gat ggg gtg cta ttg ggg cct cct ggc	1215
Asp Phe Phe Ser Arg Leu Lys Asp Gly Val Leu Leu Gly Pro Pro Gly	
361 366 371 376	
aaa gag ggg ctg tca gtg aaa gag ccc cag ctg gtg tgg ggc gga gac	1263
Lys Glu Gly Leu Ser Val Lys Glu Pro Gln Leu Val Trp Gly Gly Asp	
377 382 387 392	
gct aac cgc cct tct gcg ttc cat aaa ggt ggc tcc aga aag ggc atc	1311
Ala Asn Arg Pro Ser Ala Phe His Lys Gly Gly Ser Arg Lys Gly Ile	
393 398 403 408	
ctc tac ccc aag ccc aaa gcc tgc tgg gtg tcc ccc atg gcc aag gtc	1359
Leu Tyr Pro Lys Pro Lys Ala Cys Trp Val Ser Pro Met Ala Lys Val	
409 414 419 424	

cca gcc gag agc ccc acg ctc ccg ccc acc ttc ccc agt agc cca ggc	1407
Pro Ala Glu Ser Pro Thr Leu Pro Pro Thr Phe Pro Ser Ser Pro Gly	
425 430 435 440	
ctg ggc agc aag cgc agc ctg gag gaa gag ggt gct gcc cac agt ggg	1455
Leu Gly Ser Lys Arg Ser Leu Glu Glu Glu Gly Ala Ala His Ser Gly	
441 446 451 456	
aag aga ctg cgg gcc gtg tct ccc ttt ctt aag gag gcg gat gcc aag	1503
Lys Arg Leu Arg Ala Val Ser Pro Phe Leu Lys Glu Ala Asp Ala Lys	
457 462 467 472	
aag tgt ggg gcc aaa cct gca ggg tcc ggc ctg gtc tcc tgc ctt ctg	1551
Lys Cys Gly Ala Lys Pro Ala Gly Ser Gly Leu Val Ser Cys Leu Leu	
473 478 483 488	
ggc cca gcc ctg ggg cct gtg ccc cca gag gcc tac agg ggc acc atg	1599
Gly Pro Ala Leu Gly Pro Val Pro Pro Glu Ala Tyr Arg Gly Thr Met	
489 494 499 504	
ctg cac tgc ccg ctg aac ttc act ggc acc ccg ggc ccc ttg aag ggc	1647
Leu His Cys Pro Leu Asn Phe Thr Gly Thr Pro Gly Pro Leu Lys Gly	
505 510 515 520	
cag gct gca ctc ccc ttc agc ccc ctg gtc atc ccg gcc ttc ccg gcc	1695
Gln Ala Ala Leu Pro Phe Ser Pro Leu Val Ile Pro Ala Phe Pro Ala	
521 526 531 536	
cac ttc ctg gcc acc gca ggg ccc ctc gcc cat ggc cgc tgg cct gat	1743
His Phe Leu Ala Thr Ala Gly Pro Leu Ala His Gly Arg Trp Pro Asp	
537 542 547 552	
gca ctt ccc ccc aac gtc ctt cga cag tgc cct ccg cca cag act ttg	1791
Ala Leu Pro Pro Asn Val Leu Arg Gln Cys Pro Pro Pro Gln Thr Leu	
553 558 563 568	
ccc ggc ctc atc tgc ctg gca cgc acc acc agt cac aac cta tgc agc	1839
Pro Gly Leu Ile Cys Leu Ala Arg Thr Thr Ser His Asn Leu Cys Ser	
569 574 579 584	
gcc cca ctt ctt cca cct caa cac caa gct gta ggc cag ccc atg gtg	1887
Ala Pro Leu Leu Pro Pro Gln His Gln Ala Val Gly Gln Pro Met Val	
585 590 595 600	
ttg tgt aca ctg tgg agt cga cag ggg cct aca aca ggc agg tac tgc	1935
Leu Cys Thr Leu Trp Ser Arg Gln Gly Pro Thr Thr Gly Arg Tyr Cys	
601 606 611 616	
tgc cag ggg gct ctg aac tag tg cctgctaccc aggacaccg ggccatgcc	1988
Cys Gln Gly Ala Leu Asn *	
617 622	
ctggctgggc agcctggcac aagtgaagaa gaaggcagtg ggaaaactgg gtttatotca	2048
aggcagcagc ctgagcccag gagcagagga ccagttgtt ataaggcgct gggagaggat	2108
gggcagctcc cactgcccc gagcggagct cgaagcacco aggttgccca cggaataatcc	2168

aataaaaaga caccagtgtg aatccaaaaa aaaaaaaaaa

2208

<210> 503
<211> 1282
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (266)..(793)

<400> 503

ctagtatacc gatacgcag ctggctagcg tttaaactta agcttggtac cgagctcgga	60
tccactagtc cagtgtggtg gaattcccaa gacgagcgcg gtcgcggaag tatcgcggt	120
tacatatctc gcagccaggc gggtcctggg agaggcgcga gccaggcctg gtcggcgccc	180
gcggagaaaa gaagcagtca agcccatgaa ctacaacccc ggttgccgct ttctcctctc	240
ctaaccgtta agtgcgctaa gggcc atg gct gag gtg cac gtg atc ggg cag	292
Met Ala Glu Val His Val Ile Gly Gln	
1 5	
atc ata ggg gcc agc ggt ttc tcg gaa agt agc ctc ttc tgc aag tgg	340
Ile Ile Gly Ala Ser Gly Phe Ser Glu Ser Ser Leu Phe Cys Lys Trp	
10 15 20 25	
ggc att cac aca ggg gcg gca tgg aag ctc ctg tca ggc gtg cgg gag	388
Gly Ile His Thr Gly Ala Ala Trp Lys Leu Leu Ser Gly Val Arg Glu	
26 31 36 41	
ggc caa acg caa gtg gac acc ccg cag ata ggg gac atg gct tac tgg	436
Gly Gln Thr Gln Val Asp Thr Pro Gln Ile Gly Asp Met Ala Tyr Trp	
42 47 52 57	
tcc cac ccc atc gac ctg cac ttc gcc acc aaa ggt ctt caa ggc tgg	484
Ser His Pro Ile Asp Leu His Phe Ala Thr Lys Gly Leu Gln Gly Trp	
58 63 68 73	
ccc cgg ctc cat ttc cag gtg tgg tcc cag gac agc ttt ggc cgc tgc	532
Pro Arg Leu His Phe Gln Val Trp Ser Gln Asp Ser Phe Gly Arg Cys	
74 79 84 89	
cag ctt gca ggc tat gga ttt tgc cat gtg ccc agt agc ccg ggc acc	580
Gln Leu Ala Gly Tyr Gly Phe Cys His Val Pro Ser Ser Pro Gly Thr	
90 95 100 105	
cac cag ctg gcc tgc ccc acg tgg cgg ccc ctg ggc agt tgg cga gaa	628
His Gln Leu Ala Cys Pro Thr Trp Arg Pro Leu Gly Ser Trp Arg Glu	
106 111 116 121	
cag ttg gca cgg gct ttc gtg ggt ggt ggg ccg cag ctg ctg cat ggg	676

Gln	Leu	Ala	Arg	Ala	Phe	Val	Gly	Gly	Gly	Pro	Gln	Leu	Leu	His	Gly	
122					127					132					137	

gac	acc	atc	tac	agt	ggg	gcc	gac	cgc	tat	cgc	ctg	cac	aca	gct	gct	724
Asp	Thr	Ile	Tyr	Ser	Gly	Ala	Asp	Arg	Tyr	Arg	Leu	His	Thr	Ala	Ala	
138					143					148					153	

ggt	ggc	acc	gtg	cac	ctg	gag	atc	ggc	ctg	ctg	ctc	cgc	aac	ttc	gac	772
Gly	Gly	Thr	Val	His	Leu	Glu	Ile	Gly	Leu	Leu	Leu	Arg	Asn	Phe	Asp	
154					159					164					169	

cgc	tac	ggc	gtg	gag	tgc	tga	gg	gactctgcct	ccaacatcac	caccatccac	825
Arg	Tyr	Gly	Val	Glu	Cys	*					
170					175						

accccgagaca	cccagtgatg	ggggaggatg	gcacagtggt	caagagcaca	gactctagag	885
-------------	------------	------------	------------	------------	------------	-----

actgtcagag	ctgaccccag	ctaaggcatg	gcaccgcttc	tgtcctttct	aggacctcgg	945
------------	------------	------------	------------	------------	------------	-----

ggtccctotg	ggcccagttt	ccctatctgt	aaattgggga	cagtaaatgt	atgggggtcgc	1005
------------	------------	------------	------------	------------	-------------	------

aggggtgttga	gtgacaggag	gctgottagc	cacatgggag	gtgctcagta	aaggagagca	1065
-------------	------------	------------	------------	------------	------------	------

attottacag	gtgtctgcct	cctgaccctt	ccatccttca	ggtgtcctgt	tgccccctcc	1125
------------	------------	------------	------------	------------	------------	------

tcccaactgac	accctccgga	ggcccccatg	ttgacagacc	ctctttctcct	accttgtttc	1185
-------------	------------	------------	------------	-------------	------------	------

ccagcctgac	tctccttcog	ttctgggtcc	ccctcatctg	gtcggctccc	ctgtgtctca	1245
------------	------------	------------	------------	------------	------------	------

tcccccgacg	aaatcgtcga	cccgggacac	gatggcc	1282
------------	------------	------------	---------	------

<210> 504
 <211> 400
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (223)..(399)

<400> 504		
gccctgggtgg	gaaaagtcca caatttccca ttgatagctt tttactgcag agaaaaagg	60

aagcgtcagc	cacacaaaag cctgcgtgac cgtcgttcg gagaagctct cgaccctaac	120
------------	---	-----

tgcaagtcaact	gttacttggga tcagatcaag cgcagagact ttttgggatc cagtgggttat	180
--------------	--	-----

tctccacact	tcggagccat ttcaaccaac tctgagcaca aa	atg cag cca tcc	234
		Met Gln Pro Ser	
		1	

tct	atg	cag	cag	gcc	ctg	ccc	agt	cag	cga	ccc	tac	tgg	aca	gat	cca	282
Ser	Met	Gln	Gln	Ala	Leu	Pro	Ser	Gln	Arg	Pro	Tyr	Trp	Thr	Asp	Pro	
5					10					15					20	

agg cca gcc ctg gtt ccc tgc tgc agc cac cgt cct gac gtt cat egg	330
Arg Pro Ala Leu Val Pro Cys Cys Ser His Arg Pro Asp Val His Arg	
21 26 31 36	
agg agg ccg ggg cct ggc ctt ccc ggc aca gga ggc tgt tct gac agg	378
Ser Arg Pro Gly Pro Gly Leu Pro Gly Thr Gly Gly Cys Ser Asp Arg	
37 42 47 52	
ccc cca gct tgt ccc atc tga t	400
Pro Pro Ala Cys Pro Ile *	
53 58	

<210> 505
 <211> 1025
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (77) .. (775)

<400> 505	
attacaccag cgtggtggaa ttaaggggtgt ggcgcgagca gcgtcggttg ttggccggcg	60
gcggggccggg acgggc atg gcc ctg ctg ctg tgc ctg gtg tgc ctg acg	109
Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr	
1 5	
gcg gcg ctg gcc cac ggc tgt ctg cac tgc cac agc aac ttc tcc aag	157
Ala Ala Leu Ala His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys	
12 17 22 27	
aag ttc tcc ttc tac cgc cac cat gtg aac ttc aag tcc tgg tgg gtg	205
Lys Phe Ser Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val	
28 33 38 43	
ggc gac atc ccc gtg tca ggg gcg ctg ctc acc gac tgg agc gac gac	253
Gly Asp Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp	
44 49 54 59	
acg atg aag gag ctg cac ctg gcc atc ccc gcc aag atc acc cgg gag	301
Thr Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu	
60 65 70 75	
aag ctg gac caa gtg gcg aca gca gtg tac cag atg atg gat cag ctg	349
Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln Leu	
76 81 86 91	
tac cag ggg aag atg tac ttc ccc ggg tat ttc ccc aac gag ctg cga	397
Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu Leu Arg	
92 97 102 107	

aac atc ttc cgg gag cag gtg cac ctc atc cag aac gcc atc atc gaa	445
Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala Ile Ile Glu	
108 113 118 123	
agc cgc atc gac tgt cag cac cgc tgt ggc atc ttc cag tac gag acc	493
Ser Arg Ile Asp Cys Gln His Arg Cys Gly Ile Phe Gln Tyr Glu Thr	
124 129 134 139	
atc tcc tgc aac aac tgc aca gac tcg cac gtc gcc tgc ttt ggc tat	541
Ile Ser Cys Asn Asn Cys Thr Asp Ser His Val Ala Cys Phe Gly Tyr	
140 145 150 155	
aac tgc gag tcc tcg gcg cag tgg aag tca gct gtc cag ggc ctc ctg	589
Asn Cys Glu Ser Ser Ala Gln Trp Lys Ser Ala Val Gln Gly Leu Leu	
156 161 166 171	
aac tac ata aat aac tgg cac aaa cag gac acg agc atg aga cca cgc	637
Asn Tyr Ile Asn Asn Trp His Lys Gln Asp Thr Ser Met Arg Pro Arg	
172 177 182 187	
tcc tct gcc ttc tcc tgg cct ggg aca cac aga gcc acc ccg gcc ttc	685
Ser Ser Ala Phe Ser Trp Pro Gly Thr His Arg Ala Thr Pro Ala Phe	
188 193 198 203	
ctg gta tcg cca gcc tta agg tgt ctg gag ccc cca cac ttg gcc aac	733
Leu Val Ser Pro Ala Leu Arg Cys Leu Glu Pro Pro His Leu Ala Asn	
204 209 214 219	
ctg acc ttg gaa gat gct gct gag tgt ctc aag cag cac tga cagcagc	782
Leu Thr Leu Glu Asp Ala Ala Glu Cys Leu Lys Gln His *	
220 225 230	
tgggcctgcc ccagggcaac gtgggggcgg agactcagct ggacagcccc tgccctgtcac	842
tctggagctg ggctgctgct gcctcaggac cccctctccg accccggaca gagctgagct	902
ggccaggggcc aggagggcgg gagggagggga atgggggtgg gctgtgcgca gcatcagcgc	962
ctgggcaggt ccgcagagct gcgggatgtg attaaagtcc ctgatgtttc aaaaaaaaaa	1022
aaa	1025

<210> 506
 <211> 649
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (130)..(516)

<400> 506	
caagcctaata accgactcac tatagggaaa gctgggtacgc ctgcaggtac ggccggaatc	60

```

ccgggtcgtc tactactact aaattcgcg cgggtcgacg tgtgctgttg aaggggggag      120

actagagaa      atg gca ggg aac ctc tta tcc ggg gca ggt agg cgc ctg      168
                Met Ala Gly Asn Leu Leu Ser Gly Ala Gly Arg Arg Leu
                  1                5                10

tgg gac tgg gtg cct ctg gcg tgc aga agc ttc tct ctt ggt gtg cct      216
Trp Asp Trp Val Pro Leu Ala Cys Arg Ser Phe Ser Leu Gly Val Pro
  14                19                24                29

aga ttg atc ggt ata agg ctc act ctc ccg ccc ccc aaa gtg gtt gat      264
Arg Leu Ile Gly Ile Arg Leu Thr Leu Pro Pro Pro Lys Val Val Asp
  30                35                40                45

cgt tgg aac gag aaa agg gcc atg ttc gga gtg tat gac aac atc ggg      312
Arg Trp Asn Glu Lys Arg Ala Met Phe Gly Val Tyr Asp Asn Ile Gly
  46                51                56                61

atc ctg gga aac ttt gaa aag cac ccc aaa gaa ctg atc agg ggg ccc      360
Ile Leu Gly Asn Phe Glu Lys His Pro Lys Glu Leu Ile Arg Gly Pro
  62                67                72                77

ata tgg ctt cga ggt tgg aaa ggg aat gaa ttg caa cgt tgt atc cga      408
Ile Trp Leu Arg Gly Trp Lys Gly Asn Glu Leu Gln Arg Cys Ile Arg
  78                83                88                93

aag agg aaa atg gtt gga agt aga ata ttc gct gat gac ctg cac aac      456
Lys Arg Lys Met Val Gly Ser Arg Ile Phe Ala Asp Asp Leu His Asn
  94                99                104                109

ctt aat aaa cgc atc cgc tat ctc tac aaa cac ttt aac cga cat ggg      504
Leu Asn Lys Arg Ile Arg Tyr Leu Tyr Lys His Phe Asn Arg His Gly
  110                115                120                125

aag ttt cga tag aag agaaagctga gaacttcgga aaaggctcat ctgtcaccct      559
Lys Phe Arg  *
126

ggagaaggga aactgtactt ttccctgtga ggaaacggct ttgtattttc tctgtaataa      619

aatggggcctt ctttggaataa aaaaaaaaaa      649

```

```

<210> 507
<211> 1861
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (186)..(1832)

```

```

<400> 507
ggaactccct gtattgagga agaaattaga ctagttggct tcaaagatct aggggaatga      60

```


Thr Val Tyr Val Thr	Asp Cys Arg Val Ser Thr Ser Ala Phe Ser Lys	
207	212 217 222	
gcc ggc atg tgc ctt cgc tgc tca gcc tgt gcc ttg aac tcg gtg gtg		899
Ala Gly Met Cys Leu Arg Cys Ser Ala Cys Ala Leu Asn Ser Val Val		
223	228 233 238	
cag agc gtg ctg agc aag cgg aca ctg cag gcc cgc agc atg cac gag		947
Gln Ser Val Leu Ser Lys Arg Thr Leu Gln Ala Arg Ser Met His Glu		
239	244 249 254	
gtc atc gag ctg ctc aac gtg tgc gag gac ctg gcg ggc tcc acg ggc		995
Val Ile Glu Leu Leu Asn Val Cys Glu Asp Leu Ala Gly Ser Thr Gly		
255	260 265 270	
ctg gcc aag gag acc ttc ggg tcg ctg gag gag acg tct cca cca ccc		1043
Leu Ala Lys Glu Thr Phe Gly Ser Leu Glu Glu Thr Ser Pro Pro Pro		
271	276 281 286	
tgc tgg aac tcg gtg acg gac tca ctg ttg ctg gtg cat gag cgc tat		1091
Cys Trp Asn Ser Val Thr Asp Ser Leu Leu Leu Val His Glu Arg Tyr		
287	292 297 302	
gag cag atc tgc gag ttc tac agc cgg gcc aag aag atg aac ctc atc		1139
Glu Gln Ile Cys Glu Phe Tyr Ser Arg Ala Lys Lys Met Asn Leu Ile		
303	308 313 318	
cag agc ctc aac aag cac ctg ctc agc aac ctg gcg gcc atc ctg acg		1187
Gln Ser Leu Asn Lys His Leu Leu Ser Asn Leu Ala Ala Ile Leu Thr		
319	324 329 334	
ccg gtg aag cag gca gtc atc gag ctg agc aac gag agc cag ccc acc		1235
Pro Val Lys Gln Ala Val Ile Glu Leu Ser Asn Glu Ser Gln Pro Thr		
335	340 345 350	
ctg cag ctg gtg ctg ccc acc tac gtc agg ctg gag aag ctg ttc acg		1283
Leu Gln Leu Val Leu Pro Thr Tyr Val Arg Leu Glu Lys Leu Phe Thr		
351	356 361 366	
gcc aag gcc aac gac gca ggc act gtc agc aag ctc tgc cac ctc ttc		1331
Ala Lys Ala Asn Asp Ala Gly Thr Val Ser Lys Leu Cys His Leu Phe		
367	372 377 382	
ctg gag gcg ctc aag gag aac ttc aag gtg cac ccg gcc cac aag gtg		1379
Leu Glu Ala Leu Lys Glu Asn Phe Lys Val His Pro Ala His Lys Val		
383	388 393 398	
gcc atg atc ctg gac ccg cag cag aag ctg cgg cct gtg cca ccc tac		1427
Ala Met Ile Leu Asp Pro Gln Gln Lys Leu Arg Pro Val Pro Pro Tyr		
399	404 409 414	
cag cac gag gag atc atc ggc aag gtc tgt gag ctc atc aac gag gtg		1475
Gln His Glu Glu Ile Ile Gly Lys Val Cys Glu Leu Ile Asn Glu Val		
415	420 425 430	
aag gag tcc tgg gcc gag gag gcc gac ttc gag ccc gct gcc aag aag		1523
Lys Glu Ser Trp Ala Glu Glu Ala Asp Phe Glu Pro Ala Ala Lys Lys		

431	436	441	446	
ccc cgc tct gct gcc gtc gag aac ccc gca gct cag gaa gat gat cgg				1571
Pro Arg Ser Ala Ala Val Glu Asn Pro Ala Ala Gln Glu Asp Asp Arg				
447	452	457	462	
cta ggc aaa aat gaa gtg tac gat tac ctg cag gag ccc ctc ttc cag				1619
Leu Gly Lys Asn Glu Val Tyr Asp Tyr Leu Gln Glu Pro Leu Phe Gln				
463	468	473	478	
gct acc cct gat ctc ttc cag tac tgg tcg tgc gtt acc caa aag cac				1667
Ala Thr Pro Asp Leu Phe Gln Tyr Trp Ser Cys Val Thr Gln Lys His				
479	484	489	494	
aca aaa ctc gcc aag ctc gcc ttc tgg ctc ctg gcg gtt ccg gcc gtg				1715
Thr Lys Leu Ala Lys Leu Ala Phe Trp Leu Leu Ala Val Pro Ala Val				
495	500	505	510	
ggc gcc aga agc ggg tgt gta aat atg tgt gaa caa gcg ctt cta atc				1763
Gly Ala Arg Ser Gly Cys Val Asn Met Cys Glu Gln Ala Leu Leu Ile				
511	516	521	526	
aaa cgg agg cgg ctg ctc agt cca gaa gat atg aat aaa ctc atg ttt				1811
Lys Arg Arg Arg Leu Leu Ser Pro Glu Asp Met Asn Lys Leu Met Phe				
527	532	537	542	
ctg aaa tcc aac atg ctt taa gacttgactt cgggggaaaa aaaaaaaaaa				1861
Leu Lys Ser Asn Met Leu *				
543	548			

<210> 508
 <211> 1349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (296)..(994)

<400> 508	
agcgcccat gaattcgaag ctgtacgcct gcggtaccgg tccggaattc cgggtcgac	60
gggaggcagg agaacggaag ctgggagcag ggaaagcctt ttgtcctgag cttttctggc	120
aagggacttt gcatattggt tttgcatctc atttacttct ccattgggtc aggataaaga	180
tggggaatcc cctcctctcc aaacctgccc ccaaaccctt ccttcttgaa ccagaactct	240
cctctccccc gtactccttc ctggaccgag ctggaagccc tggcggcggc ggccc atg	298
	Met
	1
ggg ccc ttg gcg ctg ccc gcc tgg ctg cag ccc agg tat agg aag aat	346

Gly	Pro	Leu	Ala	Leu	Pro	Ala	Trp	Leu	Gln	Pro	Arg	Tyr	Arg	Lys	Asn		
2					7					12					17		
gcg	tat	ctt	ttc	atc	tat	tac	tta	atc	cag	ttc	tgt	ggc	cac	tct	tgg	394	
Ala	Tyr	Leu	Phe	Ile	Tyr	Tyr	Leu	Ile	Gln	Phe	Cys	Gly	His	Ser	Trp		
18					23					28					33		
ata	ttt	aca	aat	atg	aca	gtc	aga	ttc	ttt	tca	ttt	gga	aaa	gat	tca	442	
Ile	Phe	Thr	Asn	Met	Thr	Val	Arg	Phe	Phe	Ser	Phe	Gly	Lys	Asp	Ser		
34					39					44					49		
atg	gtt	gac	act	ttt	tat	gct	att	gga	ctt	gtg	atg	cga	ctt	tgc	caa	490	
Met	Val	Asp	Thr	Phe	Tyr	Ala	Ile	Gly	Leu	Val	Met	Arg	Leu	Cys	Gln		
50					55					60					65		
tcc	gta	tct	ctc	ctg	gaa	ctg	ctg	cac	ata	tat	gtt	ggc	att	gag	tca	538	
Ser	Val	Ser	Leu	Leu	Glu	Leu	Leu	His	Ile	Tyr	Val	Gly	Ile	Glu	Ser		
66					71					76					81		
aac	cat	ctt	ctc	cca	agg	ttt	ttg	cag	ctc	aca	gaa	aga	ata	atc	atc	586	
Asn	His	Leu	Leu	Pro	Arg	Phe	Leu	Gln	Leu	Thr	Glu	Arg	Ile	Ile	Ile		
82					87					92					97		
ctt	ttt	gtg	gtg	atc	acc	agt	caa	gag	gaa	gtc	caa	gag	aaa	tat	gtg	634	
Leu	Phe	Val	Val	Ile	Thr	Ser	Gln	Glu	Glu	Val	Gln	Glu	Lys	Tyr	Val		
98					103					108					113		
gtg	tgt	gtt	tta	ttc	gtc	ttt	tgg	aat	cta	ttg	gat	atg	gtt	agg	tac	682	
Val	Cys	Val	Leu	Phe	Val	Phe	Trp	Asn	Leu	Leu	Asp	Met	Val	Arg	Tyr		
114					119					124					129		
act	tat	agc	atg	tta	tca	gtc	ata	gga	ata	tcc	tat	gct	gtc	ttg	aca	730	
Thr	Tyr	Ser	Met	Leu	Ser	Val	Ile	Gly	Ile	Ser	Tyr	Ala	Val	Leu	Thr		
130					135					140					145		
tgg	ctc	agt	caa	aca	cta	tgg	atg	cca	att	tat	cct	ttg	tgt	gtt	ctt	778	
Trp	Leu	Ser	Gln	Thr	Leu	Trp	Met	Pro	Ile	Tyr	Pro	Leu	Cys	Val	Leu		
146					151					156					161		
gct	gaa	gca	ttt	gcc	atc	tat	caa	tcg	ctg	cct	tat	ttt	gaa	tca	ttt	826	
Ala	Glu	Ala	Phe	Ala	Ile	Tyr	Gln	Ser	Leu	Pro	Tyr	Phe	Glu	Ser	Phe		
162					167					172					177		
ggc	act	tat	tcc	acc	aag	ctg	ccc	ttt	gac	tta	tcc	atc	tat	ttc	cca	874	
Gly	Thr	Tyr	Ser	Thr	Lys	Leu	Pro	Phe	Asp	Leu	Ser	Ile	Tyr	Phe	Pro		
178					183					188					193		
tat	gtg	ctg	aaa	ata	tat	ctc	atg	atg	ctc	ttt	ata	ggt	atg	tat	ttt	922	
Tyr	Val	Leu	Lys	Ile	Tyr	Leu	Met	Met	Leu	Phe	Ile	Gly	Met	Tyr	Phe		
194					199					204					209		
acc	tac	agt	cat	cta	tac	tca	gaa	aga	aga	gac	atc	ctc	gga	atc	ttt	970	
Thr	Tyr	Ser	His	Leu	Tyr	Ser	Glu	Arg	Arg	Asp	Ile	Leu	Gly	Ile	Phe		
210					215					220					225		
ccc	att	aaa	aaa	aag	aag	atg	tga	agtagcat	tccagtgtga	cacgagaaaa	1024						
Pro	Ile	Lys	Lys	Lys	Lys	Met	*										

226

231

gagaggctgt ggattcagtg cagtaaataa aacacaggaa gtattctggg ggaaaaatac 1084
 cttgtatttg ataaaaatcc attacatgaa ataactgcac atacccccaa aactctagac 1144
 ataacaggct atgtttttca cacattgtat ttttaagaca tatatattct ccataccctg 1204
 cttcaccaaaa attcctgctt catttggtt ttatacaagt tatacttaca ttgtatgaag 1264
 tctgattatt ttcctgtaag tttaatgaga aataggagat tagctgcaat agattcaatt 1324
 aaattaagaa accaaaaaaa aaaaa 1349

<210> 509

<211> 1397

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (155)..(1258)

<220>

<221> misc_feature

<222> (1)...(1397)

<223> n = a,t,c or g

<400> 509

ccggaattcc cgggtcgacc cagcggtccg ctattttggt ggttttggtt cggttagcta 60

gatagacgat cagctgaaca ctctcttgaa ggagttccag ctaacagagg agaactactaa 120

gctccgatat ctcacctggt ctcttattga agac atg gcc gcc gcg tat ttt 172
 Met Ala Ala Ala Tyr Phe
 1

cca gac tgc ata gtc aga ccc ttt ggc tcc tca gtc aac act ttt ggg 220
 Pro Asp Cys Ile Val Arg Pro Phe Gly Ser Ser Val Asn Thr Phe Gly
 7 12 17 22

aag tta gga tgt gat ttg gac atg ttt ttg gat cta gat gaa acc aga 268
 Lys Leu Gly Cys Asp Leu Asp Met Phe Leu Asp Leu Asp Glu Thr Arg
 23 28 33 38

aac ctc agc gct cac aag atc tca gga aat ttt ctg atg gaa ttt caa 316
 Asn Leu Ser Ala His Lys Ile Ser Gly Asn Phe Leu Met Glu Phe Gln
 39 44 49 54

gtg aaa aat gtt cct tca gaa aga att gca act cag aag atc ctg tct 364
 Val Lys Asn Val Pro Ser Glu Arg Ile Ala Thr Gln Lys Ile Leu Ser
 55 60 65 70

gtg tta gga gag tgc ctt gac cac ttt ggc cct ggc tgt gtg ggt gtg 412

Val	Leu	Gly	Glu	Cys	Leu	Asp	His	Phe	Gly	Pro	Gly	Cys	Val	Gly	Val		
71					76					81					86		
caa	aaa	ata	tta	aat	gcc	cgg	tgt	ccg	ctc	gtg	agg	ttc	tca	cac	cag	460	
Gln	Lys	Ile	Leu	Asn	Ala	Arg	Cys	Pro	Leu	Val	Arg	Phe	Ser	His	Gln		
87					92					97					102		
gcc	tcc	gga	ttt	cag	tgt	gat	ttg	act	acg	aac	aat	agg	att	gcc	ttg	508	
Ala	Ser	Gly	Phe	Gln	Cys	Asp	Leu	Thr	Thr	Asn	Asn	Arg	Ile	Ala	Leu		
103					108					113					118		
aca	agt	tcc	gaa	ctc	ctt	tat	ata	tat	ggt	gcc	cta	gac	tca	aga	gtg	556	
Thr	Ser	Ser	Glu	Leu	Leu	Tyr	Ile	Tyr	Gly	Ala	Leu	Asp	Ser	Arg	Val		
119					124					129					134		
aga	gcc	ttg	gtg	ttc	agt	gta	cgg	tgc	tgg	gct	cga	gca	cat	tca	cta	604	
Arg	Ala	Leu	Val	Phe	Ser	Val	Arg	Cys	Trp	Ala	Arg	Ala	His	Ser	Leu		
135					140					145					150		
aca	agt	agt	att	cct	ggt	gca	tgg	att	aca	aat	ttc	tcc	ctt	aca	atg	652	
Thr	Ser	Ser	Ile	Pro	Gly	Ala	Trp	Ile	Thr	Asn	Phe	Ser	Leu	Thr	Met		
151					156					161					166		
atg	gtc	atc	ttt	ttt	ctc	cag	aga	aga	tca	ccc	cct	att	ctt	cca	aca	700	
Met	Val	Ile	Phe	Phe	Leu	Gln	Arg	Arg	Ser	Pro	Pro	Ile	Leu	Pro	Thr		
167					172					177					182		
cta	gat	tcc	tta	aaa	acc	cta	gca	gat	gca	gaa	gat	aaa	tgt	gta	ata	748	
Leu	Asp	Ser	Leu	Lys	Thr	Leu	Ala	Asp	Ala	Glu	Asp	Lys	Cys	Val	Ile		
183					188					193					198		
gaa	ggc	aac	aac	tgc	aca	ttt	gtt	cgt	gac	ttg	agt	aga	att	aaa	cct	796	
Glu	Gly	Asn	Asn	Cys	Thr	Phe	Val	Arg	Asp	Leu	Ser	Arg	Ile	Lys	Pro		
199					204					209					214		
tca	cag	aac	aca	gaa	aca	tta	gaa	tta	cta	ctg	aag	gaa	ttt	ttt	gag	844	
Ser	Gln	Asn	Thr	Glu	Thr	Leu	Glu	Leu	Leu	Leu	Lys	Glu	Phe	Phe	Glu		
215					220					225					230		
tat	ttt	ggc	aat	ttt	gct	ttc	gat	aaa	aat	tcc	ata	aat	att	cga	cag	892	
Tyr	Phe	Gly	Asn	Phe	Ala	Phe	Asp	Lys	Asn	Ser	Ile	Asn	Ile	Arg	Gln		
231					236					241					246		
gga	agg	gag	caa	aac	aaa	cct	gat	tct	tct	cct	ctg	tac	att	cag	aat	940	
Gly	Arg	Glu	Gln	Asn	Lys	Pro	Asp	Ser	Ser	Pro	Leu	Tyr	Ile	Gln	Asn		
247					252					257					262		
cca	ttt	gaa	act	tct	ctc	aac	ata	agc	aaa	aat	gta	agt	caa	agc	cag	988	
Pro	Phe	Glu	Thr	Ser	Leu	Asn	Ile	Ser	Lys	Asn	Val	Ser	Gln	Ser	Gln		
263					268					273					278		
ctg	caa	aaa	ttt	gta	gat	ttg	gcc	cga	gaa	agt	gcc	tgg	att	tta	caa	1036	
Leu	Gln	Lys	Phe	Val	Asp	Leu	Ala	Arg	Glu	Ser	Ala	Trp	Ile	Leu	Gln		
279					284					289					294		
cag	gaa	gat	aca	gat	cga	cct	tcc	ata	tca	agt	aat	cgg	ccc	tgg	ggg	1084	
Gln	Glu	Asp	Thr	Asp	Arg	Pro	Ser	Ile	Ser	Ser	Asn	Arg	Pro	Trp	Gly		

295	300	305	310	
ctg gta tcc cta ttg cta cca tct gct cca aac aga aag tcc ttt acc				1132
Leu Val Ser Leu Leu Leu Pro Ser Ala Pro Asn Arg Lys Ser Phe Thr				
311	316	321	326	
aag aag aaa agc aat aag ttt gca att gaa aca gtc aaa aac ttg cta				1180
Lys Lys Lys Ser Asn Lys Phe Ala Ile Glu Thr Val Lys Asn Leu Leu				
327	332	337	342	
gaa tct tta aaa ggt aac aga aca gaa aat ttc aca aaa acc agt ggg				1228
Glu Ser Leu Lys Gly Asn Arg Thr Glu Asn Phe Thr Lys Thr Ser Gly				
343	348	353	358	
gaa gag gaa caa tta gta ctc agg aca tga t gggcttgcta cattgtgtta				1279
Glu Glu Glu Gln Leu Val Leu Arg Thr *				
359	364			
aaggaactgg ggctttngcc tattccaaat gggctctgtgg gantttactt nggggaaaaa				1339
ctgggttttgg aaacttttcc acagggttctt caggcttttt cctcttggg ttgttttt				1397

<210> 510
 <211> 1562
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (521)..(1024)

<400> 510	
caagtatttc tttagagcaa tgcaaagaat ggtctaacac acccggaag ctgagactgg	60
catgagtata aagatcgtgg ataattttga aatctaaaaa tgtaaaatta atattattga	120
gggagtcac acaggaaaga ttagagcacg tgggcagagg ctgttgccca ttggtcacat	180
gtggtcagca gagagcaggt gaccagcacc ctggagcttt gcaggaagaa ccagacagcc	240
tggagctgag gttttaattg taggggccaa acaaatggg gaaaaagaca aatttagaaa	300
acaaagaaag tagatgctca actgagccag aaggaagtca ctagcaaaga ggaaaaaat	360
agagctctgg aaaaatagtg taaacagtca caagaaagg accctgtgtc atgcctgaca	420
tctggacagg tatataaaga gccaggctc agggagctcc acacctgcac ctccctctca	480
cctgctcctc tacctgatcc accctcaatc caccagaacc atg ggc tgc tgt ggc	535
Met Gly Cys Cys Gly	
1	
tgc tcc gga ggc tgt ggc tcc ggc tgt ggc ggc tgc agc tgt	583
Cys Ser Gly Gly Cys Gly Ser Gly Cys Gly Cys Gly Ser Ser Cys	

6	11	16	21	
ggg ggt tgt ggc tct ggc tgt ggg ggc tgt ggc tcc ggc cgt ggg ggc				631
Gly Gly Cys Gly Ser Gly Cys Gly Gly Cys Gly Ser Gly Arg Gly Gly				
22	27	32	37	
tgt ggc tct ggc tgt ggg ggc tgc agc tcc agc tgt ggg gga tgt ggc				679
Cys Gly Ser Gly Cys Gly Gly Cys Ser Ser Ser Cys Gly Gly Cys Gly				
38	43	48	53	
tcc aga tgt tat gtg cct gtc tgc tgc tgc aag ccc gtg tgc tcc tgg				727
Ser Arg Cys Tyr Val Pro Val Cys Cys Cys Lys Pro Val Cys Ser Trp				
54	59	64	69	
gtg cca gcc tgt tcc tgc acc agc tgt ggc tcc tgt ggg ggc tcc aag				775
Val Pro Ala Cys Ser Cys Thr Ser Cys Gly Ser Cys Gly Gly Ser Lys				
70	75	80	85	
ggg ggc tgt ggc tcc tgt ggg ggt tcc aag ggg ggc tgt ggt tct tgt				823
Gly Gly Cys Gly Ser Cys Gly Gly Ser Lys Gly Gly Cys Gly Ser Cys				
86	91	96	101	
ggc tgc tcc cag tcc agc tgt tgt aag ccc tgt tgc tgc tcc tca ggc				871
Gly Cys Ser Gln Ser Ser Cys Cys Lys Pro Cys Cys Cys Ser Ser Gly				
102	107	112	117	
tgt gga tca tcc tgc tgc cag tcc agc tgc tgc aag ccc tgc tgc tgc				919
Cys Gly Ser Ser Cys Cys Gln Ser Ser Cys Cys Lys Pro Cys Cys Cys				
118	123	128	133	
cag tcc agc tgc tgt gtc ccc gtg tgc tgc cag tcc agc tgc tgc aag				967
Gln Ser Ser Cys Cys Val Pro Val Cys Cys Gln Ser Ser Cys Cys Lys				
134	139	144	149	
ccc tgt tgc tgc cag tcc aac tgt tgt gtc cct gtg tgc tgc cag tgt				1015
Pro Cys Cys Cys Gln Ser Asn Cys Cys Val Pro Val Cys Cys Gln Cys				
150	155	160	165	
aag atc tga ggctctg gaccagacc ttcaggtttc tctgttttgg tgaaagcatt				1071
Lys Ile *				
166				
tcttatgggtt cctgagtcga gttcgtccca cacatcctcc ctgaggcacc tgcacotget				1131
ctagctcacc atccatgcac acacctcctt ccatgggtca gctctcctct gggccctgcc				1191
ttcagcctcc tcactccaga aacgtgtgtt tccctgatgc gggaggtgtc ctgccttga				1251
cgcaggcacc cagcogactg ccacgatgtt ccctgcactt ggggtgtggac catctttctt				1311
ttctccctgg gctgactgag atgcaaggtc tgacccca aggccaggcc gacgtttctg				1371
agtgatcact aagaaccagc ttotcaacca ccatcaggac cctggatcct cctgggcccgc				1431
tgccctgttct cctgtggccc aagtgtgacc aggaaggtct ctttccttcc tgttgtctcc				1491
atccgtgcgt tcttcctgcc cggactcgc cagaaatcg tcgaccggg aattccggac				1551

cggtacggca g

1562

<210> 511
<211> 2907
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (359) .. (2530)

<220>
<221> misc_feature
<222> (1) ... (2907)
<223> n = a,t,c or g

<400> 511
ccctttaaat agtatcgctc cccaccgag cgagccaaag gatcatgacg agaacggaga 60
ggccatcacc cttcttcccc cgggcgtggc gatcattatg cagtgcacgc agttttccga 120
ctgaaagcgg caagtagcgc accatattat gtagttagtc atcataaggc accaggnctt 180
acactatggc tcnnggctcgt atgtgtgtgg aatgtgagcg gatacanttc acacagnaan 240
cagtaatgac atgattacga ttttatacac tcactatagg ggaatntggc cctcgaggcc 300
aagaattcng gcacgagggg cagcttcctt gcggaagtgg tgaccgtgag agaagaag 358
atg gcg gcc cct gta gtg gcg ccg cct ggt gtg gtg gtt agt cgg gct 406
Met Ala Ala Pro Val Val Ala Pro Pro Gly Val Val Val Ser Arg Ala
1 5 10 15
aac aag cgc agc ggc gcg ggg ccg gga ggc agc ggt ggc ggg gga gcc 454
Asn Lys Arg Ser Gly Ala Gly Pro Gly Gly Ser Gly Gly Gly Gly Ala
17 22 27 32
aga ggg gcg gag gag gaa ccg ccg ccg ccc cta caa gca gtt ctg gtg 502
Arg Gly Ala Glu Glu Glu Pro Pro Pro Pro Leu Gln Ala Val Leu Val
33 38 43 48
gcc gat agc ttc gat cgc cgc ttc ttc ccc atc tcc aag gac cag cct 550
Ala Asp Ser Phe Asp Arg Arg Phe Phe Pro Ile Ser Lys Asp Gln Pro
49 54 59 64
cgg gtc ctc ttg ccc ctg gcc aat gtg gca tta att gac tac act ctg 598
Arg Val Leu Leu Pro Leu Ala Asn Val Ala Leu Ile Asp Tyr Thr Leu
65 70 75 80
gaa ttc ctg act gcc aca ggt gta cag gaa aca ttt gtc ttt tgt tgc 646
Glu Phe Leu Thr Ala Thr Gly Val Gln Glu Thr Phe Val Phe Cys Cys
81 86 91 96
tgg aaa gct gct caa atc aaa gaa cat tta ctg aag tca aag tgg tgc 694

Trp	Lys	Ala	Ala	Gln	Ile	Lys	Glu	His	Leu	Leu	Lys	Ser	Lys	Trp	Cys	
97					102					107					112	
cgc	cct	aca	tct	ctc	aat	gtg	gtt	cga	ata	att	aca	tca	gag	ctc	tat	742
Arg	Pro	Thr	Ser	Leu	Asn	Val	Val	Arg	Ile	Ile	Thr	Ser	Glu	Leu	Tyr	
113					118					123					128	
cga	tca	ctg	gga	gat	gtc	ctc	cgt	gat	gtt	gat	gcc	aag	gct	ttg	gtg	790
Arg	Ser	Leu	Gly	Asp	Val	Leu	Arg	Asp	Val	Asp	Ala	Lys	Ala	Leu	Val	
129					134					139					144	
cgc	tct	gac	ttt	ctt	ctg	gtg	tat	ggg	gat	gtc	atc	tca	aac	atc	aat	838
Arg	Ser	Asp	Phe	Leu	Leu	Val	Tyr	Gly	Asp	Val	Ile	Ser	Asn	Ile	Asn	
145					150					155					160	
atc	acc	aga	gcc	ctt	gag	gaa	cac	agg	ttg	aga	cgg	aag	cta	gaa	aaa	886
Ile	Thr	Arg	Ala	Leu	Glu	Glu	His	Arg	Leu	Arg	Arg	Lys	Leu	Glu	Lys	
161					166					171					176	
aat	gtt	tct	gtg	atg	acg	atg	atc	ttc	aag	gag	tca	tcc	ccc	agc	cac	934
Asn	Val	Ser	Val	Met	Thr	Met	Ile	Phe	Lys	Glu	Ser	Ser	Pro	Ser	His	
177					182					187					192	
cca	act	cgt	tgc	cac	gaa	gac	aat	gtg	gta	gtg	gct	gtg	gat	agt	acc	982
Pro	Thr	Arg	Cys	His	Glu	Asp	Asn	Val	Val	Val	Ala	Val	Asp	Ser	Thr	
193					198					203					208	
aca	aac	agg	gtt	ctc	cat	ttt	cag	aag	acc	cag	ggg	ctc	cgg	cgt	ttt	1030
Thr	Asn	Arg	Val	Leu	His	Phe	Gln	Lys	Thr	Gln	Gly	Leu	Arg	Arg	Phe	
209					214					219					224	
gca	ttt	cct	ctg	agc	ctg	ttt	cag	ggc	agt	agt	gat	gga	gtg	gag	gtt	1078
Ala	Phe	Pro	Leu	Ser	Leu	Phe	Gln	Gly	Ser	Ser	Asp	Gly	Val	Glu	Val	
225					230					235					240	
cga	tat	gat	tta	ctg	gat	tgt	cat	atc	agc	atc	tgt	tct	cct	cag	gtg	1126
Arg	Tyr	Asp	Leu	Leu	Asp	Cys	His	Ile	Ser	Ile	Cys	Ser	Pro	Gln	Val	
241					246					251					256	
gca	caa	ctc	ttt	aca	gac	aac	ttt	gac	tac	caa	act	cga	gat	gac	ttt	1174
Ala	Gln	Leu	Phe	Thr	Asp	Asn	Phe	Asp	Tyr	Gln	Thr	Arg	Asp	Asp	Phe	
257					262					267					272	
gtg	cga	ggg	ctc	tta	gtg	aat	gag	gag	atc	cta	ggg	aac	cag	atc	cac	1222
Val	Arg	Gly	Leu	Leu	Val	Asn	Glu	Glu	Ile	Leu	Gly	Asn	Gln	Ile	His	
273					278					283					288	
atg	cac	gta	aca	gct	aag	gaa	tat	ggg	gcc	cgt	gtc	tcc	aac	cta	cac	1270
Met	His	Val	Thr	Ala	Lys	Glu	Tyr	Gly	Ala	Arg	Val	Ser	Asn	Leu	His	
289					294					299					304	
atg	tac	tca	gct	gtc	tgt	gct	gac	gtc	atc	cgc	cga	tgg	gtc	tac	cct	1318
Met	Tyr	Ser	Ala	Val	Cys	Ala	Asp	Val	Ile	Arg	Arg	Trp	Val	Tyr	Pro	
305					310					315					320	
ctc	acc	cca	gag	gcg	aac	ttc	act	gac	agc	acc	acc	cag	agc	tgc	act	1366
Leu	Thr	Pro	Glu	Ala	Asn	Phe	Thr	Asp	Ser	Thr	Thr	Gln	Ser	Cys	Thr	

321	326	331	336	
cat tcc cgg cac aac atc tac cga ggg cct gag gtc agc ctg ggc cat				1414
His Ser Arg His Asn Ile Tyr Arg Gly Pro Glu Val Ser Leu Gly His				
337	342	347	352	
ggc agc atc cta gag gaa aat gtg ctc ctg ggc tct ggc act gtc att				1462
Gly Ser Ile Leu Glu Glu Asn Val Leu Leu Gly Ser Gly Thr Val Ile				
353	358	363	368	
ggc agc aat tgc ttt atc acc aac agt gtc att ggc ccc ggc tgc cac				1510
Gly Ser Asn Cys Phe Ile Thr Asn Ser Val Ile Gly Pro Gly Cys His				
369	374	379	384	
att gag cca ggt gat aac gtg gtg ctg gac cag acc tac ctg tgg cag				1558
Ile Glu Pro Gly Asp Asn Val Val Leu Asp Gln Thr Tyr Leu Trp Gln				
385	390	395	400	
ggt gtt cga gtg gcg gct gga gca cag atc cat cag tct ctg ctt tgt				1606
Gly Val Arg Val Ala Ala Gly Ala Gln Ile His Gln Ser Leu Leu Cys				
401	406	411	416	
gac aat gct gag gtc aag gaa cga gtg aca ctg aaa cca cgc tct gtc				1654
Asp Asn Ala Glu Val Lys Glu Arg Val Thr Leu Lys Pro Arg Ser Val				
417	422	427	432	
ctc act tcc cag gtg gtc gtg ggc cca aat atc acg ctg cct gag ggc				1702
Leu Thr Ser Gln Val Val Val Gly Pro Asn Ile Thr Leu Pro Glu Gly				
433	438	443	448	
tcg gtg atc tct ttg cac cct cca gat gca gag gaa gat gaa gat gat				1750
Ser Val Ile Ser Leu His Pro Pro Asp Ala Glu Glu Asp Glu Asp Asp				
449	454	459	464	
ggc gag ttc agt gat gat tct ggg gct gac caa gaa aag gac aaa gtg				1798
Gly Glu Phe Ser Asp Asp Ser Gly Ala Asp Gln Glu Lys Asp Lys Val				
465	470	475	480	
aag atg aaa ggt tac aat cca gca gaa gta gga gct gct ggc aag ggc				1846
Lys Met Lys Gly Tyr Asn Pro Ala Glu Val Gly Ala Ala Gly Lys Gly				
481	486	491	496	
tac ctc tgg aaa gct gca ggc atg aac atg gag gaa gag gag gaa ctg				1894
Tyr Leu Trp Lys Ala Ala Gly Met Asn Met Glu Glu Glu Glu Glu Leu				
497	502	507	512	
cag cag aat ctg tgg gga ctc aag atc aac atg gaa gaa gag agt gaa				1942
Gln Gln Asn Leu Trp Gly Leu Lys Ile Asn Met Glu Glu Glu Ser Glu				
513	518	523	528	
agt gaa agt gag caa agt atg gat tct gag gag ccg gac agc cgg gga				1990
Ser Glu Ser Glu Gln Ser Met Asp Ser Glu Glu Pro Asp Ser Arg Gly				
529	534	539	544	
ggc tcc cct cag atg gat gac atc aaa gtg ttc cag aat gaa gtt tta				2038
Gly Ser Pro Gln Met Asp Asp Ile Lys Val Phe Gln Asn Glu Val Leu				
545	550	555	560	

gga aca cta cag cgg ggc aaa gag gag aac att tct tgt gac aat ctc	2086
Gly Thr Leu Gln Arg Gly Lys Glu Glu Asn Ile Ser Cys Asp Asn Leu	
561 566 571 576	
gtc ctg gaa atc aac tct ctc aag tat gcc tat aac ata agt cta aag	2134
Val Leu Glu Ile Asn Ser Leu Lys Tyr Ala Tyr Asn Ile Ser Leu Lys	
577 582 587 592	
gag gtg atg cag gta ctg agc cac gtg gtc ctg gag ttc ccc ctg caa	2182
Glu Val Met Gln Val Leu Ser His Val Val Leu Glu Phe Pro Leu Gln	
593 598 603 608	
cag atg gat tcc ccg ctt gac tca agc cgc tac tgt gcc ctg ctg ctt	2230
Gln Met Asp Ser Pro Leu Asp Ser Ser Arg Tyr Cys Ala Leu Leu Leu	
609 614 619 624	
cct ctg cta aag gcc tgg agc cct gtt ttt agg aac tac ata aag cgc	2278
Pro Leu Leu Lys Ala Trp Ser Pro Val Phe Arg Asn Tyr Ile Lys Arg	
625 630 635 640	
gca gcc gac cat ttg gaa gcg tta gca gcc att gag gac ttc ttc cta	2326
Ala Ala Asp His Leu Glu Ala Leu Ala Ala Ile Glu Asp Phe Phe Leu	
641 646 651 656	
gag cat gaa gct ctt ggt att tcc atg gcc aag gta ctg atg gct ttc	2374
Glu His Glu Ala Leu Gly Ile Ser Met Ala Lys Val Leu Met Ala Phe	
657 662 667 672	
tac cag ctg gag atc ctg gct gag gaa aca att ctg agc tgg ttc agc	2422
Tyr Gln Leu Glu Ile Leu Ala Glu Glu Thr Ile Leu Ser Trp Phe Ser	
673 678 683 688	
caa aga gat aca act gac aag ggc cag cag ttg cgc aag aat caa cag	2470
Gln Arg Asp Thr Thr Asp Lys Gly Gln Gln Leu Arg Lys Asn Gln Gln	
689 694 699 704	
ctg cag agg ttc atc cag tgg cta aaa gag gca gaa gag gag tca tct	2518
Leu Gln Arg Phe Ile Gln Trp Leu Lys Glu Ala Glu Glu Glu Ser Ser	
705 710 715 720	
gaa gat gac tga agt cacactgcct gctcctttgg gtgtgattga gtgccctcct	2573
Glu Asp Asp *	
721	
ggctcctggg ctgggacaag tgaggaacta gctgcagagg gatgagtac caccatccag	2633
gctgagactg aaaggagcag aggctggaac tacagtattc tttccctgc tagcaaccat	2693
gtgcctccca tctgactgt ggagttggga tgtggaagtg gggctggaac aaagcttctg	2753
cctagggagg agctaagcag gcccggcagt tggaggaagg ccagaggaac agctttgtgd	2813
tccggctttc cctcagggaa cagcagagag cagttggctc tttctgctgc ttgtatatgt	2873
taatattaaa agagagtggg gtaaaaaaaaa aaaa	2907

<210> 512
 <211> 794
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (88) .. (486)

<400> 512
 cattactcac tatagggaat ttggccctcg agcagcacat tcggcacgag cgcttccacc 60
 cggaagagccc ccagggctga gtgcggc atg atc tcc atc acc gaa tgg cag 111
 Met Ile Ser Ile Thr Glu Trp Gln
 1 5
 aag att ggt gtg ggg atc acc ggt ttc ggc atc ttc ttc atc ctc ttt 159
 Lys Ile Gly Val Gly Ile Thr Gly Phe Gly Ile Phe Phe Ile Leu Phe
 9 14 19 24
 gga aca ctc ctg tac ttt gat tcc gtg ctc ctg gcc ttt gga aac ctg 207
 Gly Thr Leu Leu Tyr Phe Asp Ser Val Leu Leu Ala Phe Gly Asn Leu
 25 30 35 40
 ctg ttc ctg acg ggc ctg tcc ctc atc att ggc ctg agg aag acc ttt 255
 Leu Phe Leu Thr Gly Leu Ser Leu Ile Ile Gly Leu Arg Lys Thr Phe
 41 46 51 56
 tgg ttc ttc ttc caa cgg cac aaa ctc aag gga acc agc ttc ctc ctg 303
 Trp Phe Phe Phe Gln Arg His Lys Leu Lys Gly Thr Ser Phe Leu Leu
 57 62 67 72
 ggg ggt gtg gtt atc gtg ctc cta cgc tgg ccc ctc ctc ggc atg ttc 351
 Gly Gly Val Val Ile Val Leu Leu Arg Trp Pro Leu Leu Gly Met Phe
 73 78 83 88
 ctg gaa acc tac gga ttc ttc agc ctc ttt aag ggc ttt ttc cct gtc 399
 Leu Glu Thr Tyr Gly Phe Phe Ser Leu Phe Lys Gly Phe Phe Pro Val
 89 94 99 104
 gcc ttc ggc ttc ctg ggc aat gtc tgc aac atc ccc ttc ctg ggt gcg 447
 Ala Phe Gly Phe Leu Gly Asn Val Cys Asn Ile Pro Phe Leu Gly Ala
 105 110 115 120
 ctg ttc cgg aga ctt caa ggc act agc tgc atg gtc tga aaaacagaga 496
 Leu Phe Arg Arg Leu Gln Gly Thr Ser Ser Met Val *
 121 126 131
 tgagctcctt gaacttggat cattggttga gggggctaga gggagaatgg gaaccacccc 556
 ctcagtcccc tgcactgact cactccccga catatccgga cctccccaag tccagaagga 616
 aggaatggag ctgagcaact gacgtcaaact cccaagtcg actcaagagg ctgccaggaa 676

ggagctgagg agagaaacag aaaattgaag aaacattgga aactctgtca tgctcagtca	692
agattagatg tcaatggact agcattaata atggcaaaag aaaggaaagt gaaaaataaa	752
gttaaaaaata aagctgatac tgaggaagtg tttacaaca gtcctacaaa tcaagaaaag	812
atgcctacct cagctatttt gcctgatttt tctggctctg taatttctaa tatcagaaac	872
caaatggaaa cccttcattc tcagccacat caagaagaaa atttgtgttt tgaaaattcc	932
ttttctctta taaacctttt gcctattaat gctgtagagc ctacttcttc acagcaaata	992
cccaacagag aaacatctga agccaataaa gagagaagaa aaatgacatc aaagtcaagt	1052
gaatcaaata tatattcacc tttaacctct tttatcactg ctgattcaga actccatgac	1112
attattaaag atttggagga ttgtttgatg gtgggtctcc acacttgtgg tgatctggct	1172
ccaaatactt tgccaatatt tacctccaac tctgaaatca agggagtgtg cagtgtgggt	1232
tggtgctacc acctcttctc tgaagaattt gaaaaccagc ataaagaacg tactcaggaa	1292
aagtggggat ttccaatgtg ccactattta aaggaagaga gatgggtctg tggctgtaat	1352
gccagaatgt cagcatgttt ggcattggag cgggttgag ctggccaagg gctgcctact	1412
gaatcactct tctatcgtgc tgttcttcag gatattatta aagattgtta tggcatcacc	1472
aaatgtgatc ggcattgttg taaaatttat tccaaatgtt cttcttttct ggattatgtc	1532
agacgggtctc taaagaagct tggattagat gaggccaagc tgccagaaaa aattataatg	1592
aactactacg agaagtataa gcctcgaatg aatgagctgg aagcttttaa tatgttgaaa	1652
gttgactagg ctccctgtat agagactttg attcttctgg atcgactttg ttacctgaaa	1712
gagcaggaag atattgcatg gtctgctctt gtgaagttgt ttgatcccg taaatctccc	1772
agatgttatg ctgttattgc cctgaagaag cagcagtgat ttccattgaa gcaaattatt	1832
agatgtatct ctctatgaga cctgttgctg agattgcttt tctaaacata tatgtcctgt	1892
tatacaaaaa tttttaaatg actgttatgt attttaata ataaaataat ggctaacaac	1952
aaaaaaaaaa aaaaaa	1968

<210> 514
 <211> 1748
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (157) .. (771)

<400> 514

ataccctgc ggtaccggtc cggaattccc ggtcgaccc acgcgtccgc ggacgcgtgg 60

ggccccgaga cgcgcctggc gcggatccta aatcccgaca gctttataga gccaggcct 120

ggcaggctcc cagaacttga agccaccaga cccac atg gaa cca aag gcc tcc 174
Met Glu Pro Lys Ala Ser
1

tgt cca gct gct gca ccc ttg atg gag aga aaa ttc cat gtt ctt gtg 222
Cys Pro Ala Ala Ala Pro Leu Met Glu Arg Lys Phe His Val Leu Val
7 12 17 22

ggt gtc acg ggg agt gtc gca gcc ctg aag ttg cct ctt ctg gtg tca 270
Gly Val Thr Gly Ser Val Ala Ala Leu Lys Leu Pro Leu Leu Val Ser
23 28 33 38

aag ctt ttg gac att cct ggg ctg gaa gta gca gtg gtc aca act gag 318
Lys Leu Leu Asp Ile Pro Gly Leu Glu Val Ala Val Val Thr Thr Glu
39 44 49 54

aga gcc aaa cat ttc tac agc ccc cag gac att cct gtc acc ctc tac 366
Arg Ala Lys His Phe Tyr Ser Pro Gln Asp Ile Pro Val Thr Leu Tyr
55 60 65 70

agc gac gct gat gaa tgg gag atg tgg aag agc cgc tct gac cca gtt 414
Ser Asp Ala Asp Glu Trp Glu Met Trp Lys Ser Arg Ser Asp Pro Val
71 76 81 86

ctg cac att gac ctg cgg agg tgg gca gac ctc ctg ctg gtg gct cct 462
Leu His Ile Asp Leu Arg Arg Trp Ala Asp Leu Leu Leu Val Ala Pro
87 92 97 102

ctt gat gcc aac act ctg ggg aag gtg gcc agt ggc atc tgt gac aac 510
Leu Asp Ala Asn Thr Leu Gly Lys Val Ala Ser Gly Ile Cys Asp Asn
103 108 113 118

ttg ctt acc tgc gtc atg cgg gcc tgg gac cgc agc aag ccc ctg ctc 558
Leu Leu Thr Cys Val Met Arg Ala Trp Asp Arg Ser Lys Pro Leu Leu
119 124 129 134

ttc tgc ccg gcc atg aac acc gcc atg tgg gag cac ccg atc aca gcg 606
Phe Cys Pro Ala Met Asn Thr Ala Met Trp Glu His Pro Ile Thr Ala
135 140 145 150

cag cag gta gac cag ctc aag gcc ttt ggc tat gtc gag atc ccc tgt 654
Gln Gln Val Asp Gln Leu Lys Ala Phe Gly Tyr Val Glu Ile Pro Cys
151 156 161 166

gtg gcc aag aag ctg gtg tgc gga gat gaa ggt ctc ggg gcc atg gct 702
Val Ala Lys Lys Leu Val Cys Gly Asp Glu Gly Leu Gly Ala Met Ala
167 172 177 182

gaa gtg ggg acc atc gtg gac aaa gtg aaa gaa gtc ctc ttc cag cac 750
Glu Val Gly Thr Ile Val Asp Lys Val Lys Glu Val Leu Phe Gln His
183 188 193 198

agc ggc ttc cag cag agt tga cc tgggatttct gtcattgggtg tccctctgta 803
 Ser Gly Phe Gln Gln Ser *
 199 204

ctcagaatgg gttcaggcca agtcgggtgaa gatggatggt ggcaaaatag gaggataccc 863
 tcatttgctg aatggggggac ctgctctgag cctgcccagg ggccaggcct gctccagggt 923
 aaactggacg gaaggcccag gtctcagttt ctttcaacca ggagaggccg ctgcctagag 983
 cccctcccca ccttttctg gatgggtgag gcaagccagg agagcaagca gtgttgcct 1043
 cacgggagga ggactgagcg actgggaaaa ctgggtctta catctcacc agaacggctt 1103
 ttagaaacac cacagctgga gagtcctggc tgagccttg gagtttcagc tctttggcgg 1163
 ggtgcccagg tgccatgcga tcagcgaagc ctgcgaggtg gcaggactct gaggtttcct 1223
 gcagaccatg ccatgagatt gaaggtgcgg ggaaataaag aaaaatcacc atttaggaga 1283
 ctccattctt tccctacaac ccagctgtgg tcccagagat caggggggtgt tgccagggtgt 1343
 ggctggggaa ggggtctgggt tcacaactca ccggcactct ttagtccccg tataacatgg 1403
 tgggtaagga taaagatctg aagccagaca gcccttagtt ccaatcccag ctctgccgct 1463
 tactagcagt ggcagtttg ttcaggactt aaccttctg accttactt acctcagcta 1523
 tcttggtatc ctacctcat ggagttgcag ataggattct cgaaaatttc ttacagcata 1583
 acacctatgc cactgtggtg tctggacgta ttatatctct aagttttaga tgtttcatcc 1643
 atgtacctta tatgcccata gcactatact tacattcact tgcattgacct atctaatttc 1703
 ttattctcca aattttgtgt tagtaatctt cctcagcttc tatat 1748

<210> 515
 <211> 1976
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (47) .. (1336)

<400> 515
 gggcgaggag ggcgcgtcgc cctcttttcc cgccggcacc ctggcc atg aca ggc 55
 Met Thr Gly
 1

aag tcg gtg aag gac gtg gat cgg tac cag gct gtc ctg gcc aac ctg 103
 Lys Ser Val Lys Asp Val Asp Arg Tyr Gln Ala Val Leu Ala Asn Leu
 4 9 14 19

ctg ctg gag gag gat aac aag ttt tgt gca gat tgc cag tct aaa ggg	151
Leu Leu Glu Glu Asp Asn Lys Phe Cys Ala Asp Cys Gln Ser Lys Gly	
20 25 30 35	
ccg cga tgg gcc tct tgg aac att ggt gtg ttc atc tgc att cga tgt	199
Pro Arg Trp Ala Ser Trp Asn Ile Gly Val Phe Ile Cys Ile Arg Cys	
36 41 46 51	
gct gga atc cac agg aat ctg ggg gtg cac ata tcc agg gta aag tca	247
Ala Gly Ile His Arg Asn Leu Gly Val His Ile Ser Arg Val Lys Ser	
52 57 62 67	
gtt aac ctc gac cag tgg act caa gaa cag att cag tgc atg caa gag	295
Val Asn Leu Asp Gln Trp Thr Gln Glu Gln Ile Gln Cys Met Gln Glu	
68 73 78 83	
atg gga aat gga aag gca aac cga ctt tat gaa gcc tat ctt cct gag	343
Met Gly Asn Gly Lys Ala Asn Arg Leu Tyr Glu Ala Tyr Leu Pro Glu	
84 89 94 99	
acc ttt cgg cga cct cag ata gac cca gct gtt gaa gga ttt att cga	391
Thr Phe Arg Arg Pro Gln Ile Asp Pro Ala Val Glu Gly Phe Ile Arg	
100 105 110 115	
gac aaa tat gag aag aag aaa tac atg gac cga agt ctg gac atc aat	439
Asp Lys Tyr Glu Lys Lys Lys Tyr Met Asp Arg Ser Leu Asp Ile Asn	
116 121 126 131	
gcc ttt agg aaa gaa aaa gat gac aag tgg aaa aga ggg agc gaa cca	487
Ala Phe Arg Lys Glu Lys Asp Asp Lys Trp Lys Arg Gly Ser Glu Pro	
132 137 142 147	
gtt cca gaa aaa aaa ttg gaa cct gtt gtt ttt gag aag gtg aaa atg	535
Val Pro Glu Lys Lys Leu Glu Pro Val Val Phe Glu Lys Val Lys Met	
148 153 158 163	
cca cag aaa aaa gaa gac cca cag cta cct cgg aaa agc tcc ccg aaa	583
Pro Gln Lys Lys Glu Asp Pro Gln Leu Pro Arg Lys Ser Ser Pro Lys	
164 169 174 179	
tcc aca gcg cct gtc atg gat ttg ttg ggc ctt gat gct cct gtg gcc	631
Ser Thr Ala Pro Val Met Asp Leu Leu Gly Leu Asp Ala Pro Val Ala	
180 185 190 195	
tgc tcc att gca aat agt aag acc agc aat acc cta gag aag gat tta	679
Cys Ser Ile Ala Asn Ser Lys Thr Ser Asn Thr Leu Glu Lys Asp Leu	
196 201 206 211	
gat ctg ttg gcc tct gtt cca tcc cct tct tct tcc ggt tcc aga aag	727
Asp Leu Leu Ala Ser Val Pro Ser Pro Ser Ser Ser Gly Ser Arg Lys	
212 217 222 227	
gtt gta ggt tcc atg cca act gca ggg agt gcc ggc tct gtt cct gaa	775
Val Val Gly Ser Met Pro Thr Ala Gly Ser Ala Gly Ser Val Pro Glu	
228 233 238 243	

aat ctg aac ctg ttt ccg gag cca ggg agc aaa tca gaa gaa ata ggc	823
Asn Leu Asn Leu Phe Pro Glu Pro Gly Ser Lys Ser Glu Glu Ile Gly	
244 249 254 259	
aag aaa cag ctc tct aaa gac tcc att ctt tca ctg tat gga tcc cag	871
Lys Lys Gln Leu Ser Lys Asp Ser Ile Leu Ser Leu Tyr Gly Ser Gln	
260 265 270 275	
acg cct caa atg cct act caa gca atg ttc atg gct ccc gct cag atg	919
Thr Pro Gln Met Pro Thr Gln Ala Met Phe Met Ala Pro Ala Gln Met	
276 281 286 291	
gca tat ccc aca gcc tac ccc agc ttc ccc ggg gtt aca cct cct aac	967
Ala Tyr Pro Thr Ala Tyr Pro Ser Phe Pro Gly Val Thr Pro Pro Asn	
292 297 302 307	
agc ata atg ggg agc atg atg cct cca cca gta ggc atg gtt gct cag	1015
Ser Ile Met Gly Ser Met Met Pro Pro Pro Val Gly Met Val Ala Gln	
308 313 318 323	
cca gga gct tct ggg atg gtt gcc ccc atg gcc atg cct gca ggc tat	1063
Pro Gly Ala Ser Gly Met Val Ala Pro Met Ala Met Pro Ala Gly Tyr	
324 329 334 339	
atg ggt ggc atg cag gca tca atg atg ggt gtg ccg aat gga atg atg	1111
Met Gly Gly Met Gln Ala Ser Met Met Gly Val Pro Asn Gly Met Met	
340 345 350 355	
acc acc cag cag gct ggc tac atg gca ggc atg gca gct atg ccc cag	1159
Thr Thr Gln Gln Ala Gly Tyr Met Ala Gly Met Ala Ala Met Pro Gln	
356 361 366 371	
act gtg tat ggg gtc cag cca gct cag cag ctg caa tgg aac ctt act	1207
Thr Val Tyr Gly Val Gln Pro Ala Gln Gln Leu Gln Trp Asn Leu Thr	
372 377 382 387	
cag atg acc cag cag atg gct ggg atg aac ttc tat gga gcc aat ggc	1255
Gln Met Thr Gln Gln Met Ala Gly Met Asn Phe Tyr Gly Ala Asn Gly	
388 393 398 403	
atg atg aac tat gga cag tca atg agt ggc gga aat gga cag gca gca	1303
Met Met Asn Tyr Gly Gln Ser Met Ser Gly Gly Asn Gly Gln Ala Ala	
404 409 414 419	
aat cag act ctc agt cct cag atg tgg aaa taa aaacaaaa cacctgtatg	1354
Asn Gln Thr Leu Ser Pro Gln Met Trp Lys *	
420 425 430	
gctgccattc tottcagccc tcgctctccc ctttccacag cctccacccc tgaccccat	1414
cctctttttcc tacctctctg tttgggttag aaattgtca ataagtcatt tgggggttgg	1474
catcctgccc agccacttcc caaacatgaa gacctctctg ttgctttatg ttgtacatgc	1534
cccatagcca tcccaacgtc ctccccagtc ctctoctggc accagcacct tagaagttgt	1594
tggcagaagg cacttaaaact gtgggagaag tgtgcacacc tttgagtccc ttccctcaag	1654

gttaaagctc ctgtcagact ctcagaaggg tctgtgggtg ttgtatatta ggcaaacagg 1714
 ggaaagctta gaggtccttc tatatgtgtt aataagctgt ttctaagtgt ttaaatttga 1774
 aaagcatcat gttctcatga tttatgggaa tgaagcaagt actgaaatca aattaaatac 1834
 tccttgggtc ctgggtcagt ttgaccctag ccttgggggtg aggcaagccc cctcctatga 1894
 ggatgagcaa aaatactact ctcttcgccc tgagttgctt tctggatctg gggcttcagg 1954
 acttgctgct tcagacagcc tt 1976

<210> 516
 <211> 1823
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (114) .. (800)

<400> 516
 ccgacccact cgtccgggccc ttccagggccc tcaagcgggtt gcacacggcg cacctgtact 60
 attacgcgct gtagcgcgtg cccagtggccc tgccctgcgcg cgtgcgcgcgc ttc atg 116
 Met
 1
 atc ctg cac aac cag atc aca ggc att ggc cgc gaa gac ttt gcc acc 164
 Ile Leu His Asn Gln Ile Thr Gly Ile Gly Arg Glu Asp Phe Ala Thr
 2 7 12 17
 acc tac ttc ctg gag gag ctc aac ctc agc tac aac cgc atc acc agc 212
 Thr Tyr Phe Leu Glu Glu Leu Asn Leu Ser Tyr Asn Arg Ile Thr Ser
 18 23 28 33
 cca cag gtg cac cgc gac gcc ttc cgc aag ctg cgc ctg ctg cgc tcg 260
 Pro Gln Val His Arg Asp Ala Phe Arg Lys Leu Arg Leu Leu Arg Ser
 34 39 44 49
 ctg gac ctg tcg ggc aac cgg ctg cac atg ctg cca cct ggg ctg cct 308
 Leu Asp Leu Ser Gly Asn Arg Leu His Met Leu Pro Pro Gly Leu Pro
 50 55 60 65
 cga aat gtc cat gtg ctg aag gtc aag cgc aat gag ctg gct gcc ttg 356
 Arg Asn Val His Val Leu Lys Val Lys Arg Asn Glu Leu Ala Ala Leu
 66 71 76 81
 gca cga ggg gcg ctg gcg ggc atg gct cag ctg cgt gag ctg tac ctc 404
 Ala Arg Gly Ala Leu Ala Gly Met Ala Gln Leu Arg Glu Leu Tyr Leu
 82 87 92 97
 acc agc aac cga ctg cgc agc cga gcc ctg ggc ccc cgt gcc tgg gtg 452

Thr	Ser	Asn	Arg	Leu	Arg	Ser	Arg	Ala	Leu	Gly	Pro	Arg	Ala	Trp	Val	
98					103					108					113	
gac ctc gcc cat ctg cag ctg ctg gac atc gcc ggg aat cag ctc aca																500
Asp Leu Ala His Leu Gln Leu Leu Asp Ile Ala Gly Asn Gln Leu Thr																
114					119					124					129	
gag atc ccc gag ggg ctc ccc gag tca ctt gag tac ctg tac ctg cag																548
Glu Ile Pro Glu Gly Leu Pro Glu Ser Leu Glu Tyr Leu Tyr Leu Gln																
130					135					140					145	
aac aac aag att agt gcg gtg ccc gcc aat gcc ttc gac tcc acg ccc																596
Asn Asn Lys Ile Ser Ala Val Pro Ala Asn Ala Phe Asp Ser Thr Pro																
146					151					156					161	
aac ctc aag ggg atc ttt ctc agg ttt aac aag ctg gct gtg ggc tcc																644
Asn Leu Lys Gly Ile Phe Leu Arg Phe Asn Lys Leu Ala Val Gly Ser																
162					167					172					177	
gtg gtg gac agt gcc ttc cgg agg ctg aag cac ctg cag gtc ttg gac																692
Val Val Asp Ser Ala Phe Arg Arg Leu Lys His Leu Gln Val Leu Asp																
178					183					188					193	
att gaa ggc aac tta gag ttt ggt gac att tcc aag gac cgt ggc cgc																740
Ile Glu Gly Asn Leu Glu Phe Gly Asp Ile Ser Lys Asp Arg Gly Arg																
194					199					204					209	
ttg ggg aag gaa aag gag gag gag gaa gag gag gag gag gag gaa gag																788
Leu Gly Lys Glu Lys Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu																
210					215					220					225	
gaa aca aga tag tga caaggtgatg cagatgtgac ctaggatgat ggaccgccgg																843
Glu Thr Arg *																
226																
actctttttct gcagcacacg cctgtgtgtgt gtgagccccc cactctgccg tgctcacaca																903
gacacaccca gctgcacaca tgaggcatcc cacatgacac gggctgacac agtctcatat																963
ccccaccctt tcccacggcg tgtcccacgg ccagacacat gcacacacat cacaccctca																1023
aacaccacgc tcagccacac acaactaccc tccaaaccac cacagtctct gtcacacccc																1083
cactaccgct gccacgcct ctgaatcatg cagggaaagg tctgcccctg cctgggcaca																1143
cacaggcacc cattccctcc ccctgctgac atgtgtatgc gtatgcatac acaccacaca																1203
cacacacatg cacaagtcac gtgcgaacag cctccaaag cctatgccac agacagctct																1263
tgcccagcc agaatcagcc atagcagctc gccgtctgcc ctgtccatct gtccgtccgt																1323
tccttgaga agacacaagg gtatccatgc tctgtggcca ggtgcctgcc accctctgga																1383
actcacaaaa gctggctttt attcctttcc catcctatgg ggacaggagc cttcaggact																1443
gctggcctgg cctggcccac cctgctcctc caggtgctgg gcagtcactc tgctaagagt																1503

ccctccctgc cacgccctgg caggacacag gcacttttcc aatgggcaag ccagtggaag 1563
gcaggattgg aagagcccc tgggtgctgc tggggccttg gggcaggagt gaagcagagg 1623
tgatggggct gggctgagcc agggaggaag gaccagctg cacctaggag acacctttgt 1683
tcttcaggcc tgtgggggaa gtccgggtg cctttatttt ttattctttt ctaaggaaaa 1743
aaatgataaa aatctcaaag ctgatttttc ttgttataga aaaactaata taaaagcatt 1803
atccctaaaa aaaaaaaaaa 1823

<210> 517
<211> 6027
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1650)

<400> 517

atg caa gct acc aag act gaa tca gga aga aat gga aaa cct gga cag 48
Met Gln Ala Thr Lys Thr Glu Ser Gly Arg Asn Gly Lys Pro Gly Gln
1 5 10

ccc agt aac agg tgt cat tat ttg ctt aat caa ggc tgg gtt gct aac 96
Pro Ser Asn Arg Cys His Tyr Leu Leu Asn Gln Gly Trp Val Ala Asn
17 22 27 32

tct ggg aaa gga gga aga acc aac att cca gat aag gag ctt aaa tct 144
Ser Gly Lys Gly Gly Arg Thr Asn Ile Pro Asp Lys Glu Leu Lys Ser
33 38 43 48

gga gat gac cca gaa aat gtt cac atc act tcc ttt caa tat ttg gcc 192
Gly Asp Asp Pro Glu Asn Val His Ile Thr Ser Phe Gln Tyr Leu Ala
49 54 59 64

tta gct gcc ttc cca cgg ggc agg gct cgg gac ctg cag ctc gcc atg 240
Leu Ala Ala Phe Pro Arg Gly Arg Ala Arg Asp Leu Gln Leu Ala Met
65 70 75 80

act gag cct ccc cac ccc tcc gtg ggc tcc tgt gca gcc cga gcc tcc 288
Thr Glu Pro Pro His Pro Ser Val Gly Ser Cys Ala Ala Arg Ala Ser
81 86 91 96

ctg acg agc gct gcc ccc tgc tcc acg gcg ccc agt ccc atc aac cac 336
Leu Thr Ser Ala Ala Pro Cys Ser Thr Ala Pro Ser Pro Ile Asn His
97 102 107 112

ccg aag gct gag gag tgt ggg tgc acg gca cgg gac tgg cag gca gct 384
Pro Lys Ala Glu Glu Cys Gly Cys Thr Ala Arg Asp Trp Gln Ala Ala
113 118 123 128

cca cct gca gcc cgg gtg cgg gat cca ctg ggt gaa gcc agc tgg gct	432
Pro Pro Ala Ala Arg Val Arg Asp Pro Leu Gly Glu Ala Ser Trp Ala	
129 134 139 144	
cct gag tct gag tat gta tgt aac tgc tct gtg gtt gga agc ctg aat	480
Pro Glu Ser Glu Tyr Val Cys Asn Cys Ser Val Val Gly Ser Leu Asn	
145 150 155 160	
gtg aat cgc tgc aac cag acc aca ggg cag tgt gag tgt cgg cca ggt	528
Val Asn Arg Cys Asn Gln Thr Thr Gly Gln Cys Glu Cys Arg Pro Gly	
161 166 171 176	
tat cag ggg ctt cac tgt gaa acc tgc aaa gag ggc ttt tac cta aat	576
Tyr Gln Gly Leu His Cys Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn	
177 182 187 192	
tac act tct ggg ctc tgt cag cca tgt gac tgt agt cca cat gga gct	624
Tyr Thr Ser Gly Leu Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala	
193 198 203 208	
ctc agc ata ccg tgc aac agt tct ggg aaa tgc cag tgc aaa gtg ggt	672
Leu Ser Ile Pro Cys Asn Ser Ser Gly Lys Cys Gln Cys Lys Val Gly	
209 214 219 224	
gtc att ggc tct ata tgt gac cga tgc caa gat gga tat tat ggc ttt	720
Val Ile Gly Ser Ile Cys Asp Arg Cys Gln Asp Gly Tyr Tyr Gly Phe	
225 230 235 240	
agt aag aat ggc tgc ttg ccc tgc caa tgc aat aat cgg tct gcc agt	768
Ser Lys Asn Gly Cys Leu Pro Cys Gln Cys Asn Asn Arg Ser Ala Ser	
241 246 251 256	
tgc gat gcc ctc aca ggt gct tgt tta aac tgc cag gaa aat agc aaa	816
Cys Asp Ala Leu Thr Gly Ala Cys Leu Asn Cys Gln Glu Asn Ser Lys	
257 262 267 272	
gga aat cac tgt gaa gaa tgt aaa gaa gga ttt tat cag agt cct gat	864
Gly Asn His Cys Glu Glu Cys Lys Glu Gly Phe Tyr Gln Ser Pro Asp	
273 278 283 288	
gcc act aaa gaa tgt ctt cgc tgc cct tgt tca gca gtg aca tct aca	912
Ala Thr Lys Glu Cys Leu Arg Cys Pro Cys Ser Ala Val Thr Ser Thr	
289 294 299 304	
ggc agc tgc tct ata aaa tcg agt gaa ttg gaa cct gaa tgt gac cag	960
Gly Ser Cys Ser Ile Lys Ser Ser Glu Leu Glu Pro Glu Cys Asp Gln	
305 310 315 320	
tgt aaa gat ggt tac ata ggc ccg aac tgc aat aaa tgt gaa aat ggc	1008
Cys Lys Asp Gly Tyr Ile Gly Pro Asn Cys Asn Lys Cys Glu Asn Gly	
321 326 331 336	
tat tac aat ttt gac agc atc tgt aga aag tgc caa tgt cac ggc cat	1056
Tyr Tyr Asn Phe Asp Ser Ile Cys Arg Lys Cys Gln Cys His Gly His	
337 342 347 352	
gtg gac cca gtt aaa act cca aag att tgt aag ccc gag agt ggt gag	1104

Val Asp Pro Val Lys Thr Pro Lys Ile Cys Lys Pro Glu Ser Gly Glu	
353 358 363 368	
tgc atc aac tgc ctc cat aac acc act ggg ttt tgg tgt gag aac tgc	1152
Cys Ile Asn Cys Leu His Asn Thr Thr Gly Phe Trp Cys Glu Asn Cys	
369 374 379 384	
cta gaa ggt tat gtt cac gac ctc gag gga aat tgc atc aag aaa gaa	1200
Leu Glu Gly Tyr Val His Asp Leu Glu Gly Asn Cys Ile Lys Lys Glu	
385 390 395 400	
gtt att ctt cca aca cct gaa ggt tct acc att ttg gtt tcc aat gcc	1248
Val Ile Leu Pro Thr Pro Glu Gly Ser Thr Ile Leu Val Ser Asn Ala	
401 406 411 416	
tct ttg acc aca tca gtg ccc acc cct gtt ata aat agt act ttt acc	1296
Ser Leu Thr Thr Ser Val Pro Thr Pro Val Ile Asn Ser Thr Phe Thr	
417 422 427 432	
cct aca acc ctg cag act atc ttt tca gta agc act tct gaa aac agc	1344
Pro Thr Thr Leu Gln Thr Ile Phe Ser Val Ser Thr Ser Glu Asn Ser	
433 438 443 448	
act tca gct tta gct gat gta tca tgg acc caa ttt aac atc atc att	1392
Thr Ser Ala Leu Ala Asp Val Ser Trp Thr Gln Phe Asn Ile Ile Ile	
449 454 459 464	
ttg aca gtc atc atc att gtt gtg gtg ctg cta atg gga ttt gtg ggg	1440
Leu Thr Val Ile Ile Ile Val Val Val Leu Leu Met Gly Phe Val Gly	
465 470 475 480	
gct gta tat atg tac cgc gag tac caa aac cgg aaa ctc aat gcc ccc	1488
Ala Val Tyr Met Tyr Arg Glu Tyr Gln Asn Arg Lys Leu Asn Ala Pro	
481 486 491 496	
ttt tgg acc atc gag ctg aaa gaa gac aat atc agt ttc agc agc tac	1536
Phe Trp Thr Ile Glu Leu Lys Glu Asp Asn Ile Ser Phe Ser Ser Tyr	
497 502 507 512	
cat gac agc att ccc aat gca gat gtt tgc gga ttg ttg gaa gat gat	1584
His Asp Ser Ile Pro Asn Ala Asp Val Ser Gly Leu Leu Glu Asp Asp	
513 518 523 528	
ggc aat gaa gtg gct ccc aat ggg cag ctg acc ctg acg acg ccc ata	1632
Gly Asn Glu Val Ala Pro Asn Gly Gln Leu Thr Leu Thr Thr Pro Ile	
529 534 539 544	
cat aac tac aaa gcc taa ggagct agaactgttc tgaattgtta aaccacagt	1686
His Asn Tyr Lys Ala *	
545 550	
cttgctaaga cagagtcagc cctgggccca gacaaagcct ggctagagtt tgctgagaaa	1746
gcaaaggcaa atagtgcac tgaaattttc aggtacaaat ttgtaatgcg cttagcctat	1806
ctattgctct tagttttccc atgaagatct gaagcgttca ctgtcattag gacttgaagt	1866

aaagtatatatt tttgtaccaa accacatggg agtatggaaa ggctgaaccc catagtgcag	1926
cccaaaacca ctttgacctc cagatagact cctggggaag cattcaccaa gccagtggta	1986
acaagatgat gaatgtggag ggggaaaaga ctgctggaag acttcatctc cattcctgaa	2046
acattttttt taaaacagtg tcagggatta tattcgtttt actatacaaa aggacatcat	2106
tgaggaaaag cttgtttcta ggctgtatca cagtaaataa tcttgattgt ttctagaaca	2166
ggggtagaaa agtccaaga tcttcagaag ggcttggttt tttcctcca ggattcctgc	2226
tcagtgatga gttgaaagca caggataagc ttctaaggga ggaaggcagc attggggagc	2286
aggaggctga tggctctcct caggtctca gtgtaaatga taaattgtct aaaaataagg	2346
aatattcctg cctctagaga aataaggtgt acatagttaa tgtagcatat ctggtcgacg	2406
ttgtatttgt atctatttgt aaaaaaaaaa tcatgtcata ttttatcatc tggaatttat	2466
ttgtacagca gttaatggtg ttgtaaaaag aaaaatatgg ggattgctta aaatactgta	2526
aaatagatgg caatattgct agagctggga ctctggtgag catccgtcat ttttagtcct	2586
tcttgaggac attgctgaaa tttataagag gtogaatgtt tctttctttc ctttctcagt	2646
ctaaaagtag agttatatgc tctttgactt actatgattc aagcaataga ttttgaagtc	2706
agtaatcgtt aagctgggac ataggatgca ttctccaaaa acattaatct aattagacat	2766
tagccaccct atatatatta catagattaa tataaaacat atcctcatta aaaaatgttt	2826
ttcttgaatg taaaagatag tcttccaaag gatagaaata ttttagttcc aagagaaaag	2886
ccatcatatt acttgggac tctagttttc atgcctatga aatatttata atcctccctc	2946
accccaaata aaaaatctcc tacatgtgaa catagcctgt cactcatttg ccatgaggta	3006
tgtgccatct cctgcagtg ctatagtctt ccattgtct tctgtctgg ttaatgagca	3066
gctttgtaga tgggtgtgtc tagttagttc ttgctttttg atggagtttt ttcctagagg	3126
ccaactactg ttgctctcgt ttattatgat attgacattt tgggttaagc aaggtgggtg	3186
ggaaagggtg tcagatgtta aatataactt attaggagga acagtgaact gtgaagtgg	3246
tagaaaaaaaa aaaaaaactt cttattagat tagacctagg aaattcaagc tgacccttt	3306
gcctaacttc cctagagaaa aacctagaac ttgggtcatcc ctttatagga gaccctaag	3366
ttgttctcag gggttgaga tgatgttctg gagggagtac aagcaaataa tctacttctg	3426
gtaatctgag ggtgctttgc gtatttggcc attgctcaga agaatagagg ttacattata	3486
ttacattata tgaaaattat ttagtttttc tatagccctt ttagttttgc aaagcacttt	3546
tccatatgtg tgcctctct tccacaccat agccccctga ggaagtaatt gttgtcccca	3606

ttttatagat gaaaaggctg aggcacagag gagctaaata tottgttcaa ggctatacaa	3666
tgtgtgtgat tattaggctt ggaatcaggg cctctaactc taaagcacat gttttttcaa	3726
ctatatgcag aaattgccta gccatggaca caagaaagct gggaggaaga gttctacttg	3786
tggatgtttt taattttttt taaatatcag gagcaatcca gggccataca gctatgaagc	3846
acttagtgaa aagaacacaa gaagatttac taactgaagt tagtattagt gattagaaaa	3906
caaaactgcc agtttgtgct tcattaaggt gaactcatct ctccaagcag gaagggaaaa	3966
tttgctttcc ctagcagttg ctgcatatgt gtgtacagac tgcacaattc taagaaattg	4026
tgcaaaatgg catacctgtc tttctcccag atacaccgcc ccctgcccc cccaaaaaag	4086
gtcaggatta aagggtggtga gaagtgaaca tttattaaac agaagttaaa ccaatagaga	4146
gaaaggaggt ttgttggagt ctaaggaggat tttgaccatg tagaaattcc ttgaaacaga	4206
ccttaaaagg tattgaaaaa ttgaatcaca aagaaagttt acctttaaat acttgtaaat	4266
ggctcctaga tcatggttat aatttttctc aatgggaaaa aaagtcttaa aatttgtttt	4326
aaataagatc ctctaattgc tcgagctttt tgattctgga aataatttgc tttaaaatat	4386
aaatcaatca gaaagtgatc taccactgaa atcattctag gaaactagca tgggatgcac	4446
tgcacaatgt tctttcctct aaaggcatgg gcccataaa ctgtggcatc tggcagcagg	4506
atgccatcag tccttttagaa agcctaattt tgggcccgggt gcggtggctc acgcctgtaa	4566
tcccagcact ttgggaggcc gagggcgggtg gatcacaagg tcaggagttc gagaccagcc	4626
tgggtcaacat ggcgaaatcc cgtctctact aaaaacacaa aaattagccg ggtgtacgtg	4686
cctgtagtct cagctacttg ggaggctgag gcaggagaat cacttgaacc tgggaggcag	4746
aggttacagt gagccgagat ggcgccattt cactccagcc tgggcgacag agcaagactc	4806
tgtctcaaaa aaaaggaaga aaaagaaagc ctaatatagg gagaatgttt gtgtaaggat	4866
tggaaatctg tttattttta aataagatag cactgatgtg aatcttattt ggaaattaca	4926
gatactgcca ttaagcgatg cttttatctt cattaattca ttttggttaag cgcctatgca	4986
tttctgatgg ttaggtgccc taggtagtgt taagtatgtc cgtgtcctcc ctactcccc	5046
tctcgctccc tctaccctct atcccctagg gttcttttat taatggaatt tctccagtta	5106
tagagaaaaa aatgacattt gaaaactaaa gtcattttat attaatacta aggtcctgtg	5166
ggcctagtgc gttactcttc ccagtgatac ctagatttta agagtagaga acagaggaaa	5226
catgggatga gaggagagag gttttttaga caacatttgt agacacctca aattatatca	5286

ctgttctcta gcgccaatat tcccaggtaa attgaccatt aaagcaatac tcaactgacct 5346
 actagtttat tttggtcagc tgagtaccat caggatattt aaccctttaa gtgctgtttt 5406
 gggagtagaa aactaaagca acaatacttc ctcttgacag ctttgattgg aatgggggta 5466
 ttagatcatt cacottgggc ctacactttt taggatgctt ggtgaacata acaccactta 5526
 taatgaacat ccctgggtcc tatattttgg gctatgtggg taggaattgt tacttggtgc 5586
 tgcagcagca gccctagaaa gtaagcccag ggcttcagat ctaagttagt ccaaaaagcta 5646
 aatgatttaa agtcaagttg taatgctagg cataagcact ctataatata ttaaattata 5706
 ggccgagcaa ttaggggaatg tttctgaaac attaaacttg tatttatgtc actaaaattc 5766
 taacacaaaac ttaaaaaatg tgtctcatac atatgctgta ctaggcttca tcatgcattt 5826
 ctaaatgtgt gtatgatttg aatatatgaa agaatttata caagagtgtt atttaaaatt 5886
 attaaaaata aatgtatata atttgtacct attgtagatt tggtgtttac ttttttgtgt 5946
 ggtcagagtt gtttcatgtc ttcaaataca tgccaaggat catttacttt cagcccactt 6006
 cataaaaaatc tttgaactct t 6027

<210> 518
 <211> 787
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (249)..(464)

<400> 518
 ccggaattcc cggggcgacg ccggcgtagc ataaataccc ttgaataaaa tggttagctt 60
 tcttctcaca gaggaagatg cagtatatgg tggttgtaga aataaatgaa gctttacttt 120
 aagttctggg atacatgtgc aggatgtgca gggttggttac ataggtaaac ttgtgccatg 180
 gtgggttgct gcacctatca acccatcacc taggtattaa gcccgcatg cattagctat 240
 ttttccta atg ctc tcc ttc ccc cac cta acc ccc caa caa ccc aaa tgc 290
 Met Leu Ser Phe Pro His Leu Thr Pro Gln Gln Pro Lys Cys
 1 5 10
 cca tca atg ata gac tgg ata aag aaa ata tgg tac ata tac acc atg 338
 Pro Ser Met Ile Asp Trp Ile Lys Lys Ile Trp Tyr Ile Tyr Thr Met
 15 20 25 30
 gaa tac tat gca acc ata aaa agg aat gag atc atg ttc ttt gca ggg 386
 Glu Tyr Tyr Ala Thr Ile Lys Arg Asn Glu Ile Met Phe Phe Ala Gly

31	36	41	46	
aca tgg atg gag atg gaa gcc att atc ctc agc aaa cta atg cag gac				434
Thr Trp Met Glu Met Glu Ala Ile Ile Leu Ser Lys Leu Met Gln Asp				
47	52	57	62	
tat atg ttc tca ctt ata agt ggg agc tga a caataagaac atatggaaac				485
Tyr Met Phe Ser Leu Ile Ser Gly Ser *				
63	68			
aggaggaga acaatataca ctggggcctg ttttgggagt gcagtggagg agaagagcat				545
taggaagaat agctaatagca tgctggtctt aatacctagg tgatggggtg ataagtgcag				605
caaaccacca tggcacatgt ttacctatgt aacaaacctg cacatcctgc acacgtaccc				665
tggaacttaa aaaaacaaaa taaaataaaag tgggtataaa taccactgcc gaactgcctc				725
tgggctgcta ttttgggtcc agtcctatgc atggccctct ctgcaaggaa cagtacctgt				785
gc				787

<210> 519
 <211> 1388
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (37) .. (963)

<400> 519	
atttggccct cgaggccaag aattcggcac gagaag atg gcg ggg aag aag aat	54
Met Ala Gly Lys Lys Asn	
1	

gtt ctg tcg tct ctc gca gtt tac gcg gaa gat tca gag ccc gag tct	102
Val Leu Ser Ser Leu Ala Val Tyr Ala Glu Asp Ser Glu Pro Glu Ser	
7 12 17 22	

gat ggc gag gct gga atc gag gcg gtg ggc agc gcg gct gag gag aaa	150
Asp Gly Glu Ala Gly Ile Glu Ala Val Gly Ser Ala Ala Glu Glu Lys	
23 28 33 38	

ggc gga ttg gta tct gat gcc tat ggg gag gat gac ttt tct cgt cta	198
Gly Gly Leu Val Ser Asp Ala Tyr Gly Glu Asp Asp Phe Ser Arg Leu	
39 44 49 54	

ggg ggt gat gaa gat ggt tat gaa gaa gaa gaa gat gag aac agt aga	246
Gly Gly Asp Glu Asp Gly Tyr Glu Glu Glu Glu Asp Glu Asn Ser Arg	
55 60 65 70	

cag tcg gaa gat gac gat tca gag act gaa aaa cct gag gct gat gac	294
Gln Ser Glu Asp Asp Asp Ser Glu Thr Glu Lys Pro Glu Ala Asp Asp	

71	76	81	86	
cca aag gat aat aca gaa gca gaa aag cga gac ccc cag gaa ctc gtg				342
Pro Lys Asp Asn Thr Glu Ala Glu Lys Arg Asp Pro Gln Glu Leu Val				
87	92	97	102	
gcc tcc ttt tct gaa aga gtt cgg aac atg tgc cct gat gaa atc aag				390
Ala Ser Phe Ser Glu Arg Val Arg Asn Met Ser Pro Asp Glu Ile Lys				
103	108	113	118	
atc ccg cca gaa ccc cct ggc aga tgt tca aat cac ttg caa gac aag				438
Ile Pro Pro Glu Pro Pro Gly Arg Cys Ser Asn His Leu Gln Asp Lys				
119	124	129	134	
atc cag aag ctt tat gaa cga aag ata aag gag gga atg gat atg aac				486
Ile Gln Lys Leu Tyr Glu Arg Lys Ile Lys Glu Gly Met Asp Met Asn				
135	140	145	150	
tac att atc caa agg aag aaa gaa ttt cgg aac cct agc atc tac gag				534
Tyr Ile Ile Gln Arg Lys Lys Glu Phe Arg Asn Pro Ser Ile Tyr Glu				
151	156	161	166	
aag ctg atc cag ttc tgt gcc att gac gag ctt ggc acc aac tac cca				582
Lys Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr Asn Tyr Pro				
167	172	177	182	
aag gat atg ttt gat ccc cat ggc tgg tct gag gac tcc tac tat gag				630
Lys Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser Tyr Tyr Glu				
183	188	193	198	
gca tta gcc aag gcc cag aaa att gag atg gac aaa ttg gaa aag gcc				678
Ala Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu Glu Lys Ala				
199	204	209	214	
aaa aag gag cga aca aaa att gag ttt gtg acg ggc acc aaa aaa ggc				726
Lys Lys Glu Arg Thr Lys Ile Glu Phe Val Thr Gly Thr Lys Lys Gly				
215	220	225	230	
acc acg acc aac gcc acg tcc acc acc act acc act gcc agc aca gct				774
Thr Thr Thr Asn Ala Thr Ser Thr Thr Thr Thr Thr Ala Ser Thr Ala				
231	236	241	246	
gtt gca gat gct cag aag aga aag agc aag tgg gat tgc gct atc cca				822
Val Ala Asp Ala Gln Lys Arg Lys Ser Lys Trp Asp Ser Ala Ile Pro				
247	252	257	262	
gtg aca acg ata gcc cag ccc acc atc ctc acc acc aca gcc acc ctg				870
Val Thr Thr Ile Ala Gln Pro Thr Ile Leu Thr Thr Thr Ala Thr Leu				
263	268	273	278	
cca gct gtt gtc acg gtc acc acc agc gcc agc ggc tcc aag acc acc				918
Pro Ala Val Val Thr Val Thr Thr Ser Ala Ser Gly Ser Lys Thr Thr				
279	284	289	294	
gtc atc tct gct gtg ggc acc att gtg aag aag gcc aag cag tga cct				966
Val Ile Ser Ala Val Glu Gly Thr Ile Val Lys Lys Ala Lys Gln *				
295	300	305		

gagggggccac cctaggactt gaaaggaccg tgcagcccag tgaccactgc ccagtgggag 1026
 gcgccacttt gtatatttca ggactgggac ctactcccca gatgccacct gagaggagct 1086
 tctgtttggc attccagatg gaaggacagg cagcacggga gccagggcgt gtggacaggg 1146
 tctgtccacg caccacctgg ggtctgccgc ctattaaaag tgccgtattc ttacctcttg 1206
 gcattctcaga tgcactggcc tctcctgcat tctgtttgca ggcaaagtct tcagctcaca 1266
 tgtcccccaa gactcaatag tcttggttgg gactattgcc tcaggggtga caacaggggtg 1326
 atggaggcct gggacgctgt tcagaggggt gacccaagaa gtdaccgttg ttatccgtgt 1386
 at 1388

<210> 520
 <211> 1562
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (37)..(1137)

<400> 520
 atttggccct cgaggccaag aattcggcac gagaag atg gcg ggg aag aag aat 54
 Met Ala Gly Lys Lys Asn
 1
 gtt ctg tcg tct ctc gca gtt tac gcg gaa gat tca gag ccc gag tct 102
 Val Leu Ser Ser Leu Ala Val Tyr Ala Glu Asp Ser Glu Pro Glu Ser
 7 12 17 22
 gat ggc gag gct gga atc gag gcg gtg ggc agc gcg gct gag gag aaa 150
 Asp Gly Glu Ala Gly Ile Glu Ala Val Gly Ser Ala Ala Glu Glu Lys
 23 28 33 38
 ggc gga ttg gta tct gat gcc tat ggg gag gat gac ttt tct cgt cta 198
 Gly Gly Leu Val Ser Asp Ala Tyr Gly Glu Asp Asp Phe Ser Arg Leu
 39 44 49 54
 ggg ggt gat gaa gat ggt tat gaa gaa gaa gaa gat gag aac agt aga 246
 Gly Gly Asp Glu Asp Gly Tyr Glu Glu Glu Glu Asp Glu Asn Ser Arg
 55 60 65 70
 cag tcg aga cgg tgt ttc act atg ttt ccc agt ctg gtt tca aac ttc 294
 Gln Ser Arg Arg Cys Phe Thr Met Phe Pro Ser Leu Val Ser Asn Phe
 71 76 81 86
 tgg cct caa gca att ccc ctg cct cac cct ccc aaa gtg ctg gga tta/ 342
 Trp Pro Gln Ala Ile Pro Leu Pro His Pro Pro Lys Val Leu Gly Leu
 87 92 97 102

cag gaa gat gac gat tca gag act gaa aaa cct gag gct gat gac cca	390
Gln Glu Asp Asp Asp Ser Glu Thr Glu Lys Pro Glu Ala Asp Asp Pro	
103 108 113 118	
aag gat aat aca gaa gca gaa aag cga gac ccc cag gaa ctc gtg gcc	438
Lys Asp Asn Thr Glu Ala Glu Lys Arg Asp Pro Gln Glu Leu Val Ala	
119 124 129 134	
tcc ttt tct gaa aga gtt cgg aac atg tcg cct gat gaa atc aag atc	486
Ser Phe Ser Glu Arg Val Arg Asn Met Ser Pro Asp Glu Ile Lys Ile	
135 140 145 150	
ccg cca gaa ccc cct ggc aga tgt tca aat cac ttg caa gac aag atc	534
Pro Pro Glu Pro Pro Gly Arg Cys Ser Asn His Leu Gln Asp Lys Ile	
151 156 161 166	
cag aag ctt tat gaa cga aag ata aag gag gga atg gat atg aac tac	582
Gln Lys Leu Tyr Glu Arg Lys Ile Lys Glu Gly Met Asp Met Asn Tyr	
167 172 177 182	
att atc caa agg aag aaa gaa ttt cgg aac cct agc atc tac gag aag	630
Ile Ile Gln Arg Lys Lys Glu Phe Arg Asn Pro Ser Ile Tyr Glu Lys	
183 188 193 198	
ctg atc cag ttc tgt gcc att gac gag ctt ggc acc aac tac cca aag	678
Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr Asn Tyr Pro Lys	
199 204 209 214	
gat atg ttt gat ccc cat ggc tgg tct gag gac tcc tac tat gag gca	726
Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser Tyr Tyr Glu Ala	
215 220 225 230	
tta gcc aag gcc cag aaa att gag atg gac aaa ttg gaa aag gcc aaa	774
Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu Glu Lys Ala Lys	
231 236 241 246	
aag gag cga aca aaa gct tgt tgc agg gac gtg tct gca gcg cct ggg	822
Lys Glu Arg Thr Lys Ala Cys Cys Arg Asp Val Ser Ala Ala Pro Gly	
247 252 257 262	
gaa ccg agc tgt cct tcc cct gtg cgg gcg ggc acc gcc tcc tcc tgg	870
Glu Pro Ser Cys Pro Ser Pro Val Arg Ala Gly Thr Ala Ser Ser Trp	
263 268 273 278	
att gag ttt gtg acg ggc acc aaa aaa ggc acc acg acc aac gcc aca	918
Ile Glu Phe Val Thr Gly Thr Lys Lys Gly Thr Thr Thr Asn Ala Thr	
279 284 289 294	
tcc acc acc act acc act gcc agc aaa gct gtt gca gat gct cag aag	966
Ser Thr Thr Thr Thr Thr Ala Ser Lys Ala Val Ala Asp Ala Gln Lys	
295 300 305 310	
aga aag agc aag tgg gat tcg gct atc cca gtg aca acg ata gcc cag	1014
Arg Lys Ser Lys Trp Asp Ser Ala Ile Pro Val Thr Thr Ile Ala Gln	
311 316 321 326	

ccc acc atc ctc acc acc aca gcc acc ctg cca gct gtt gtc acg gtc	1062
Pro Thr Ile Leu Thr Thr Thr Ala Thr Leu Pro Ala Val Val Thr Val	
327 332 337 342	
acc acc agc gcc agc ggc tcc aag acc acc gtc atc tct gct gtg ggc	1110
Thr Thr Ser Ala Ser Gly Ser Lys Thr Thr Val Ile Ser Ala Val Gly	
343 348 353 358	
acc att gtg aag aag gcc aag cag tga cctga gggggccaccc taggacttga	1162
Thr Ile Val Lys Lys Ala Lys Gln *	
359 364	
aaggaccgtg cagcccagtg accactgccc agtgggaggc gccactttgt atatttcagg	1222
actgggacct actccccaga tgccacctga gaggagcttc tgtttggcat tccagatgga	1282
aggacaggca gcacgggagc caggcgctgt ggacagggtc tgtccacgca ccacctgggg	1342
tctgccgcct attaaaagtg ccgtattctt acctottggc atctcagatg cactggcctc	1402
tcctgcattc tgtttgcagg caaatgcttc agctcacatg tcccccaaga ctcaatagtc	1462
ttggttggga ctattgcctc agggttgaca acagggtgat ggaggcctgg gacgctgttc	1522
agaggggtga cccaagaagt caccgttgtt atccgtgtat	1562

<210> 521
 <211> 1340
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (37)..(915)

<400> 521	
atttggccct cgaggccaag aattcggcac gagaag atg gcg ggg aag aag aat	54
Met Ala Gly Lys Lys Asn	
1	
gtt ctg tcg tct ctc gca gtt tac gcg gaa gat tca gag ccc gag tct	102
Val Leu Ser Ser Leu Ala Val Tyr Ala Glu Asp Ser Glu Pro Glu Ser	
7 12 17 22	
gat ggc gag gct gga atc gag gcg gtg ggc agc gcg gct gag gag aaa	150
Asp Gly Glu Ala Gly Ile Glu Ala Val Gly Ser Ala Ala Glu Glu Lys	
23 28 33 38	
ggc gga ttg gta tct gat gcc tat ggg gag gat gac ttt tct cgt cta	198
Gly Gly Leu Val Ser Asp Ala Tyr Gly Glu Asp Asp Phe Ser Arg Leu	
39 44 49 54	
ggg ggt gat gaa gat ggt tat gaa gaa gaa gaa gat gag aac agt aga	246
Gly Gly Asp Glu Asp Gly Tyr Glu Glu Glu Glu Asp Glu Asn Ser Arg	

55	60	65	70	
cag tcg gat aat aca gaa gca gaa aag cga gac ccc cag gaa ctc gtg				294
Gln Ser Asp Asn Thr Glu Ala Glu Lys Arg Asp Pro Gln Glu Leu Val				
71	76	81	86	
gcc tcc ttt tct gaa aga gtt cgg aac atg tcg cct gat gaa atc aag				342
Ala Ser Phe Ser Glu Arg Val Arg Asn Met Ser Pro Asp Glu Ile Lys				
87	92	97	102	
atc ccg cca gaa ccc cct ggc aga tgt tca aat cac ttg caa gac aag				390
Ile Pro Pro Glu Pro Pro Gly Arg Cys Ser Asn His Leu Gln Asp Lys				
103	108	113	118	
atc cag aag ctt tat gaa cga aag ata aag gag gga atg gat atg aac				438
Ile Gln Lys Leu Tyr Glu Arg Lys Ile Lys Glu Gly Met Asp Met Asn				
119	124	129	134	
tac att atc caa agg aag aaa gaa ttt cgg aac cct agc atc tac gag				486
Tyr Ile Ile Gln Arg Lys Lys Glu Phe Arg Asn Pro Ser Ile Tyr Glu				
135	140	145	150	
aag ctg atc cag ttc tgt gcc att gac gag ctt ggc acc aac tac cca				534
Lys Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr Asn Tyr Pro				
151	156	161	166	
aag gat atg ttt gat ccc cat ggc tgg tct gag gac tcc tac tat gag				582
Lys Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser Tyr Tyr Glu				
167	172	177	182	
gca tta gcc aag gcc cag aaa att gag atg gac aaa ttg gaa aag gcc				630
Ala Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu Glu Lys Ala				
183	188	193	198	
aaa aag gag cga aca aaa att gag ttt gtg acg ggc acc aaa aaa ggc				678
Lys Lys Glu Arg Thr Lys Ile Glu Phe Val Thr Gly Thr Lys Lys Gly				
199	204	209	214	
acc acg acc aac gcc acg tcc acc acc act acc act gcc agc aca gct				726
Thr Thr Thr Asn Ala Thr Ser Thr Thr Thr Thr Thr Ala Ser Thr Ala				
215	220	225	230	
gtt gca gat gct cag aag aga aag agc aag tgg gat tcg gct atc cca				774
Val Ala Asp Ala Gln Lys Arg Lys Ser Lys Trp Asp Ser Ala Ile Pro				
231	236	241	246	
gtg aca acg ata gcc cag ccc acc atc ctc acc acc aca gcc acc ctg				822
Val Thr Thr Ile Ala Gln Pro Thr Ile Leu Thr Thr Thr Ala Thr Leu				
247	252	257	262	
cca gct gtt gtc acg gtc acc acc agc gcc agc ggc tcc aag acc acc				870
Pro Ala Val Val Thr Val Thr Thr Ser Ala Ser Gly Ser Lys Thr Thr				
263	268	273	278	
gtc atc tct gct gtg ggc acc att gtg aag aag gcc aag cag tga cct				918
Val Ile Ser Ala Val Gly Thr Ile Val Lys Lys Ala Lys Gln *				
279	284	289		

gagggggccac cctaggactt gaaaggaccg tgcagcccag tgaccactgc ccagtgggag 978
gcgccacttt gtatatattca ggactgggac ctactcccca gatgccacct gagaggagct 1038
tctgttttggc attccagatg gaaggacagg cagcacggga gccaggcgct gtggacaggg 1098
tctgtccacg caccacctgg ggtctgccgc ctattaaag tgccgtattc ttacctcttg 1158
gcatctcaga tgcaactggcc tctcctgcat tctgtttgca ggcaaatgct tcagctcaca 1218
tgtcccccaa gactcaatag tcttggttgg gactattgcc tcagggttga caacaggggtg 1278
atggaggcct gggacgctgt tcagaggggt gaccaagaa gtcaccgttg ttatccgtgt 1338
at 1340

<210> 522
<211> 827
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (114)..(593)

<400> 522
ggactgtggc gaatgatgta tataactatc tattcgatga tgaagatacc ccaccaaacc 60
caaaaaaaga gatctctcga ggatccgaat tcgcgggccgc gtcgacgagc aac atg 116
Met
1
ccc aag ttt tat tgt gac tac tgc gat aca tac ctc acc cat gac tct 164
Pro Lys Phe Tyr Cys Asp Tyr Cys Asp Thr Tyr Leu Thr His Asp Ser
2 7 12 17
cca tct gtg aga aag aca cac tgc agt gga agg aaa cac aaa gag aat 212
Pro Ser Val Arg Lys Thr His Cys Ser Gly Arg Lys His Lys Glu Asn
18 23 28 33
gtg aaa gac tat tat cag aaa tgg atg gaa gag cag gct cag agc ctg 260
Val Lys Asp Tyr Tyr Gln Lys Trp Met Glu Glu Gln Ala Gln Ser Leu
34 39 44 49
att gac aaa aca acg gct gca ttt caa caa gga aag ata cct cct act 308
Ile Asp Lys Thr Thr Ala Ala Phe Gln Gln Gly Lys Ile Pro Pro Thr
50 55 60 65
cca ttc tct gct cct cct cct gca ggg gcg atg ata cca cct ccc ccc 356
Pro Phe Ser Ala Pro Pro Pro Ala Gly Ala Met Ile Pro Pro Pro Pro
66 71 76 81
agc ctt ccg ggt cct cct cgc cct ggt atg atg cca gca ccc cat atg 404

Ser Leu Pro Gly Pro Pro Arg Pro Gly Met Met Pro Ala Pro His Met
82 87 92 97

ggg ggc cct ccc atg atg cca atg atg ggc cct cct cct cct ggg atg 452
Gly Gly Pro Pro Met Met Pro Met Met Gly Pro Pro Pro Pro Gly Met
98 103 108 113

atg cca gtg gga cct gct cct gga atg agg ccg ccc atg gga ggc cat 500
Met Pro Val Gly Pro Ala Pro Gly Met Arg Pro Pro Met Gly Gly His
114 119 124 129

atg cca atg atg cct ggg ccc cca atg atg aga cct cct gcc cgt ccc 548
Met Pro Met Met Pro Gly Pro Pro Met Met Arg Pro Pro Ala Arg Pro
130 135 140 145

atg atg gtg ccc act cgg ccc gga atg act cga cca gac aga taa gga 596
Met Met Val Pro Thr Arg Pro Gly Met Thr Arg Pro Asp Arg *
146 151 156

tagaggggag gccttattgt atcggtttta tatttatatt ctgcttcacc aggagatcat 656

gctgctgtga tactgagttt tctaaacagc ataaggaaga cttgctcccc tgtcctatga 716

aagagaatag ttttggaggg gagaagtggg acaaaaaaga tgcagttttc ctttgtattg 776

ggaaatgtga aaataaaatt gtcaactcct tcagttaata aaaaaaaaaa a 827

<210> 523
<211> 1612
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (248) .. (994)

<400> 523
catttgtata ccgtgaccca gcctggctag cgtttaaact taagcttggg accgagctcg 60

gatccactag tccagtgtgg tggaattcat ctttgtatga tgtggcttta aattttttaa 120

aagcaatgct gtctgtgaat aacatggcta atttcttcgt aggggtgattt ctaacctaga 180

agcaagaaat ttggggccaa gattaacacc cctcctgcag gaggaagaca gccaccagcg 240

gctgctc atg ggg ctg atg gtg tct gag cta aaa gac cat ttt ttg aga 289
Met Gly Leu Met Val Ser Glu Leu Lys Asp His Phe Leu Arg
1 5 10

cac cta cag ggt gta gaa aag aag aaa att gaa cag atg gtt ctg gac 337
His Leu Gln Gly Val Glu Lys Lys Lys Ile Glu Gln Met Val Leu Asp
15 20 25 30

tac att tca aaa ctg ctg gat ctc att tgc cac atc gta gaa acc aat 385

Tyr	Ile	Ser	Lys	Leu	Leu	Asp	Leu	Ile	Cys	His	Ile	Val	Glu	Thr	Asn		
31					36					41					46		
tgg	agg	aaa	cat	aat	ctt	cat	tcc	tgg	gtt	ctc	cac	ttc	aat	agt	cgt		433
Trp	Arg	Lys	His	Asn	Leu	His	Ser	Trp	Val	Leu	His	Phe	Asn	Ser	Arg		
47					52					57					62		
ggc	agt	gct	gct	gaa	ttt	gca	gtt	ttt	cac	atc	atg	acc	agg	att	ctg		481
Gly	Ser	Ala	Ala	Glu	Phe	Ala	Val	Phe	His	Ile	Met	Thr	Arg	Ile	Leu		
63					68					73					78		
gaa	gct	aca	aac	agt	ttg	ttt	tta	cct	ctg	cct	cct	ggt	ttt	cat	act		529
Glu	Ala	Thr	Asn	Ser	Leu	Phe	Leu	Pro	Leu	Pro	Pro	Gly	Phe	His	Thr		
79					84					89					94		
ctg	cac	acc	atc	ctc	ggg	gtc	cag	tgt	ctc	cct	ttg	cat	aac	ctg	ctg		577
Leu	His	Thr	Ile	Leu	Gly	Val	Gln	Cys	Leu	Pro	Leu	His	Asn	Leu	Leu		
95					100					105					110		
cat	tgc	att	gac	agt	gga	gtg	ttg	ctt	ctc	act	gaa	aca	gct	gtc	ata		625
His	Cys	Ile	Asp	Ser	Gly	Val	Leu	Leu	Leu	Thr	Glu	Thr	Ala	Val	Ile		
111					116					121					126		
agg	ctc	atg	aaa	gat	ctg	gat	aat	aca	gag	aaa	aat	gaa	aaa	ctg	aaa		673
Arg	Leu	Met	Lys	Asp	Leu	Asp	Asn	Thr	Glu	Lys	Asn	Glu	Lys	Leu	Lys		
127					132					137					142		
ttc	agt	atc	att	gtg	cgg	ctt	cct	ccg	ctt	att	ggg	cag	aag	att	tgt		721
Phe	Ser	Ile	Ile	Val	Arg	Leu	Pro	Pro	Leu	Ile	Gly	Gln	Lys	Ile	Cys		
143					148					153					158		
aga	ctt	tgg	gat	cat	cct	atg	agt	tct	aac	atc	att	tcg	cgg	aac	cac		769
Arg	Leu	Trp	Asp	His	Pro	Met	Ser	Ser	Asn	Ile	Ile	Ser	Arg	Asn	His		
159					164					169					174		
gtg	acg	cga	ctg	ctt	cag	aac	tat	aag	aaa	cag	cct	cgg	aat	tct	atg		817
Val	Thr	Arg	Leu	Leu	Gln	Asn	Tyr	Lys	Lys	Gln	Pro	Arg	Asn	Ser	Met		
175					180					185					190		
att	aac	aag	tca	tcg	ttc	agt	gta	gaa	ttt	ctg	cct	ctg	aac	tac	ttc		865
Ile	Asn	Lys	Ser	Ser	Phe	Ser	Val	Glu	Phe	Leu	Pro	Leu	Asn	Tyr	Phe		
191					196					201					206		
att	gaa	att	ctg	aca	gat	ata	gag	tcc	tcc	aat	caa	gcc	ctg	tat	cct		913
Ile	Glu	Ile	Leu	Thr	Asp	Ile	Glu	Ser	Ser	Asn	Gln	Ala	Leu	Tyr	Pro		
207					212					217					222		
ttt	gaa	gga	cat	gac	aat	gtg	gat	gca	gaa	ttt	gta	gag	gaa	gca	gct		961
Phe	Glu	Gly	His	Asp	Asn	Val	Asp	Ala	Glu	Phe	Val	Glu	Glu	Ala	Ala		
223					228					233					238		
ctg	aaa	cac	acc	gcg	atg	ctt	tta	ggc	tta	tga	aaaagaaa	acgcaattgg					1012
Leu	Lys	His	Thr	Ala	Met	Leu	Leu	Gly	Leu	*							
239					244					249							
atctgctgct	gccatttttaa	tcttgctcat	taaccttact	cctttgagaa	ttctttaaca												1072

atattttaaaa ttggttaacaa aaatagttta gccataattg tttagccatg tgagtttcag 1132
 gttggtacac gttcagacag aactgctgta tcacattcca attttgaata gccagtgagc 1192
 aatcaagtgt agagaaatga taaatggcct aagaaggcat acagtggcat aaacgatgct 1252
 cttcctagta gcttaatagg ccacaagota gtttctgttg cactctgaaa taaaatatgc 1312
 tttaaaaatg tagggaacag tgcttagaaa agcaaaaact aggtgtgtca ttgaaataat 1372
 aggcataaaa attaaatggt acataagaac actatttgga aagagggtcc ttttaaaaac 1432
 tgaatttgta ctaaatacaga tttgccatgt ccagtacaga ataatttgta cttagtattt 1492
 gcagcagggt ttgtctttgt gaattcagat gaaacatatt tttttttttt tatttataaa 1552
 aggttgattt aggaatatatt tgtcagtcac taaaaaacct gaaaacataa aaaaaaaaaa 1612

<210> 524
 <211> 955
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (3)..(866)

<400> 524
 ca atg tcg ttg cac gcg tac gta agc ttg gat cct cta gag cgg ccg 47
 Met Ser Leu His Ala Tyr Val Ser Leu Asp Pro Leu Glu Arg Pro
 1 5 10
 cgg gca gac ccg gag gga acg gag gaa gcg gtc atg tct cgc tac acg 95
 Arg Ala Asp Pro Glu Gly Thr Glu Glu Ala Val Met Ser Arg Tyr Thr
 16 21 26 31
 agg ccc ccc aac acc tcc ctg ttc atc agg aac gtc gcg gac gcc acc 143
 Arg Pro Pro Asn Thr Ser Leu Phe Ile Arg Asn Val Ala Asp Ala Thr
 32 37 42 47
 agg cct gag gac ttg cgc cgt gag ttt ggt cga tat ggc cct ata gta 191
 Arg Pro Glu Asp Leu Arg Arg Glu Phe Gly Arg Tyr Gly Pro Ile Val
 48 53 58 63
 gac gtt tac att cca ctt gac ttc tac act cgc cgc cca aga gga ttt 239
 Asp Val Tyr Ile Pro Leu Asp Phe Tyr Thr Arg Arg Pro Arg Gly Phe
 64 69 74 79
 gct tat gtt caa ttt gaa gat gtt cga gat gct gaa gat gct ctt tat 287
 Ala Tyr Val Gln Phe Glu Asp Val Arg Asp Ala Glu Asp Ala Leu Tyr
 80 85 90 95
 aac ctc aat aga aag tgg gta tgt ggc cgt cag att gaa ata cag ttt 335
 Asn Leu Asn Arg Lys Trp Val Cys Gly Arg Gln Ile Glu Ile Gln Phe

96	101	106	111	
gca caa ggt gat cgc aaa aca cca ggc caa atg aaa tca aaa gaa cgt				383
Ala Gln Gly Asp Arg Lys Thr Pro Gly Gln Met Lys Ser Lys Glu Arg				
112	117	122	127	
cat cct tgt tct cca agt gat cac agg aga tca aga agc ccc agc caa				431
His Pro Cys Ser Pro Ser Asp His Arg Arg Ser Arg Ser Pro Ser Gln				
128	133	138	143	
aga aga act cga agt aga agt tct tca tgg gga aga aat agg agg cgg				479
Arg Arg Thr Arg Ser Arg Ser Ser Ser Trp Gly Arg Asn Arg Arg Arg				
144	149	154	159	
tca gac agc ctt aaa gag tct cga cac agg cga ttt tct tat agc cag				527
Ser Asp Ser Leu Lys Glu Ser Arg His Arg Arg Phe Ser Tyr Ser Gln				
160	165	170	175	
tct aaa tct cgt tcc aaa tca tta cca agg cgg tct acc tca gca agg				575
Ser Lys Ser Arg Ser Lys Ser Leu Pro Arg Arg Ser Thr Ser Ala Arg				
176	181	186	191	
cag tca aga act cca aga agg aat ttt ggc tct aga gga cgg tca agg				623
Gln Ser Arg Thr Pro Arg Arg Asn Phe Gly Ser Arg Gly Arg Ser Arg				
192	197	202	207	
tcc aag tcc tta caa aag agg tcc aag tca ata gga aaa tca cag tca				671
Ser Lys Ser Leu Gln Lys Arg Ser Lys Ser Ile Gly Lys Ser Gln Ser				
208	213	218	223	
agt tca cct caa aag cag act agc tca gga aca aaa tca aga tca cat				719
Ser Ser Pro Gln Lys Gln Thr Ser Ser Gly Thr Lys Ser Arg Ser His				
224	229	234	239	
gga aga cat tct gac tca ata gca aga tcc ccg tgt aaa tct ccc aaa				767
Gly Arg His Ser Asp Ser Ile Ala Arg Ser Pro Cys Lys Ser Pro Lys				
240	245	250	255	
ggg tat acc aat tct gaa act aaa gta caa aca gca aag cat tct cat				815
Gly Tyr Thr Asn Ser Glu Thr Lys Val Gln Thr Ala Lys His Ser His				
256	261	266	271	
ttt cgg tca cat tcc aga tct cga agt tat cgt cat aaa aac agt tgg				863
Phe Arg Ser His Ser Arg Ser Arg Ser Tyr Arg His Lys Asn Ser Trp				
272	277	282	287	
tga acag caacagaaaag agcaccacgc cgtctttaat ataagttatt aaactctcat				920
*				
288				
tatgttaaataaaaaattctt taaggcatac agaaa				955

<210> 525
<211> 2593

<213> Homo sapiens

<221> CDS

<222> (263) .. (1960)

aaggtaccgct ccqgaattcc cgggtcgacg atttcgtcac actggcacag acacaagcag 60

ggacacacgc agacacacgc acactcgcgc gcgcattcctc ccgccagcct gccgcctgc 120

tcgccggcgc ccggaagccc ctctgcccgc tggatgatct gaaagctgcc tctctccttc 180

atttatatca ccagcttgct ttttgctgag aaagcttcct gccctggaag atggcaccct 240

tcccatcca gacaccttgg ga atg aat tat gag gga gcc agg agt gag aga 292
Met Asn Tyr Glu Gly Ala Arg Ser Glu Arg
1 5

gag aac cac gct gct gat gac tcc gag gga ggg gcc ctg gac atg tgc 340
Glu Asn His Ala Ala Asp Asp Ser Glu Gly Gly Ala Leu Asp Met Cys
11 16 21 26

tgc agt gag agg cta ccg ggt ctc ccc cag ccg ata gtg atg gag gca 388
Cys Ser Glu Arg Leu Pro Gly Leu Pro Gln Pro Ile Val Met Glu Ala
27 32 37 42

ctg gac gag gct gaa ggg ctc cag gac tca cag aga gag atg ccg cca 436
Leu Asp Glu Ala Glu Gly Leu Gln Asp Ser Gln Arg Glu Met Pro Pro
43 48 53 58

ccc cct cct ccc tog ccg ccc tca gat cca gct cag aag cca cca cct 484
Pro Pro Pro Pro Ser Pro Pro Ser Asp Pro Ala Gln Lys Pro Pro Pro
59 64 69 74

cga ggc gct ggg agc cac tcc ctc act gtc agg agc agc ctg tgc ctg 532
Arg Gly Ala Gly Ser His Ser Leu Thr Val Arg Ser Ser Leu Cys Leu
75 80 85 90

ttc	gct	gcc	tca	cag	ttc	ctg	ctt	gcc	tgt	ggg	gtg	ctc	tgg	ttc	agc	580
Phe	Ala	Ala	Ser	Gln	Phe	Leu	Leu	Ala	Cys	Gly	Val	Leu	Trp	Phe	Ser	
91					96					101					106	

ggt tat ggc cac atc tgg tca cag aac gcc aca aac ctc gtc tcc tct 628
Gly Tyr Gly His Ile Trp Ser Gln Asn Ala Thr Asn Leu Val Ser Ser
107 112 117 122

ttg	ctg	acg	ctc	ctg	aaa	cag	ctg	gaa	ccc	acg	gcc	tgg	ott	gac	tct	676
Leu	Leu	Thr	Leu	Leu	Lys	Gln	Leu	Glu	Pro	Thr	Ala	Trp	Leu	Asp	Ser	
123					128					133					138	

ggg acg tgg gga gtc ccc agt ctg ctg ctg gtc ttt ctg tcc gtg ggc 724
Gly Thr Trp Gly Val Pro Ser Leu Leu Leu Val Phe Leu Ser Val Gly
139 144 149 154

ctg gtc ctc gtt acc acc ctg gtg tgg cac ctc ctg agg aca ccc cca 772

Leu Val Leu Val Thr Thr Leu Val Trp His Leu Leu Arg Thr Pro Pro	
155 160 165 170	
gag cca ccc acc cca ctg ccc cct gag gac agg cgc cag tca gtg agc	820
Glu Pro Pro Thr Pro Leu Pro Pro Glu Asp Arg Arg Gln Ser Val Ser	
171 176 181 186	
cgc cag ccc tcc ttc acc tac tca gag tgg atg gag gag aag atc gag	868
Arg Gln Pro Ser Phe Thr Tyr Ser Glu Trp Met Glu Glu Lys Ile Glu	
187 192 197 202	
gat gac ttc ctg gac ctc gac ccg gtg ccc gag act cct gtg ttt gat	916
Asp Asp Phe Leu Asp Leu Asp Pro Val Pro Glu Thr Pro Val Phe Asp	
203 208 213 218	
tgt gtg atg gac atc aag cct gag gct gac ccc acc tca ctc acc gtc	964
Cys Val Met Asp Ile Lys Pro Glu Ala Asp Pro Thr Ser Leu Thr Val	
219 224 229 234	
aag tcc atg ggt ctg cag gag agg agg ggt tcc aat gtc tcc ctg acc	1012
Lys Ser Met Gly Leu Gln Glu Arg Arg Gly Ser Asn Val Ser Leu Thr	
235 240 245 250	
ctg gac atg tgc act ccg ggc tgc aac gag gag ggc ttt ggc tat ctc	1060
Leu Asp Met Cys Thr Pro Gly Cys Asn Glu Glu Gly Phe Gly Tyr Leu	
251 256 261 266	
atg tcc cca cgt gag gag tcc gcc cgc gag tac ctg ctc agc gcc tcc	1108
Met Ser Pro Arg Glu Glu Ser Ala Arg Glu Tyr Leu Leu Ser Ala Ser	
267 272 277 282	
cgt gtc ctc caa gca gaa gag ctt cat gaa aag gcc ctg gac cct ttc	1156
Arg Val Leu Gln Ala Glu Glu Leu His Glu Lys Ala Leu Asp Pro Phe	
283 288 293 298	
ctg ctg cag gcg gaa ttc ttt gaa atc ccc atg aac ttt gtg gat ccg	1204
Leu Leu Gln Ala Glu Phe Phe Glu Ile Pro Met Asn Phe Val Asp Pro	
299 304 309 314	
aaa gag tac gac atc cct ggg ctg gtg cgg aag aac cgg tac aaa acc	1252
Lys Glu Tyr Asp Ile Pro Gly Leu Val Arg Lys Asn Arg Tyr Lys Thr	
315 320 325 330	
ata ctt ccc aac cct cac agc aga gtg tgt ctg acc tca cca gac cct	1300
Ile Leu Pro Asn Pro His Ser Arg Val Cys Leu Thr Ser Pro Asp Pro	
331 336 341 346	
gac gac cct ctg agt tcc tac atc aat gcc aac tac atc cgg ggc tat	1348
Asp Asp Pro Leu Ser Ser Tyr Ile Asn Ala Asn Tyr Ile Arg Gly Tyr	
347 352 357 362	
ggg gag gag aag gtg tac atc gcc act cag gga ccc atc gtc agc	1396
Gly Gly Glu Glu Lys Val Tyr Ile Ala Thr Gln Gly Pro Ile Val Ser	
363 368 373 378	
acg gtc gcc gac ttc tgg cgc atg gtg tgg cag gag cac acg ccc atc	1444
Thr Val Ala Asp Phe Trp Arg Met Val Trp Gln Glu His Thr Pro Ile	

379	384	389	394	
att gtc atg atc acc aac atc gag gag atg aac gag aaa tgc acc gag				1492
Ile Val Met Ile Thr Asn Ile Glu Glu Met Asn Glu Lys Cys Thr Glu				
395	400	405	410	
tat tgg ccg gag gag cag gtg gcg tac gac ggt gtt gag atc act gtg				1540
Tyr Trp Pro Glu Glu Gln Val Ala Tyr Asp Gly Val Glu Ile Thr Val				
411	416	421	426	
cag aaa gtc att cac acg gag gat tac cgg ctg cga ctc atc tcc ctc				1588
Gln Lys Val Ile His Thr Glu Asp Tyr Arg Leu Arg Leu Ile Ser Leu				
427	432	437	442	
aag agt ggg act gag gag cga ggc ctg aag cat tac tgg ttc aca tcc				1636
Lys Ser Gly Thr Glu Glu Arg Gly Leu Lys His Tyr Trp Phe Thr Ser				
443	448	453	458	
tgg ccc gac cag aag acc cca gac cgg gcc ccc cca ctc ctg cac ctg				1684
Trp Pro Asp Gln Lys Thr Pro Asp Arg Ala Pro Pro Leu Leu His Leu				
459	464	469	474	
gtg cgg gag gtg gag gag gca gcc cag cag gag ggg ccc cac tgt gcc				1732
Val Arg Glu Val Glu Glu Ala Ala Gln Gln Glu Gly Pro His Cys Ala				
475	480	485	490	
ccc atc atc gtc cac tgc agt gca ggg att ggg agg acc ggc tgc ttc				1780
Pro Ile Ile Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Cys Phe				
491	496	501	506	
att gcc acc agc atc tgc tgc cag cag ctg cgg cag gag ggt gta gtg				1828
Ile Ala Thr Ser Ile Cys Cys Gln Gln Leu Arg Gln Glu Gly Val Val				
507	512	517	522	
gac atc ctg aag acc acg tgc cag ctc cgt cag gac agg ggc ggc atg				1876
Asp Ile Leu Lys Thr Thr Cys Gln Leu Arg Gln Asp Arg Gly Gly Met				
523	528	533	538	
atc cag cac tgc gag cag tac cag ttt gtg cac cac gtc atg agc ctc				1924
Ile Gln His Cys Glu Gln Tyr Gln Phe Val His His Val Met Ser Leu				
539	544	549	554	
tac gaa aag cag ctg tcc cac cag tcc cca gaa tga ctgc gcttctccta				1974
Tyr Glu Lys Gln Leu Ser His Gln Ser Pro Glu *				
555	560	565		
caaggggtctc tgggcactgc ccagcctgag tctcgccct caccagggc cctgcctcgg				2034
gtcctggggc tgctccccgc ttctctccct tcagtcagct ccctctgtcc tctgtcagcc				2094
tggcctgacc cctaccctcc agcattgctc ttctactgt acatattggg gagtgggggg				2154
cagggctcggg aagggacatg ccaggccagg cgtggggccc cggggcctga cccacaccac				2214
gcagaccccg ggctccagtt tttaacgatg gttccatcaa tacctgatcc agaattgttc				2274
cgtgctacac tttgtgtcct gctgcaatgt gttctgtctg tccatccatc tctgccctct				2334

gtaccggaca ctgtgtctcc tcagccagga aggggtaatg agctccagcc cctaagcaac 2394
 eggacttgcc tgccctggcc tcaccgcac ttctccaaa aggcagatga cggggagtta 2454
 ggcattggga gctccagaag gtcaccagag agctttcagc tgaggagag ttctctaggt 2514
 tggagtgggc atcacagcca ggggtggcctc tgggtgtcag atgctctcag gagggtgccc 2574
 agcctgtgag gcactggca 2593

<210> 526
 <211> 1733
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (215)..(1372)

<400> 526
 cggccagtgc atagctaaaa ttaacctca ctaaaggga taagcttgcg gccggggcg 60
 cggcggcgag agcgaaagag gaaactgcag aggaggaagc tgcgccgcag cccgagccgc 120
 ccggcatccc cgccgcctct gcgcccgcgc cgcgcccccg gcgccccctc cccagcgcgc 180
 ccccgggcgc tctccgcgc cgcgctcgtc ggcc atg gcc cgg gag aac gcc 232
 Met Ala Arg Glu Asn Gly
 1
 gag agc agc tcc tcc tgg aaa aag caa gct gaa gac atc aag aag atc 280
 Glu Ser Ser Ser Ser Trp Lys Lys Gln Ala Glu Asp Ile Lys Lys Ile
 7 12 17 22
 ttc gag ttc aaa gag acc ctc gga acc ggg gcc ttt tcc gaa gtg gtt 328
 Phe Glu Phe Lys Glu Thr Leu Gly Thr Gly Ala Phe Ser Glu Val Val
 23 28 33 38
 tta gct gaa gag aag gca act ggc aag ctc ttt gct gtg aag tgt atc 376
 Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu Phe Ala Val Lys Cys Ile
 39 44 49 54
 cct aag aag gcg ctg aag ggc aag gaa agc agc ata gag aat gag ata 424
 Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser Ser Ile Glu Asn Glu Ile
 55 60 65 70
 gcc gtc ctg aga aag att aag cat gaa aat att gtt gcc ctg gaa gac 472
 Ala Val Leu Arg Lys Ile Lys His Glu Asn Ile Val Ala Leu Glu Asp
 71 76 81 86
 att tat gaa agc cca aat cac ctg tac ttg gtc atg cag ctg gtg tcc 520
 Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu Val Met Gln Leu Val Ser
 87 92 97 102

ggt gga gag ctg ttt gac cgg ata gtg gag aag ggg ttt tat aca gag	568
Gly Gly Glu Leu Phe Asp Arg Ile Val Glu Lys Gly Phe Tyr Thr Glu	
103 108 113 118	
aag gat gcc agc act ctg atc cgc caa gtc ttg gac gcc gtg tac tat	616
Lys Asp Ala Ser Thr Leu Ile Arg Gln Val Leu Asp Ala Val Tyr Tyr	
119 124 129 134	
ctc cac aga atg ggc atc gtc cac aga gac ctc aag ccc gaa aat ctc	664
Leu His Arg Met Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn Leu	
135 140 145 150	
ttg tac tac agt caa gat gag gag tcc aaa ata atg atc agt gac ttt	712
Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys Ile Met Ile Ser Asp Phe	
151 156 161 166	
gga ttg tca aaa atg gag ggc aaa gga gat gtg atg tcc act gcc tgt	760
Gly Leu Ser Lys Met Glu Gly Lys Gly Asp Val Met Ser Thr Ala Cys	
167 172 177 182	
gga act cca ggc tat gtc gct cct gaa gtc ctc gcc cag aaa cct tac	808
Gly Thr Pro Gly Tyr Val Ala Pro Glu Val Leu Ala Gln Lys Pro Tyr	
183 188 193 198	
agc aaa gcc gtt gac tgc tgg tcc atc gga gtg att gcc tac atc ttg	856
Ser Lys Ala Val Asp Cys Trp Ser Ile Gly Val Ile Ala Tyr Ile Leu	
199 204 209 214	
ctc tgc ggc tac cct cct ttt tat gat gaa aat gac tcc aag ctc ttt	904
Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu Asn Asp Ser Lys Leu Phe	
215 220 225 230	
gag cag atc ctc aag gcg gaa tat gag ttt gac tct ccc tac tgg gat	952
Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe Asp Ser Pro Tyr Trp Asp	
231 236 241 246	
gac atc tcc gac tct gca aaa gac ttc att cgg aac ctg atg gag aag	1000
Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile Arg Asn Leu Met Glu Lys	
247 252 257 262	
gac ccg aat aaa aga tac acg tgt gag cag gca gct cgg cac cca tgg	1048
Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln Ala Ala Arg His Pro Trp	
263 268 273 278	
atc gct ggt gac aca gcc ctc aac aaa aac atc cac gag tcc gtc agc	1096
Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn Ile His Glu Ser Val Ser	
279 284 289 294	
gcc cag atc cgg aaa aac ttt gcc aag agc aaa tgg aga caa gca ttt	1144
Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser Lys Trp Arg Gln Ala Phe	
295 300 305 310	
aat gcc acg gcc gtc gtg aga cat atg aga aaa cta cac ctc ggc agc	1192
Asn Ala Thr Ala Val Val Arg His Met Arg Lys Leu His Leu Gly Ser	
311 316 321 326	

agc ctg gac agt tca aat gca agt gtt tgc agc agc ctc agt ttg gcc	1240
Ser Leu Asp Ser Ser Asn Ala Ser Val Ser Ser Ser Leu Ser Leu Ala	
327 332 337 342	
agc caa aaa gac tgt ctg gca cct tcc acg ctc tgt agt ttc att tct	1288
Ser Gln Lys Asp Cys Leu Ala Pro Ser Thr Leu Cys Ser Phe Ile Ser	
343 348 353 358	
tct tgc tgc ggg gtc tca gga gtt gga gcc gag cgg aga ccc agg ccc	1336
Ser Ser Ser Gly Val Ser Gly Val Gly Ala Glu Arg Arg Pro Arg Pro	
359 364 369 374	
acc act gtg acg gca gtg cac tct gga agc aag tga ctgg ccctggaggt	1386
Thr Thr Val Thr Ala Val His Ser Gly Ser Lys *‡	
375 380 385	
ggggcccggg gtcggggctg gggaagggga gccccagggt cgccagagcc gcgagccact	1446
ccagcgagac cccaccttgc atggtgcccc ttctgcata ggactggaag accgaagttt	1506
ttttatggcc atattttcta ctgcaattct gaagtgttca tttctcaca actgtactga	1566
ctcgaggggc gctgatttca taggatctgg tgctgtatat acgaatcttg caaagctcta	1626
actgaacgga ccttcttatt cctctccct aacaccatcg tttccactct tctcagtgt	1686
ggtaaccgtc tatggtgtgt tttttcatta atgacaaaaa aaaaaaa	1733

<210> 527
 <211> 731
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (109)..(639)

<400> 527	
ctcactatag ggaatttggc cctcgagcaa gaagttcggc acgaggcgca ctctctaagg	60
ccccgggtga agccccacct ctgctgcgcg cacgctgcgg tgcgggtc atg gcg cgg	117
Met Ala Arg	
1	
cta ccg aag ctg gca gtc ttt gat ttg gat tac act ctc tgg cct ttc	165
Leu Pro Lys Leu Ala Val Phe Asp Leu Asp Tyr Thr Leu Trp Pro Phe	
4 9 14 19	
tgg gtc gac acg cac gta gac cct ccg ttc cat aag agc agt gat gga	213
Trp Val Asp Thr His Val Asp Pro Pro Phe His Lys Ser Ser Asp Gly	
20 25 30 35	
act gta cga gat agg cgg ggc caa gac gtc cga ctg tac cca gag gtg	261
Thr Val Arg Asp Arg Arg Gly Gln Asp Val Arg Leu Tyr Pro Glu Val	

36	41	46	51	
cct gag gtc cta aaa cga ttg cag agc ctt ggg gtg ccc ggt gcg gct				309
Pro Glu Val Leu Lys Arg Leu Gln Ser Leu Gly Val Pro Gly Ala Ala				
52	57	62	67	
gct tca agg aca agt gag ata gaa ggg gcc aac cag cta ctg gag ctc				357
Ala Ser Arg Thr Ser Glu Ile Glu Gly Ala Asn Gln Leu Leu Glu Leu				
68	73	78	83	
ttt gac ctc ttc agg tac ttt gtt cat cgg gaa atc tat cca ggc agc				405
Phe Asp Leu Phe Arg Tyr Phe Val His Arg Glu Ile Tyr Pro Gly Ser				
84	89	94	99	
aag atc aca cac ttt gag agg ttg cag cag aag act gga att cct ttc				453
Lys Ile Thr His Phe Glu Arg Leu Gln Gln Lys Thr Gly Ile Pro Phe				
100	105	110	115	
tcc cag atg atc ttc ttt gat gat gag agg cgg aat att gta gac gtc				501
Ser Gln Met Ile Phe Phe Asp Asp Glu Arg Arg Asn Ile Val Asp Val				
116	121	126	131	
agc aaa ctg ggt gtt acc tgc att cac atc cag aat gga atg aat ctt				549
Ser Lys Leu Gly Val Thr Cys Ile His Ile Gln Asn Gly Met Asn Leu				
132	137	142	147	
caa act cta agt caa ggg tta gag aca ttt gcg aag gcc caa act ggg				597
Gln Thr Leu Ser Gln Gly Leu Glu Thr Phe Ala Lys Ala Gln Thr Gly				
148	153	158	163	
cct ttg agg tcc agc ctt gag gag agc cca ttt gag gcc taa actgaaa				646
Pro Leu Arg Ser Ser Leu Glu Glu Ser Pro Phe Glu Ala *				
164	169	174		
ggaaatcaag aaggcatttt caggtgcatt tgtaatttat taaagttcat ctgtgtgtga				706
cagaagagat tttaaaaaaaa aaaaa				731

<210> 528
 <211> 1746
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (107) .. (505)

<400> 528	
attgttaggg agacccaagc ttgctagcgt ttaaacttaa gcttggtacc gagctcggat	60
ccactagtcc agtgtggtgg aattcaagcg gcgagtaaga tggaag atg agg agg	115
	Met Arg Arg
	1

tcg ctg aga gct ggg aag agg cgg cag aca gcg ggg aaa tcc aaa tot	163
Ser Leu Arg Ala Gly Lys Arg Arg Gln Thr Ala Gly Lys Ser Lys Ser	
4 9 14 19	
cct ccc aaa gtg ccc att gtg att cag gac gat agc ctt ccc gcg ggg	211
Pro Pro Lys Val Pro Ile Val Ile Gln Asp Asp Ser Leu Pro Ala Gly	
20 25 30 35	
ccc cct cca cag atc cgc atc ctc aag agg ccc acc agc aac ggt gtg	259
Pro Pro Pro Gln Ile Arg Ile Leu Lys Arg Pro Thr Ser Asn Gly Val	
36 41 46 51	
gtc agc agc ccc aac tcc acc agc agg ccc acc ctt cca gtc aag tcc	307
Val Ser Ser Pro Asn Ser Thr Ser Arg Pro Thr Leu Pro Val Lys Ser	
52 57 62 67	
cta gca cag cga gag gcc gag tac gcc gag gcc cgg aag cgg atc ctg	355
Leu Ala Gln Arg Glu Ala Glu Tyr Ala Glu Ala Arg Lys Arg Ile Leu	
68 73 78 83	
ggc agc gcc agc ccc gag gag gag cag gag aaa ccc atc ctc gac agg	403
Gly Ser Ala Ser Pro Glu Glu Glu Gln Glu Lys Pro Ile Leu Asp Arg	
84 89 94 99	
cca acc agg atc tcc caa ccc gaa gac agc agg cag ccc aat aat gtg	451
Pro Thr Arg Ile Ser Gln Pro Glu Asp Ser Arg Gln Pro Asn Asn Val	
100 105 110 115	
atc aga cag cct ttg ggt cct gat ggg tct caa ggc ttc aaa cag cgc	499
Ile Arg Gln Pro Leu Gly Pro Asp Gly Ser Gln Gly Phe Lys Gln Arg	
116 121 126 131	
aga taa atgcaggcaa gaaaagatgc cgccgttgct gccgtcaccc cctcctgggt	555
Arg *	
132	
cgctccgccac gggttgcact gccgtggcag acagctggac ttgagcagag ggaacgacct	615
gacttacttg cactgtgac ccccttgctc cgccactgt gacctgaac cccatgcact	675
gtgacctccc cctttctccc ccttcccact gtgattggca catcgacaag ggctgtccca	735
agtcaatgga aagggaaagg gtgggggtta ggggaagggt ggggggaccc agcaaggact	795
cagagagtca gacagtgcc cttggccact tggggtaaag ccagtgccag caataacagt	855
ttatcatgct cattaatttg ggatttcaaa acacaaatga aaactcacac ccacccaccc	915
ccaagtgc atgtccatca cttaaaaagt aagttccatt tgaaaatatc ctttcttttt	975
tttttcttcc tatttttggt tgtttataca aatatctgat ttgcaagaaa aagtgcattg	1035
gaggggtttt agtggtttta tgaattttta attaagaaag ggtagtttgg tagtctactt	1095
aaaaatgttt ctgggaaatt cactagaaac attaaccaat aggatttttg tgagcttagc	1155
ttctgtattc ctactgccgc ccagaaaagg ggcagggtc tgcagccgcc aggacagacg	1215

agcaccocat gcctatacct ccctccccga gctaagtccc agggcatctg ggccttgcc 1275
 ggagactggg ctagctctgt aggctcggag agcctgggga ggggtgccaac cccacctcta 1335
 gtattttggg agatagggaa agtgaaccga cttccccttc ccatacccct cagggtggtt 1395
 ccctaccagc caggcttact acttctagaa gaaagcagag tgccagggag tgagattgca 1455
 tccctgggct tagaagtgc ggagagaaga cttgtttagt attttgccat cagcacaagg 1515
 aaaaccagga gagagtctgc ctccaggact ctgagccttc tgccctgtat gttcagaagg 1575
 tggataggtc ttcccactcc agcatggctt gaactcttag gggctctgcag tgctccatct 1635
 ccattggtgg cccagctca gtaactatac ctggtacatt tccgtgtgtgc aatcagtacc 1695
 ttgaaggcag aacattctga ataaagttgg aaaaagaaca aaaaaaaaaa a 1746

<210> 529
 <211> 612
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (118)..(486)

<400> 529
 catcgaaagg cttgatgtct ataactatct attcgatgat gaagataccc caccaaacc 60
 aaaaaaagag atctctcgag gatccgaatt cgcggccgcg tcgaccgcgg ccgcaag 117
 atg gcg ccg cag aaa gac agg aag ccc aag agg tca acc tgg agg ttt 165
 Met Ala Pro Gln Lys Asp Arg Lys Pro Lys Arg Ser Thr Trp Arg Phe
 1 5 10 15
 aat ttg gac ctt act cat cca gta gaa gat gga att ttt gat tct gga 213
 Asn Leu Asp Leu Thr His Pro Val Glu Asp Gly Ile Phe Asp Ser Gly
 17 22 27 32
 aat ttt gag caa ttt cta cgg gag aag gtt aaa gtc aat ggc aaa act 261
 Asn Phe Glu Gln Phe Leu Arg Glu Lys Val Lys Val Asn Gly Lys Thr
 33 38 43 48
 gga aat ctc ggg aat gtt gtt cac att gaa cgc ttc aag aat aaa atc 309
 Gly Asn Leu Gly Asn Val Val His Ile Glu Arg Phe Lys Asn Lys Ile
 49 54 59 64
 aca gtt gtt tct gag aaa cag ttc tct aaa agg tat ttg aaa tac ctt 357
 Thr Val Val Ser Glu Lys Gln Phe Ser Lys Arg Tyr Leu Lys Tyr Leu
 65 70 75 80
 acc aag aaa tac ctt aag aag aac aat ctt cgt gat tgg ctt cga gtg 405
 Thr Lys Lys Tyr Leu Lys Lys Asn Asn Leu Arg Asp Trp Leu Arg Val

81	86	91	96	
gtt gca tct gac aag gag acc tac gaa ctt cgt tac ttc cag att agt				453
Val Ala Ser Asp Lys Glu Thr Tyr Glu Leu Arg Tyr Phe Gln Ile Ser				
97	102	107	112	
caa gat gaa gat gaa tca gag tcg gag gac tag gcaaaggc tccccttaca				504
Gln Asp Glu Asp Glu Ser Glu Ser Glu Asp *				
113	118	123		
gggctttgct tattaataaaa ataatgaag tatacatgag aaataccaag aaattggctt				564
ttagttttatc agtgaataaaa aaatattata ctcttgaaaa aaaaaaaa				612

<210> 530
 <211> 4586
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (586) .. (2556)

<400> 530			
caggctccct caggatgcac tggtgccagt cagcgttact cattttattc cctagggAAC			60
agtggggtttg gtagaactct cttctaaatc tctttttcat agaatttAAA ttataaattg			120
gtcattttact gttgtcacac aatattgcgt tgctgaattt tccactgatt atattcattt			180
tatttctctc cagaacttgg tttcttggtt ttctgctcac tgtccacacc cactccaccc			240
caaggctgga ataattctct tggagcaaaa aaatcatctt tttctttgta tttcattgaa			300
cgttctcttt acagtgttag gtaaaccgct gctgcgcgtt ttgtcccgcg tctcgccccg			360
tccgtctcct gactggccgc tcttgctctt cctcccgtt tttcttctct cgtcttgccg			420
tctgaagatg ccctcggcca ccagccacag cgggagcggc agcaagtcgt ccggaccgcc			480
accgccgtcg gggtctccgg gagtgaggcg gccgcgggag cgggggccgc cgcgccggct			540
tctcagcacc ccgcaaccgg caccggcgct gtccagaccg aggcc			594
	atg aag cag		
	Met Lys Gln		
	1		
att ctc ggg gtg atc gac aag aaa ctt cgg aac ctg gag aag aaa aag			642
Ile Leu Gly Val Ile Asp Lys Lys Leu Arg Asn Leu Glu Lys Lys Lys			
4	9	14	19
ggg aag ctt gat gat tac cag gaa cga atg aac aaa ggg gaa agg ctt			690
Gly Lys Leu Asp Asp Tyr Gln Glu Arg Met Asn Lys Gly Glu Arg Leu			
20	25	30	35

aat caa gat cag ctg gat gcc gtt tct aag tac cag gaa gtc aca aat	738
Asn Gln Asp Gln Leu Asp Ala Val Ser Lys Tyr Gln Glu Val Thr Asn	
36 41 46 51	
aat ttg gag ttt gca aaa gaa tta cag agg agt ttc atg gca cta agt	786
Asn Leu Glu Phe Ala Lys Glu Leu Gln Arg Ser Phe Met Ala Leu Ser	
52 57 62 67	
caa gat att cag aaa aca ata aag aag aca gca cgt cgg gag cag ctt	834
Gln Asp Ile Gln Lys Thr Ile Lys Lys Thr Ala Arg Arg Glu Gln Leu	
68 73 78 83	
atg aga gaa gaa gct gaa cag aaa cgt tta aaa act gta ctt gag cta	882
Met Arg Glu Glu Ala Glu Gln Lys Arg Leu Lys Thr Val Leu Glu Leu	
84 89 94 99	
cag tat gtt ttg gac aaa ttg gga gat gat gaa gtg cgg act gac ctg	930
Gln Tyr Val Leu Asp Lys Leu Gly Asp Asp Glu Val Arg Thr Asp Leu	
100 105 110 115	
aaa caa ggt ttg aat gga gtg cca ata ttg tcc gaa gag gag ttg tca	978
Lys Gln Gly Leu Asn Gly Val Pro Ile Leu Ser Glu Glu Glu Leu Ser	
116 121 126 131	
ttg ttg gat gaa ttc tat aag cta gta gac cct gaa cgg gac atg agc	1026
Leu Leu Asp Glu Phe Tyr Lys Leu Val Asp Pro Glu Arg Asp Met Ser	
132 137 142 147	
ttg agg ttg aat gaa cag tat gaa cat gcc tcc att cac ctg tgg gac	1074
Leu Arg Leu Asn Glu Gln Tyr Glu His Ala Ser Ile His Leu Trp Asp	
148 153 158 163	
ctg ctg gaa ggg aag gaa aaa cct gta tgt gga acc acc tat aaa gtt	1122
Leu Leu Glu Gly Lys Glu Lys Pro Val Cys Gly Thr Thr Tyr Lys Val	
164 169 174 179	
cta aag gaa att gtt gag cgt gtt ttt cag tca aac tac ttt gac agc	1170
Leu Lys Glu Ile Val Glu Arg Val Phe Gln Ser Asn Tyr Phe Asp Ser	
180 185 190 195	
acc cac aac cac cag aat ggg ctg tgt gag gaa gaa gag gca gcc tca	1218
Thr His Asn His Gln Asn Gly Leu Cys Glu Glu Glu Glu Ala Ala Ser	
196 201 206 211	
gca cct gca gtt gaa gac cag gta cct gaa gct gaa cct gag cca gca	1266
Ala Pro Ala Val Glu Asp Gln Val Pro Glu Ala Glu Pro Glu Pro Ala	
212 217 222 227	
gaa gag tac act gag caa agt gaa gtt gaa tca aca gag tat gta aat	1314
Glu Glu Tyr Thr Glu Gln Ser Glu Val Glu Ser Thr Glu Tyr Val Asn	
228 233 238 243	
aga cag ttc atg gca gaa aca cag ttc acc agt ggt gaa aag gag cag	1362
Arg Gln Phe Met Ala Glu Thr Gln Phe Thr Ser Gly Glu Lys Glu Gln	
244 249 254 259	
gta gat gag tgg aca gtt gaa acg gtt gag gtg gta aat tca ctc cag	1410

Val Asp Glu Trp Thr	Val Glu Thr Val Glu Val Val Asn Ser Leu Gln	
260	265	270 275
cag caa cct cag gct gca tcc cct tca gta cca gag ccc cac tct ttg		1458
Gln Gln Pro Gln Ala Ala Ser Pro Ser Val Pro Glu Pro His Ser Leu		
276	281	286 291
act cca gtg gct cag gca gat ccc ctt gtg aga aga cag cga gta caa		1506
Thr Pro Val Ala Gln Ala Asp Pro Leu Val Arg Arg Gln Arg Val Gln		
292	297	302 307
gac ctt atg gca caa atg cag ggt ccc tat aat ttc ata cag gat tca		1554
Asp Leu Met Ala Gln Met Gln Gly Pro Tyr Asn Phe Ile Gln Asp Ser		
308	313	318 323
atg ctg gat ttt gaa aat cag aca ctt gat cct gcc att gta tct gca		1602
Met Leu Asp Phe Glu Asn Gln Thr Leu Asp Pro Ala Ile Val Ser Ala		
324	329	334 339
cag cct atg aat cca aca caa aac atg gac atg ccc cag ctg gtt tgc		1650
Gln Pro Met Asn Pro Thr Gln Asn Met Asp Met Pro Gln Leu Val Cys		
340	345	350 355
cct cca gtt cat tct gaa tct aga ctt gct cag cct aat caa gtt cct		1698
Pro Pro Val His Ser Glu Ser Arg Leu Ala Gln Pro Asn Gln Val Pro		
356	361	366 371
gta caa cca gaa gcg aca cag gtt cct ttg gta tca tcc aca agt gag		1746
Val Gln Pro Glu Ala Thr Gln Val Pro Leu Val Ser Ser Thr Ser Glu		
372	377	382 387
ggg tac aca gca tct caa ccc ttg tac cag cct tct cat gct aca gag		1794
Gly Tyr Thr Ala Ser Gln Pro Leu Tyr Gln Pro Ser His Ala Thr Glu		
388	393	398 403
caa cga cca cag aag gaa cca att gat cag att cag gca aca atc tct		1842
Gln Arg Pro Gln Lys Glu Pro Ile Asp Gln Ile Gln Ala Thr Ile Ser		
404	409	414 419
tta aat aca gac cag act aca gca tca tca tcc ctt cct gct gcg tct		1890
Leu Asn Thr Asp Gln Thr Thr Ala Ser Ser Ser Leu Pro Ala Ala Ser		
420	425	430 435
cag cct caa gta ttt cag gct ggg aca agc aaa cct tta cat agc agt		1938
Gln Pro Gln Val Phe Gln Ala Gly Thr Ser Lys Pro Leu His Ser Ser		
436	441	446 451
gga atc aat gta aat gca gct cca ttc caa tcc atg caa acg gtg ttc		1986
Gly Ile Asn Val Asn Ala Ala Pro Phe Gln Ser Met Gln Thr Val Phe		
452	457	462 467
aat atg aat gcc cca gtt cct cct gtt aat gaa cca gaa act tta aaa		2034
Asn Met Asn Ala Pro Val Pro Pro Val Asn Glu Pro Glu Thr Leu Lys		
468	473	478 483
cag caa aat cag tac cag gcc agt tat aac cag agc ttt tct agt cag		2082
Gln Gln Asn Gln Tyr Gln Ala Ser Tyr Asn Gln Ser Phe Ser Ser Gln		

484	489	494	499	
cct cac caa gta gaa caa aca gag ctt cag caa gaa cag ctt caa aca				2130
Pro His Gln Val Glu Gln Thr Glu Leu Gln Gln Glu Gln Leu Gln Thr				
500	505	510	515	
gtg gtt ggc act tac cat ggt tcc cca gac cag tcc cat caa gtg act				2178
Val Val Gly Thr Tyr His Gly Ser Pro Asp Gln Ser His Gln Val Thr				
516	521	526	531	
ggt aac cac cag cag cct cct cag cag aac act gga ttt cca cgt agc				2226
Gly Asn His Gln Gln Pro Pro Gln Gln Asn Thr Gly Phe Pro Arg Ser				
532	537	542	547	
aat cag ccc tat tac aat agt cgt ggt gtg tct cgt gga ggc tcc cgt				2274
Asn Gln Pro Tyr Tyr Asn Ser Arg Gly Val Ser Arg Gly Gly Ser Arg				
548	553	558	563	
ggt gct aga ggc ttg atg aat gga tac cgg ggc cct gcc aat gga ttc				2322
Gly Ala Arg Gly Leu Met Asn Gly Tyr Arg Gly Pro Ala Asn Gly Phe				
564	569	574	579	
aga gga gga tat gat ggt tac cgc cct tca ttc tct aac act cca aac				2370
Arg Gly Gly Tyr Asp Gly Tyr Arg Pro Ser Phe Ser Asn Thr Pro Asn				
580	585	590	595	
agt ggt tat aca cag tct cag ttc agt gct ccc cgg gat tac tct ggc				2418
Ser Gly Tyr Thr Gln Ser Gln Phe Ser Ala Pro Arg Asp Tyr Ser Gly				
596	601	606	611	
tat caa cgg gat gga tat cag cag aat ttc aag cga ggc tct ggg cag				2466
Tyr Gln Arg Asp Gly Tyr Gln Gln Asn Phe Lys Arg Gly Ser Gly Gln				
612	617	622	627	
agt gga cca cgg gga gcc cca cga ggt cgt gga ggg ccc cca aga ccc				2514
Ser Gly Pro Arg Gly Ala Pro Arg Gly Arg Gly Gly Pro Pro Arg Pro				
628	633	638	643	
aac aga ggg atg ccg caa atg aac act cag caa gtg aat taa tctgatt				2563
Asn Arg Gly Met Pro Gln Met Asn Thr Gln Gln Val Asn *				
644	649	654		
cacaggatta tgtttaatcg ccaaaaacac actggccagt gtaccataat atgttaccag				2623
aagagttatt atctatttgt tctccctttc aggaaactta ttgtaaaggg actgttttca				2683
tcccataaag acaggactac aattgtcagc tttctattac ctggatatgg aaggaaaacta				2743
tttttactct gcatgttctg tctaagcgt catcttgagc cttgcacatg atactcagat				2803
tcctcaccct tgcttaggag taaaacaata tactttacag ggtgataata atctccatag				2863
ttatttgaag tggcttgaaa aaggcaagat tgacttttat gacattggat aaaatctaca				2923
aatcagccct cgagttattc aatgataact gacaaactaa attatttccc tagaaaggaa				2983
gatgaaagga gtggagtgtg gtttggcaga acaactgcat ttcacagctt ttccagttaa				3043

attggagcac tgaacgttca gatgcatacc aaattatgca tgggtcctaa tcacacatat	3103
aaggctggct accagctttg acacagcact gttcatctgg ccaaacaact gtggttaaaa	3163
acacatgtaa aatgcttttt aacagctgat actgtataag acaaagccaa gatgcaaaat	3223
taggctttga ttggcacttt ttgaaaaata tgcaacaaat atgggatgta atccggatgg	3283
ccgcttctgt acttaatgtg aaatatattag ataccttttt gaacacttaa cagtttcttt	3343
gagacaatga cttttgtaag gatttggtact atctatcatt ccttatgaca tgtacattgt	3403
ctgtcactaa tccttggatt ttgctgtatt gtcacctaaa ttggtacagg tactgatgaa	3463
aatctctagt ggataatcat aacactctcg gtcacatggt tttccttcag cttgaaagct	3523
tttttttaaa aggaaaagat accaaatgcc tgctgctacc acccttttca attgctatct	3583
tttgaaaggc accagtatgt gttttagatt gatttccctg tttcagggaa atcacggaca	3643
gtagtttcag ttctgatggg ataagcaaaa caaataaaac gtttataaaa gttgtatctt	3703
gaaacactgg tgttcaacag ctagcagctt atgtgattca ccccatgcc a cgttagtgtc	3763
acaaatttta tggtttatct ccagcaacat ttctctagta cttgcactta ttatcttttg	3823
tctaatttaa ccttaactga attctccgtt tctcctggag gcatttatat tcagtataa	3883
ttccttccct tagatgcata gggagagtct ctaaatttga tggaaatgga cacttgagta	3943
gtgacttagc cttatgtact ctgttggaa ttgtgctagc agtttgagca ctagttctgt	4003
gtgcctatga agttaatgct gcttattgtc tcattctgac ttcattggaga attaatccca	4063
cctttaagca aaggctacta agttaatggg attttctgtg cagaaattaa attttatttt	4123
cagcatttag ccaggaatt cttccagtag gtgctcagct atttaaaaac aaaactattc	4183
tcaaacattc atcattagac aactggagtt tttgctgggt ttgtaacct ccaaaatgga	4243
taggctgttg aacattccac attcaaaagt tttgtagggg ggtgggaaat gggggatctt	4303
caatgtttat tttaaaataa aataaataag ttcttgactt ttctcatggg tggttgttgg	4363
tacatcatat tggaagggt aaccctgtta ctttggcaaa tgagtatttt ttgctagca	4423
cctccocttg cgtgctttta atgacatctg cctgggatgt accacaacca tatgttacct	4483
gtatcttagg ggaatggata aaatatattgt ggtttactgg gtaatcccta gatgatgtat	4543
gcttgcagtc ctatataaaa ctaaatttgc taataaaaaa aaa	4586

<211> 2682
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (25)..(2286)

<400> 531

ccgaccagtt tgtgtgacat ttgt	atg tgc agt atc tct gta ttt gaa gac	51
	Met Cys Ser Ile Ser Val Phe Glu Asp	
	1 5	
cct gtg gat atg ccc tgt gga cat gac ttt tgt aga gga tgt tgg gag	99	
Pro Val Asp Met Pro Cys Gly His Asp Phe Cys Arg Gly Cys Trp Glu		
10 15 20 25		
tcg ttt ttg aat ctg aaa att caa gaa ggg gaa gct cac aac att ttt	147	
Ser Phe Leu Asn Leu Lys Ile Gln Glu Gly Glu Ala His Asn Ile Phe		
26 31 36 41		
tgc cct gca tat gat tgc ttc caa ctt gta cct ggg gat atc ata aaa	195	
Cys Pro Ala Tyr Asp Cys Phe Gln Leu Val Pro Gly Asp Ile Ile Lys		
42 47 52 57		
agt gta gtt tca aag gag atg gac aaa cga tac cta cag ttt gat att	243	
Ser Val Val Ser Lys Glu Met Asp Lys Arg Tyr Leu Gln Phe Asp Ile		
58 63 68 73		
aag gcc ttt gtt gaa aat aat cct gcc att aaa tgg tgt cct act cca	291	
Lys Ala Phe Val Glu Asn Asn Pro Ala Ile Lys Trp Cys Pro Thr Pro		
74 79 84 89		
ggc tgt gac aga gca gta aga cta acg aaa caa ggg tca aat aca tct	339	
Gly Cys Asp Arg Ala Val Arg Leu Thr Lys Gln Gly Ser Asn Thr Ser		
90 95 100 105		
gga tct gat aca ctc agc ttc cca ttg ctg aga gct cct gct gtt gat	387	
Gly Ser Asp Thr Leu Ser Phe Pro Leu Leu Arg Ala Pro Ala Val Asp		
106 111 116 121		
tgt gga aaa gga cac ctc ttc tgc tgg gag tgc ctt ggt gaa gca cat	435	
Cys Gly Lys Gly His Leu Phe Cys Trp Glu Cys Leu Gly Glu Ala His		
122 127 132 137		
gag cct tgt gac tgc caa aca tgg aag aat tgg ctg caa aaa ata acc	483	
Glu Pro Cys Asp Cys Gln Thr Trp Lys Asn Trp Leu Gln Lys Ile Thr		
138 143 148 153		
gaa atg aaa cca gaa gaa ctt gtg gga gtt agt gaa gcc tac gag gat	531	
Glu Met Lys Pro Glu Glu Leu Val Gly Val Ser Glu Ala Tyr Glu Asp		
154 159 164 169		
gcc gcc aat tgt ctc tgg tta tta act aac tcc aag cct tgt gcc aac	579	
Ala Ala Asn Cys Leu Trp Leu Leu Thr Asn Ser Lys Pro Cys Ala Asn		
170 175 180 185		

tgt aag tct cca ata cag aag aat gaa ggc tgc aat cac atg cag tgt	627
Cys Lys Ser Pro Ile Gln Lys Asn Glu Gly Cys Asn His Met Gln Cys	
186 191 196 201	
gct aag tgc aag tat gac ttt tgc tgg att tgc ctt gaa gag tgg aaa	675
Ala Lys Cys Lys Tyr Asp Phe Cys Trp Ile Cys Leu Glu Glu Trp Lys	
202 207 212 217	
aaa cat agt tgc tcc act gga ggt tat tac aga tgt act cgc tat gaa	723
Lys His Ser Ser Ser Thr Gly Gly Tyr Tyr Arg Cys Thr Arg Tyr Glu	
218 223 228 233	
gtc att caa cac gtg gag gag caa tcc aag gaa atg act gtg gag gct	771
Val Ile Gln His Val Glu Glu Gln Ser Lys Glu Met Thr Val Glu Ala	
234 239 244 249	
gag aaa aaa cac aaa cga ttt cag gaa ctt gac aga ttt atg cac tat	819
Glu Lys Lys His Lys Arg Phe Gln Glu Leu Asp Arg Phe Met His Tyr	
250 255 260 265	
tat aca aga ttt aaa aac cat gag cat agt tat cag cta gaa caa cgc	867
Tyr Thr Arg Phe Lys Asn His Glu His Ser Tyr Gln Leu Glu Gln Arg	
266 271 276 281	
ctt ctt aaa aca gcc aaa gaa aag atg gag caa ttg agc aga gct ctc	915
Leu Leu Lys Thr Ala Lys Glu Lys Met Glu Gln Leu Ser Arg Ala Leu	
282 287 292 297	
aaa gaa act gaa gga ggc tgt cca gat acc act ttc att gaa gat gca	963
Lys Glu Thr Glu Gly Gly Cys Pro Asp Thr Thr Phe Ile Glu Asp Ala	
298 303 308 313	
gtt cat gtg ctc tta aaa act cgg cgc att ctc aag tgt tct tat cca	1011
Val His Val Leu Leu Lys Thr Arg Arg Ile Leu Lys Cys Ser Tyr Pro	
314 319 324 329	
tat gga ttt ttc ttg gaa cct aaa agc aca aag aaa gaa att ttt gaa	1059
Tyr Gly Phe Phe Leu Glu Pro Lys Ser Thr Lys Lys Glu Ile Phe Glu	
330 335 340 345	
cta atg caa aca gac cta gaa atg gtc act gaa gac ctt gcc cag aaa	1107
Leu Met Gln Thr Asp Leu Glu Met Val Thr Glu Asp Leu Ala Gln Lys	
346 351 356 361	
gtc aat agg cct tac ctt cgc aca ccc cgc cac aag atc atc aaa gca	1155
Val Asn Arg Pro Tyr Leu Arg Thr Pro Arg His Lys Ile Ile Lys Ala	
362 367 372 377	
gca tgc ctt gta cag cag aag agg caa gaa ttc ctg gca tct gtg gct	1203
Ala Cys Leu Val Gln Gln Lys Arg Gln Glu Phe Leu Ala Ser Val Ala	
378 383 388 393	
cgg gga gta gct cct gca gac tca cca gaa gct cca agg cgc agc ttt	1251
Arg Gly Val Ala Pro Ala Asp Ser Pro Glu Ala Pro Arg Arg Ser Phe	
394 399 404 409	
gct ggt gga aca tgg gat tgg gaa tat tta gga ttt gca tca cca gag	1299

Ala Gly Gly Thr Trp Asp Trp Glu Tyr Leu Gly Phe Ala Ser Pro Glu	
410 415 420 425	
gaa tat gct gaa ttt cag tat cgg agg agg cac aga caa cgt cgt cga	1347
Glu Tyr Ala Glu Phe Gln Tyr Arg Arg Arg His Arg Gln Arg Arg Arg	
426 431 436 441	
gga gat gtt cac agt cta ctc agt aat cct cca gac cct gat gag cca	1395
Gly Asp Val His Ser Leu Leu Ser Asn Pro Pro Asp Pro Asp Glu Pro	
442 447 452 457	
agt gaa agc act tta gat att cca gaa ggc ggc agc agc agc cgc agg	1443
Ser Glu Ser Thr Leu Asp Ile Pro Glu Gly Gly Ser Ser Ser Arg Arg	
458 463 468 473	
cct ggc aca tcc gtg gta agt tct gca tct atg agt gtg ctg cac agc	1491
Pro Gly Thr Ser Val Val Ser Ser Ala Ser Met Ser Val Leu His Ser	
474 479 484 489	
tct tcc ctg cgt gac tac acc cct gcc agt cgc tct gaa aac cag gac	1539
Ser Ser Leu Arg Asp Tyr Thr Pro Ala Ser Arg Ser Glu Asn Gln Asp	
490 495 500 505	
tct ctt cag gct ctg agt tcc ttg gat gaa gac gat ccc aat ata ctt	1587
Ser Leu Gln Ala Leu Ser Ser Leu Asp Glu Asp Asp Pro Asn Ile Leu	
506 511 516 521	
ctt gca ata cag tta tca ctg caa gag tct ggg ctg gcc ctc gat gaa	1635
Leu Ala Ile Gln Leu Ser Leu Gln Glu Ser Gly Leu Ala Leu Asp Glu	
522 527 532 537	
gaa act aga gac ttc ctc agt aat gaa gca tcc tta ggt gcg ata ggc	1683
Glu Thr Arg Asp Phe Leu Ser Asn Glu Ala Ser Leu Gly Ala Ile Gly	
538 543 548 553	
act tct tta cct tcc agg ctg gac tct gtc ccc aga aat aca gat agc	1731
Thr Ser Leu Pro Ser Arg Leu Asp Ser Val Pro Arg Asn Thr Asp Ser	
554 559 564 569	
cct cgg gct gca ttg agc agc tct gag ctt ttg gaa ctt ggt gac agc	1779
Pro Arg Ala Ala Leu Ser Ser Ser Glu Leu Leu Glu Leu Gly Asp Ser	
570 575 580 585	
ctc atg aga cta gga gca gag aat gac cca ttt tca act gac acc ctg	1827
Leu Met Arg Leu Gly Ala Glu Asn Asp Pro Phe Ser Thr Asp Thr Leu	
586 591 596 601	
agc tca cac cct ctc agt gag gca aga agt gat ttc tgt ccc tca tct	1875
Ser Ser His Pro Leu Ser Glu Ala Arg Ser Asp Phe Cys Pro Ser Ser	
602 607 612 617	
agt gat cct gac tca gct ggc cag gac ccc aac atc aat gac aat ctt	1923
Ser Asp Pro Asp Ser Ala Gly Gln Asp Pro Asn Ile Asn Asp Asn Leu	
618 623 628 633	
ctc ggc aac atc atg gct tgg ttt cat gac atg aac cct cag agt att	1971
Leu Gly Asn Ile Met Ala Trp Phe His Asp Met Asn Pro Gln Ser Ile	

634	639	644	649	
gcc ctg att cct cca gca act aca gaa atc agt gca gat tcc cag ctc				2019
Ala Leu Ile Pro Pro Ala Thr Thr Glu Ile Ser Ala Asp Ser Gln Leu				
650	655	660	665	
ccc tgt atc aaa gat ggg tca gaa ggt gtg aag gat gtg gaa atg gtg				2067
Pro Cys Ile Lys Asp Gly Ser Glu Gly Val Lys Asp Val Glu Met Val				
666	671	676	681	
ctg cca gaa gat tca atg ttt gaa gat gcc agt gtc agt gaa ggt aga				2115
Leu Pro Glu Asp Ser Met Phe Glu Asp Ala Ser Val Ser Glu Gly Arg				
682	687	692	697	
gga acc cag ata gaa gaa aat cct ttg gaa gaa aat att ctg gcg ggg				2163
Gly Thr Gln Ile Glu Glu Asn Pro Leu Glu Glu Asn Ile Leu Ala Gly				
698	703	708	713	
gaa gca gca tct caa gct ggt gac agt ggt aac gag gca gcc aac aga				2211
Glu Ala Ala Ser Gln Ala Gly Asp Ser Gly Asn Glu Ala Ala Asn Arg				
714	719	724	729	
gga gat ggt tca gat gtt tca agt caa aca cct caa acc tca agt gac				2259
Gly Asp Gly Ser Asp Val Ser Ser Gln Thr Pro Gln Thr Ser Ser Asp				
730	735	740	745	
tgg ctt gaa caa gta cat tta gtg tga actgc acacatctgg gctctaaatg				2311
Trp Leu Glu Gln Val His Leu Val *				
746	751			
aattacaggt acagatggta tgctaggtgg agtatgcttg atagagactt tgattcactt				2371
aattccaact cagtataaa ccaactgacat taggggttgaa tacagagaag ttcccttgaa				2431
tggtagcttc atttttttatt ttaaccttac agggaatttc ctttgtactt aattgaatag				2491
cttttccct ttttctgac aaaaagaaga gcaagagaaa gagaaacaaa aatgaaataa				2551
ataagttgta ttccacactc taagaaaatg cagtcctcta tttagcctag gcttgacaat				2611
acttaaattg aacatttaaa ctaaaggctt actcctaata ctttgggtgg ctttccttta				2671
aaaaaaaaa a				2682

<210> 532
 <211> 1583
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (374) .. (1558)

 <400> 532

Lys Glu Leu Asp Glu Tyr Met His Gly Gly Lys Lys Met Gly Ser Lys	
173 178 183 188	
gaa gag gaa aat ggg caa ggt cat ctc aaa agg aaa cga cct gtc aaa	985
Glu Glu Glu Asn Gly Gln Gly His Leu Lys Arg Lys Arg Pro Val Lys	
189 194 199 204	
gac agg cta ggg aac aga cca gaa atg aac tat aaa ggt cga tac gag	1033
Asp Arg Leu Gly Asn Arg Pro Glu Met Asn Tyr Lys Gly Arg Tyr Glu	
205 210 215 220	
atc aca gcg gaa gat tct caa gag aaa gtg gct gat gaa att tca ttc	1081
Ile Thr Ala Glu Asp Ser Gln Glu Lys Val Ala Asp Glu Ile Ser Phe	
221 226 231 236	
agg tta cag gaa cca aag aaa gac ctg ata gcc cga gta gtg agg att	1129
Arg Leu Gln Glu Pro Lys Lys Asp Leu Ile Ala Arg Val Val Arg Ile	
237 242 247 252	
att ggt aac aaa aag gca att gaa ctt ctg atg gaa acc gct gaa gtt	1177
Ile Gly Asn Lys Lys Ala Ile Glu Leu Leu Met Glu Thr Ala Glu Val	
253 258 263 268	
gaa caa aat ggt ggt ctc ttt ata atg aat ggt agt cga aga aga aca	1225
Glu Gln Asn Gly Gly Leu Phe Ile Met Asn Gly Ser Arg Arg Arg Thr	
269 274 279 284	
cca ggt gga gtt ttt ctg aat ctc ttg aaa aac act cct agt atc agc	1273
Pro Gly Gly Val Phe Leu Asn Leu Leu Lys Asn Thr Pro Ser Ile Ser	
285 290 295 300	
gag gaa caa att aag gac att ttc tac att gaa aac caa aag gaa tat	1321
Glu Glu Gln Ile Lys Asp Ile Phe Tyr Ile Glu Asn Gln Lys Glu Tyr	
301 306 311 316	
gaa aat aaa aaa gct gct agg aag agg aga aca caa gtg ttg ggg aaa	1369
Glu Asn Lys Lys Ala Ala Arg Lys Arg Arg Thr Gln Val Leu Gly Lys	
317 322 327 332	
aag atg aaa caa gct att aaa agt cta aat ttt caa gaa gat gat gat	1417
Lys Met Lys Lys Gln Ala Ile Lys Ser Leu Asn Phe Gln Glu Asp Asp Asp	
333 338 343 348	
aca tca cga gaa act ttt gca agt gac acg aat gag gcc ttg gcc tct	1465
Thr Ser Arg Glu Thr Phe Ala Ser Asp Thr Asn Glu Ala Leu Ala Ser	
349 354 359 364	
ctt gat gag tca cag gaa gga cat gca gaa gcc aag ttg gag gca gag	1513
Leu Asp Glu Ser Gln Glu Gly His Ala Glu Ala Lys Leu Glu Ala Glu	
365 370 375 380	
gaa gcc att gaa gtt gat cat tct cat gat ttg gac atc ttt taa gta	1561
Glu Ala Ile Glu Val Asp His Ser His Asp Leu Asp Ile Phe *	
381 386 391	
cattttcaac agtttgagga ct	1583

<210> 533
 <211> 2734
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (116)..(1477)

<220>
 <221> misc_feature
 <222> (1)...(2734)
 <223> n = a,t,c or g

<400> 533
 aaggatcctt aattaaatta atcccccccc ctccagatag taaataatct cggaaggcg 60
 agaaagaagc tgtctccatc ttgtctgtat ccgctgctct tgtgacgttg tggag atg 118
 Met
 1
 ggg agc gtc ctg ggg ctg tgc tcc atg gcg agc tgg ata cca tgt ttg 166
 Gly Ser Val Leu Gly Leu Cys Ser Met Ala Ser Trp Ile Pro Cys Leu
 2 7 12 17
 tgt gga agt gcc ccg tgt ttg cta tgc cga tgc tgt cct agt gga aac 214
 Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys Cys Pro Ser Gly Asn
 18 23 28 33
 aac tcc act gta act aga ttg atc tat gca ctt ttc ttg ctt gtt gga 262
 Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu Phe Leu Leu Val Gly
 34 39 44 49
 gta tgt gta gct tgt gta atg ttg ata cca gga atg gaa gaa caa ctg 310
 Val Cys Val Ala Cys Val Met Leu Ile Pro Gly Met Glu Glu Gln Leu
 50 55 60 65
 aat aag att cct gga ttt tgt gag aat gag aaa ggt gtt gtc cct tgt 358
 Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu Lys Gly Val Val Pro Cys
 66 71 76 81
 aac att ttg gtt ggc tat aaa gct gta tat cgt ttg tgc ttt ggt ttg 406
 Asn Ile Leu Val Gly Tyr Lys Ala Val Tyr Arg Leu Cys Phe Gly Leu
 82 87 92 97
 gct atg ttc tat ctt ctt ctc tct tta cta atg atc aaa gtg aag agt 454
 Ala Met Phe Tyr Leu Leu Leu Ser Leu Leu Met Ile Lys Val Lys Ser
 98 103 108 113
 agc agt gat cgt aga gct gca gtg cac aat gga ttt tgg ttc ttt aaa 502
 Ser Ser Asp Pro Arg Ala Ala Val His Asn Gly Phe Trp Phe Phe Lys
 114 119 124 129
 ttt gct gca gca att gca att att att ggg gca ttc ttc att cca gaa 550

Phe	Ala	Ala	Ala	Ile	Ala	Ile	Ile	Ile	Gly	Ala	Phe	Phe	Ile	Pro	Glu	
130					135					140					145	
gga	act	ttt	aca	act	gtg	tgg	ttt	tat	gta	ggc	atg	gca	ggg	gcc	ttt	598
Gly	Thr	Phe	Thr	Thr	Val	Trp	Phe	Tyr	Val	Gly	Met	Ala	Gly	Ala	Phe	
146					151					156					161	
tgt	ttc	atc	ctc	ata	caa	cta	gtc	tta	ctt	att	gat	ttt	gca	cat	tca	646
Cys	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	Asp	Phe	Ala	His	Ser	
162					167					172					177	
tgg	aat	gaa	tcg	tgg	gtt	gaa	aaa	atg	gaa	gaa	ggg	aac	tcg	aga	tgt	694
Trp	Asn	Glu	Ser	Trp	Val	Glu	Lys	Met	Glu	Glu	Gly	Asn	Ser	Arg	Cys	
178					183					188					193	
tgg	tat	gca	gcc	ttg	tta	tca	gct	aca	gct	ctg	aat	tat	ctg	ctg	tct	742
Trp	Tyr	Ala	Ala	Leu	Leu	Ser	Ala	Thr	Ala	Leu	Asn	Tyr	Leu	Leu	Ser	
194					199					204					209	
tta	gtt	gct	atc	gtc	ctg	ttc	ttt	gtc	tac	tac	act	cat	cca	gcc	agt	790
Leu	Val	Ala	Ile	Val	Leu	Phe	Phe	Val	Tyr	Tyr	Thr	His	Pro	Ala	Ser	
210					215					220					225	
tgt	tca	gaa	aac	aag	gcg	ttc	atc	agt	gtc	aac	atg	ctc	ctc	tgc	gtt	838
Cys	Ser	Glu	Asn	Lys	Ala	Phe	Ile	Ser	Val	Asn	Met	Leu	Leu	Cys	Val	
226					231					236					241	
ggg	gct	tct	gta	atg	tct	ata	ctg	cca	aaa	atc	caa	gaa	tca	caa	cca	886
Gly	Ala	Ser	Val	Met	Ser	Ile	Leu	Pro	Lys	Ile	Gln	Glu	Ser	Gln	Pro	
242					247					252					257	
aga	tct	ggg	ttg	tta	cag	tct	tca	gta	att	aca	gtc	tac	aca	atg	tat	934
Arg	Ser	Gly	Leu	Leu	Gln	Ser	Ser	Val	Ile	Thr	Val	Tyr	Thr	Met	Tyr	
258					263					268					273	
ttg	aca	tgg	tca	gct	atg	acc	aat	gaa	cca	gaa	aca	aat	tgc	aac	cca	982
Leu	Thr	Trp	Ser	Ala	Met	Thr	Asn	Glu	Pro	Glu	Thr	Asn	Cys	Asn	Pro	
274					279					284					289	
agt	cta	cta	agc	ata	att	ggc	tac	aat	aca	aca	agc	act	gtc	cca	aag	1030
Ser	Leu	Leu	Ser	Ile	Ile	Gly	Tyr	Asn	Thr	Thr	Ser	Thr	Val	Pro	Lys	
290					295					300					305	
gaa	ggg	cag	tca	gtc	cag	tgg	tgg	cat	gct	caa	gga	att	ata	gga	cta	1078
Glu	Gly	Gln	Ser	Val	Gln	Trp	Trp	His	Ala	Gln	Gly	Ile	Ile	Gly	Leu	
306					311					316					321	
att	ctc	ttt	ttg	ttg	tgt	gta	ttt	tat	tcc	agc	atc	cgt	act	tca	aac	1126
Ile	Leu	Phe	Leu	Leu	Cys	Val	Phe	Tyr	Ser	Ser	Ile	Arg	Thr	Ser	Asn	
322					327					332					337	
aat	agt	cag	gtt	aat	aaa	ctg	act	cta	aca	agt	gat	gaa	tct	aca	tta	1174
Asn	Ser	Gln	Val	Asn	Lys	Leu	Thr	Leu	Thr	Ser	Asp	Glu	Ser	Thr	Leu	
338					343					348					353	
ata	gaa	gat	ggg	gga	gct	aga	agt	gat	gga	tca	ctg	gag	gat	ggg	gac	1222
Ile	Glu	Asp	Gly	Gly	Ala	Arg	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Gly	Asp	

354	359	364	369	
gat gtt cac cga gct gta gat aat gaa agg gat ggt gtc act tac agt				1270
Asp Val His Arg Ala Val Asp Asn Glu Arg Asp Gly Val Thr Tyr Ser				
370	375	380	385	
tat tcc ttc ttt cac ttc atg ctt ttc ctg gct tca ctt tat atc atg				1318
Tyr Ser Phe Phe His Phe Met Leu Phe Leu Ala Ser Leu Tyr Ile Met				
386	391	396	401	
atg acc ctt acc aac tgg tac agg tat gaa ccc tct cgt gag atg aaa				1366
Met Thr Leu Thr Asn Trp Tyr Arg Tyr Glu Pro Ser Arg Glu Met Lys				
402	407	412	417	
agt cag tgg aca gct gtc tgg gtg aaa atc tct tcc agt tgg att ggc				1414
Ser Gln Trp Thr Ala Val Trp Val Lys Ile Ser Ser Ser Trp Ile Gly				
418	423	428	433	
atc gtg ctg tat gtt tgg aca ctc gtg gca cca ctt gtt ctt aca aat				1462
Ile Val Leu Tyr Val Trp Thr Leu Val Ala Pro Leu Val Leu Thr Asn				
434	439	444	449	
cgt gat ttt gac tga gtgagacttc tagcatgaaa gtcccacttt gattattgct				1517
Arg Asp Phe Asp *				
450				
tatttgaaaa cagtattccc aacttttgta aagttgtgta tgtttttgct tcccatgtaa				1577
cttctccagt gttctggcat gaattagatt ttactgcttg tcattttggt attttcttac				1637
caagtgcatt gatatgtgaa gtagaatgaa ttgcagagga aagttttatg aatatggtga				1697
tgagtttagta aaagtggcca ctattgggct tattctctgc tctatagttg tgaaatgaag				1757
agtgaaaaca aatttgtttg actatttttaa aattatatta gaccttaagc tgttttagca				1817
agcattaaag caaatgtatg gctgcctttt gaaatatttg atgtgttgcc tggcaggata				1877
ctgcaaagaa catggtttat tttaaaattt ataaacaagt cacttaaagc ccagttgtct				1937
gaaaaatctt ataaggtttt acccttgata cggaatttac acaggtaggg agtgtttagt				1997
ggacaatagt gtaggttatg gatggaggtg tcggtactaa attgaataac gagtaaataa				2057
tcttacttgg gtagagatgg cctttgccaa caaagtgaac tgttttggtt gttttaaact				2117
catgaagtat gggttcagtg gaaatgtttg gaactctgaa ggatttagac aaggttttga				2177
aaaggataat catgggtagg aaggaagtgt ttgaaagtca ctttgaaagt tagttttggg				2237
ccagcacggt agctcaccct tgtaatocca gcactttggg aggctgaggt gggtagatta				2297
cttgagccca ggaattcaag accagcctgg gcaacatggt gaaaccctgt ttcataaaaa				2357
aataatctgg gctttgtagc atatgcctgt ggtcccagct actgaggagg ctgaggtggg				2417
aggattgctt gagcccagga ggcagaggtt gcagtgagcc aaggtcacgt cactgcactc				2477

tagcctgggc aacagagtaa gacaaaaaat atatatatat tgaaaatcaa aggaggcaaa	2537
attttgacag ggaaggaagt aactgcaaaa cactaggctt tagtaggtac ttatataaaa	2597
tctagtccag ttctcttcat ttaaaaaaat gaagacacga agtacagact taaatagctc	2657
agatangcaa ttaggaaatt tcaagttggc caataatagc attctctctg acatttaaaa	2717
ataatttcta ttcaaaa	2734

<210> 534
 <211> 3024
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1554)

<400> 534

atg gcg gag gct gca gct ccc gga aca aca gtc aca aca tcg gga gca	48
Met Ala Glu Ala Ala Pro Gly Thr Thr Val Thr Thr Ser Gly Ala	
1 5 10	
gga gca gca gcg gcg gag gcg gcg gag acg gcg gaa gca gtc tcc ccg	96
Gly Ala Ala Ala Glu Ala Ala Glu Thr Ala Glu Ala Val Ser Pro	
17 22 27 32	
act ccg atc ccc aca gtc acc gcc ccg tcc ccg agg gcg ggc gga ggg	144
Thr Pro Ile Pro Thr Val Thr Ala Pro Ser Pro Arg Ala Gly Gly Gly	
33 38 43 48	
gtc ggc ggc agc gac ggc agc gac ggt agt ggc ggc agg ggc gac agt	192
Val Gly Gly Ser Asp Gly Ser Asp Gly Ser Gly Gly Arg Gly Asp Ser	
49 54 59 64	
ggc gcg tat gac ggc agc ggt gcg tgc ggc ggc agc gac gcg tgc gat	240
Gly Ala Tyr Asp Gly Ser Gly Ala Cys Gly Gly Ser Asp Ala Cys Asp	
65 70 75 80	
ggc agc ggc gac agc agc ggc gac agc tgg act aaa cag gtc act tgt	288
Gly Ser Gly Asp Ser Ser Gly Asp Ser Trp Thr Lys Gln Val Thr Cys	
81 86 91 96	
aga tat ttt aag tat ggg att tgt aag gaa gga gat aac tgt cgc tac	336
Arg Tyr Phe Lys Tyr Gly Ile Cys Lys Glu Gly Asp Asn Cys Arg Tyr	
97 102 107 112	
tcg cat gac ctc tct gac cgt ctg tgt ggt gta gtg tgc aag tat ttt	384
Ser His Asp Leu Ser Asp Arg Leu Cys Gly Val Val Cys Lys Tyr Phe	
113 118 123 128	
cag cga ggg tac tgt att tat gga gac cgc tgc aga tgt gaa cat agc	432

Gln	Arg	Gly	Tyr	Cys	Ile	Tyr	Gly	Asp	Arg	Cys	Arg	Cys	Glu	His	Ser		
129					134					139					144		
aag	cca	ttg	aaa	cag	gaa	gaa	gca	act	gct	aca	gag	cta	act	aca	aag	480	
Lys	Pro	Leu	Lys	Gln	Glu	Glu	Ala	Thr	Ala	Thr	Glu	Leu	Thr	Thr	Lys		
145					150					155					160		
tca	tcc	ctt	gct	gct	tcc	tca	agt	ctc	tca	tcg	ata	gtt	gga	cca	ctt	528	
Ser	Ser	Leu	Ala	Ala	Ser	Ser	Ser	Leu	Ser	Ser	Ile	Val	Gly	Pro	Leu		
161					166					171					176		
gtt	gaa	atg	aat	aca	ggc	gaa	gct	gag	tca	aga	aat	tca	aac	ttt	gca	576	
Val	Glu	Met	Asn	Thr	Gly	Glu	Ala	Glu	Ser	Arg	Asn	Ser	Asn	Phe	Ala		
177					182					187					192		
act	gta	gta	gca	ggc	tca	gag	gac	tgg	gtg	aat	gct	att	gag	ttt	gtt	624	
Thr	Val	Val	Ala	Gly	Ser	Glu	Asp	Trp	Val	Asn	Ala	Ile	Glu	Phe	Val		
193					198					203					208		
cct	ggg	caa	ccc	tac	tgt	ggc	cgt	act	gcg	cct	tcc	tgc	act	gaa	gca	672	
Pro	Gly	Gln	Pro	Tyr	Cys	Gly	Arg	Thr	Ala	Pro	Ser	Cys	Thr	Glu	Ala		
209					214					219					224		
ccc	ctg	cag	ggc	tca	gtg	acc	aag	gaa	gaa	tca	gag	aaa	gag	caa	acc	720	
Pro	Leu	Gln	Gly	Ser	Val	Thr	Lys	Glu	Glu	Ser	Glu	Lys	Glu	Gln	Thr		
225					230					235					240		
gcc	gtg	gag	aca	aag	aag	cag	ctg	tgc	ccc	tat	gct	gca	gtg	gga	gag	768	
Ala	Val	Glu	Thr	Lys	Lys	Gln	Leu	Cys	Pro	Tyr	Ala	Ala	Val	Gly	Glu		
241					246					251					256		
tgc	cga	tac	ggg	gag	aac	tgt	gtg	tat	ctc	cac	gga	gat	tct	tgt	gac	816	
Cys	Arg	Tyr	Gly	Glu	Asn	Cys	Val	Tyr	Leu	His	Gly	Asp	Ser	Cys	Asp		
257					262					267					272		
atg	tgt	ggg	ctg	cag	gtc	ctg	cat	cca	atg	gat	gct	gcc	cag	aga	tcg	864	
Met	Cys	Gly	Leu	Gln	Val	Leu	His	Pro	Met	Asp	Ala	Ala	Gln	Arg	Ser		
273					278					283					288		
cag	cat	atc	aaa	tcg	tgc	att	gag	gcc	cat	gag	aag	gac	atg	gag	ctc	912	
Gln	His	Ile	Lys	Ser	Cys	Ile	Glu	Ala	His	Glu	Lys	Asp	Met	Glu	Leu		
289					294					299					304		
tca	ttt	gcc	gtg	cag	cgc	agc	aag	gac	atg	gtg	tgt	ggg	atc	tgc	atg	960	
Ser	Phe	Ala	Val	Gln	Arg	Ser	Lys	Asp	Met	Val	Cys	Gly	Ile	Cys	Met		
305					310					315					320		
gag	gtg	gtc	tat	gag	aaa	gcc	aac	ccc	agt	gag	cgc	cgc	ttc	ggg	atc	1008	
Glu	Val	Val	Tyr	Glu	Lys	Ala	Asn	Pro	Ser	Glu	Arg	Arg	Phe	Gly	Ile		
321					326					331					336		
ctc	tcc	aac	tgc	aac	cac	acc	tac	tgt	ctc	aag	tgc	att	cgc	aag	tgg	1056	
Leu	Ser	Asn	Cys	Asn	His	Thr	Tyr	Cys	Leu	Lys	Cys	Ile	Arg	Lys	Trp		
337					342					347					352		
agg	agt	gct	aag	caa	ttt	gag	agc	aag	atc	ata	aag	tcc	tgc	cca	gaa	1104	
Arg	Ser	Ala	Lys	Gln	Phe	Glu	Ser	Lys	Ile	Ile	Lys	Ser	Cys	Pro	Glu		

353	358	363	368	
tgc cgg atc aca tct	aac ttt gtc att cca	agt gag tac tgg gtg gag		1152
Cys Arg Ile Thr Ser	Asn Phe Val Ile Pro	Ser Glu Tyr Trp Val Glu		
369	374	379	384	
gag aaa gaa gag aag	cag aaa ctc att ctg	aaa tac aag gag gca atg		1200
Glu Lys Glu Glu Lys	Gln Lys Leu Ile Leu	Lys Tyr Lys Glu Ala Met		
385	390	395	400	
agc aac aag gcg tgc	agg tat ttt gat gaa	gga cgt ggg agc tgc cca		1248
Ser Asn Lys Ala Cys	Arg Tyr Phe Asp Glu	Gly Arg Gly Ser Cys Pro		
401	406	411	416	
ttt gga ggg aac tgt	ttt tac aag cat gcg	tac cct gat ggc cgt aga		1296
Phe Gly Gly Asn Cys	Phe Tyr Lys His Ala	Tyr Pro Asp Gly Arg Arg		
417	422	427	432	
gag gag cca cag aga	cag aaa gtg gga aca	tca agc aga tac cgg gcc		1344
Glu Glu Pro Gln Arg	Gln Lys Val Gly Thr	Ser Ser Arg Tyr Arg Ala		
433	438	443	448	
caa cga agg aac cac	ttc tgg gaa ctc att	gag gaa aga gag aac agc		1392
Gln Arg Arg Asn His	Phe Trp Glu Leu Ile	Glu Glu Arg Glu Asn Ser		
449	454	459	464	
aac ccc ttt gac aac	gat gaa gaa gag gtt	gtc acc ttt gag ctg ggc		1440
Asn Pro Phe Asp Asn	Asp Glu Glu Glu Val	Val Thr Phe Glu Leu Gly		
465	470	475	480	
gag atg ttg ctt atg	ctt ttg gct gca ggt	ggg gac gac gaa cta aca		1488
Glu Met Leu Leu Met	Leu Leu Ala Ala Gly	Gly Asp Asp Glu Leu Thr		
481	486	491	496	
gac tct gaa gat gag	tgg gac ttg ttt cat	gat gag ctg gaa gat ttt		1536
Asp Ser Glu Asp Glu	Trp Asp Leu Phe His	Asp Glu Leu Glu Asp Phe		
497	502	507	512	
tat gac ttg gat cta	tag caacct tgcgtggcgt	gtgaactggg ctgctgacct		1590
Tyr Asp Leu Asp Leu	*			
513	518			
cagacagcag ctgtcccctg	tgggtgggtgtg gcagtgcctg	tgttctctcc taggcaggcc		1650
tctcaactcc aggtgctgtc	ctaagaattt ttaccaggg	cctgtcttct caaccctca		1710
cctttccctg aggagtgtgt	tgttttccct gttgaaaaaa	gttacaaaaa taaatcttaa		1770
agttagtttt ttgtaacacg	aatttaactg tcagacagtt	agtgtagggtg tgttgcgta		1830
tctgtttttca accagattgc	atztatggac ttttcacaca	ctcattttga ggaccccagg		1890
ttcaaaaagta aaagcagtgg	ccctgctttg ggggtccaaga	ataggagtga tgggtgaagg		1950
gacctaagct ggccaatagc	cctctgcccc agacatggga	tgtggatcct tgaggtttct		2010
ggtgaaatct gcacatctgt	gtttttatat ctgttccta	ccctgtaatc cctaccacgt		2070

gcacttggtc tgtgggtttg gtctcttggt taattgcaca caagtaatac tactgggtaa 2130
ccagaatcag gtgtgaatgt gttgagattt tttactgttt tgcattgatag gaaaattgag 2190
aaagaatacg tataaaagat agagagggcat aacatcaatg cagagttgga agttggctcc 2250
caagggctga catgggtgtga gtgtgtgggt gtgtgataag cttctcatcc ctgcatagat 2310
gcagtattct tagccttagt agaaaaacct ggttttagtgg tttaagcctt gtgtggcaga 2370
tagatcttaa agggcaaagc agtatattgg tagttgtcaa tatagcagtg ctagctctgt 2430
ctatataaat agagaaatgg ggtagccat agagggttaa actacctggg ttatcccata 2490
taataacaca aactgggtct tggatacaca gttgtattta atgttttacg atctagcctt 2550
tccagtacag gcactttctg agaaaccttt gtctcactt gaggcatttt gttgtcgggt 2610
ttttgtgttt gtttttgtgg gtatttgcct cattccaccc ctgagctttc aggtagacag 2670
acgtgattca aaactctgtt ctaagggtgtt tattgtagtg gagtaatggg tttgcagtga 2730
taagtcatac ttttccaccg aaagggaggg cttgggaatc cctgagatta gctaaagtta 2790
agttgttggg agaattcctt gattggaaat tgtacctttg tgttttgttg ctctgtttcc 2850
tgaaaataac tcggggatgc tcctggtttg tccatctact gctttgatcc cttggatccc 2910
acctattctt tcactttaag aaaaaacaaa taattgttgc agaggctctt gtattttgca 2970
gctgcccttt tgtaagaagc acttttccca aataaaacaa ttaaaaaaaaa aaaa 3024

<210> 535
<211> 1411
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (158) .. (1333)

<400> 535
gcgctcagat acgcgacgcg tagcaggcgg ggaccgaacg ggtgcctcag tgccttccc 60
ctccccctgc ctggcctcgc cgtcctctcc ccgcagccgg accggaacta tgtgatcccc 120
gaagttccgg ggcctttgct gtgtgggata aacagta atg gcg gag gct gca act 175
Met Ala Glu Ala Ala Thr
1 1
ccc gga aca aca gcc aca aca tca gga gca gga gcg gca gcg gcg acg 223
Pro Gly Thr Thr Ala Thr Ser Gly Ala Gly Ala Ala Ala Ala Thr
7 12 17 22

gcg gca gca gcc tcc ccc acc ccg atc ccc aca gtc acc gcc ccg tcc	271
Ala Ala Ala Ala Ser Pro Thr Pro Ile Pro Thr Val Thr Ala Pro Ser	
23 28 33 38	
ctg ggg gcg ggc gga ggg ggc ggc ggc agc gac ggc agc ggc ggc ggc	319
Leu Gly Ala Gly Gly Gly Gly Gly Gly Ser Asp Gly Ser Gly Gly Gly	
39 44 49 54	
tgg act aaa cag gtc acc tgc agg tat ttt atg cat ggg gtt tgt aag	367
Trp Thr Lys Gln Val Thr Cys Arg Tyr Phe Met His Gly Val Cys Lys	
55 60 65 70	
gaa gga gac aac tgt cgc tac tcg cat gac ctc tct gac agt ccg tat	415
Glu Gly Asp Asn Cys Arg Tyr Ser His Asp Leu Ser Asp Ser Pro Tyr	
71 76 81 86	
agt gta gtg tgc aag tat ttt cag cga ggg tac tgt att tat gga gac	463
Ser Val Val Cys Lys Tyr Phe Gln Arg Gly Tyr Cys Ile Tyr Gly Asp	
87 92 97 102	
cgc tgc aga tat gaa cat agc aaa cca ttg aaa cag gaa gaa gca act	511
Arg Cys Arg Tyr Glu His Ser Lys Pro Leu Lys Gln Glu Glu Ala Thr	
103 108 113 118	
gct aca gag cta act aca aag tca tcc ctt gct gct tcc tca agt ctc	559
Ala Thr Glu Leu Thr Thr Lys Ser Ser Leu Ala Ala Ser Ser Ser Leu	
119 124 129 134	
tca tcg ata gtt gga cca ctt gtt gaa atg aat aca ggc gaa gct gag	607
Ser Ser Ile Val Gly Pro Leu Val Glu Met Asn Thr Gly Glu Ala Glu	
135 140 145 150	
tca aga aat tca aac ttt gca act gta gga gca ggt tca gag gac tgg	655
Ser Arg Asn Ser Asn Phe Ala Thr Val Gly Ala Gly Ser Glu Asp Trp	
151 156 161 166	
gtg aat gct att gag ttt gtt cct ggg caa ccc tac tgt ggc cgt act	703
Val Asn Ala Ile Glu Phe Val Pro Gly Gln Pro Tyr Cys Gly Arg Thr	
167 172 177 182	
gcg cct tcc tgc act gaa gca ccc ctg cag ggc tca gtg acc aag gaa	751
Ala Pro Ser Cys Thr Glu Ala Pro Leu Gln Gly Ser Val Thr Lys Glu	
183 188 193 198	
gaa tca gag aaa gag caa acc gcc gtg gag aca aag aag cag ctg tgc	799
Glu Ser Glu Lys Glu Gln Thr Ala Val Glu Thr Lys Lys Gln Leu Cys	
199 204 209 214	
ccc tat gct gca gtg gga gag tgc cga tac ggg gag aac tgt gtg tat	847
Pro Tyr Ala Ala Val Gly Glu Cys Arg Tyr Gly Glu Asn Cys Val Tyr	
215 220 225 230	
ctc cac gga gat tct tgt gac atg tgt ggg ctg cag ctc ctg cat cca	895
Leu His Gly Asp Ser Cys Asp Met Cys Gly Leu Gln Leu Leu His Pro	
231 236 241 246	

atg gat gct gcc cag aga tcg cag cat atc aaa tcg tgc att gag gcc	943
Met Asp Ala Ala Gln Arg Ser Gln His Ile Lys Ser Cys Ile Glu Ala	
247 252 257 262	
cat gag aag gac atg gag ctc tca ttt gcc gtg cag cgc agc aag gac	991
His Glu Lys Asp Met Glu Leu Ser Phe Ala Val Gln Arg Ser Lys Asp	
263 268 273 278	
atg gtg tgt ggg atc tgc atg gag gtg gtc tat gag aaa gcc aac ccc	1039
Met Val Cys Gly Ile Cys Met Glu Val Val Tyr Glu Lys Ala Asn Pro	
279 284 289 294	
agt gag cgc cgc ttc ggg atc ctc tcc aac tgc aac cac acc tac tgt	1087
Ser Glu Arg Arg Phe Gly Ile Leu Ser Asn Cys Asn His Thr Tyr Cys	
295 300 305 310	
ctc aag tgc att tgc acg tgg agg agt gct aag caa ttt gag agc aag	1135
Leu Lys Cys Ile Cys Thr Trp Arg Ser Ala Lys Gln Phe Glu Ser Lys	
311 316 321 326	
atc ata aag tcc tgc cca gaa tgc cag atc aca tct aac tta gtc att	1183
Ile Ile Lys Ser Cys Pro Glu Cys Gln Ile Thr Ser Asn Leu Val Ile	
327 332 337 342	
cca agt gag tac tgg gtt gag gag aaa gaa gag aag cag aaa ctc gtt	1231
Pro Ser Glu Tyr Trp Val Glu Glu Lys Glu Glu Lys Gln Lys Leu Val	
343 348 353 358	
cag aaa tac aaa gag tca atg agc atc aag gcg tgc acg tat ttt gat	1279
Gln Lys Tyr Lys Glu Ser Met Ser Ile Lys Ala Cys Thr Tyr Phe Asp	
359 364 369 374	
gaa gga cat ggg agc tgc cca ttt gga ggg aac tgc ttt tac aag cat	1327
Glu Gly His Gly Ser Cys Pro Phe Gly Gly Asn Cys Phe Tyr Lys His	
375 380 385 390	
gcg taa agaggaggag agaggagcca cggagctaaa accgctcgtg ccgaattctt	1383
Ala *	
391	
ggcctcgagg gccaaattcc ctatagtg	1411

<210> 536
 <211> 1755
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (55) .. (942)

gcccgcaccg acggggagaa cgtattttacc gggcagtc aa agatctattc ctac	57
atg	
Met	

agc ccg aac aaa tgc tct gga atg cgt ttc ccc ctt cag gaa gag aac	105
Ser Pro Asn Lys Cys Ser Gly Met Arg Phe Pro Leu Gln Glu Glu Asn	
2 7 12 17	
tca gtt aca cat cac gaa gtc aaa tgc cag ggg aaa cca tta gcc gga	153
Ser Val Thr His His Glu Val Lys Cys Gln Gly Lys Pro Leu Ala Gly	
18 23 28 33	
atc tac agg aaa cga gaa gag aaa aga aat gct ggg aac gca gta cgg	201
Ile Tyr Arg Lys Arg Glu Glu Lys Arg Asn Ala Gly Asn Ala Val Arg	
34 39 44 49	
agc gcc atg aag tcc gag gaa cag aag atc aaa gac gcc agg aaa ggt	249
Ser Ala Met Lys Ser Glu Glu Gln Lys Ile Lys Asp Ala Arg Lys Gly	
50 55 60 65	
ccc ctg gta cct ttt cca aac caa aaa tct gaa gca gca gaa cct cca	297
Pro Leu Val Pro Phe Pro Asn Gln Lys Ser Glu Ala Ala Glu Pro Pro	
66 71 76 81	
aaa act cca ccc tca tct tgt gat tcc acc aat gca gcc atc gcc aag	345
Lys Thr Pro Pro Ser Ser Cys Asp Ser Thr Asn Ala Ala Ile Ala Lys	
82 87 92 97	
caa gcc ctg aaa aag ccc atc aag ggc aaa cag gcc ccc cga aaa aaa	393
Gln Ala Leu Lys Lys Pro Ile Lys Gly Lys Gln Ala Pro Arg Lys Lys	
98 103 108 113	
gct caa gga aaa acg caa cag aat cgc aaa ctt acg gat ttc tac cct	441
Ala Gln Gly Lys Thr Gln Gln Asn Arg Lys Leu Thr Asp Phe Tyr Pro	
114 119 124 129	
gtc cga agg agc tcc agg aag agc aaa gcc gag ctg cag tct gaa gaa	489
Val Arg Arg Ser Ser Arg Lys Ser Lys Ala Glu Leu Gln Ser Glu Glu	
130 135 140 145	
agg aaa aga ata gat gaa ttg att gaa agt ggg aag gaa gaa gga atg	537
Arg Lys Arg Ile Asp Glu Leu Ile Glu Ser Gly Lys Glu Glu Gly Met	
146 151 156 161	
aag att gac ctc atc gat ggc aaa ggc agg ggt gtg att gcc acc aag	585
Lys Ile Asp Leu Ile Asp Gly Lys Gly Arg Gly Val Ile Ala Thr Lys	
162 167 172 177	
cag ttc tcc cgg ggt gac ttt gtg gtg gaa tac cac ggg gac ctc atc	633
Gln Phe Ser Arg Gly Asp Phe Val Val Glu Tyr His Gly Asp Leu Ile	
178 183 188 193	
gag atc acc gac gcc aag aaa cgg gag gct ctg tac gca cag gac oct	681
Glu Ile Thr Asp Ala Lys Lys Arg Glu Ala Leu Tyr Ala Gln Asp Pro	
194 199 204 209	
tcc acg ggc tgc tac atg tac tat ttt cag tat ctg agc aaa acc tac	729
Ser Thr Gly Cys Tyr Met Tyr Tyr Phe Gln Tyr Leu Ser Lys Thr Tyr	
210 215 220 225	

tgc gtg gat gca act aga gag aca aat cgc cta gga aga ctg atc aat	777
Cys Val Asp Ala Thr Arg Glu Thr Asn Arg Leu Gly Arg Leu Ile Asn	
226 231 236 241	
cac agc aaa tgt ggg aac tgc caa acc aaa ctg cac gac atc gac ggc	825
His Ser Lys Cys Gly Asn Cys Gln Thr Lys Leu His Asp Ile Asp Gly	
242 247 252 257	
gta cct cac ctc atc ctc atc gcc tcc cga gac atc gcg gct ggg gag	873
Val Pro His Leu Ile Leu Ile Ala Ser Arg Asp Ile Ala Ala Gly Glu	
258 263 268 273	
gag ctc ctg tat gac tat ggg gac cgc agc aag gct tcc att gaa gcc	921
Glu Leu Leu Tyr Asp Tyr Gly Asp Arg Ser Lys Ala Ser Ile Glu Ala	
274 279 284 289	
cac ccg tgg ctg aag cat taa cc ggtgggcccc gtgccctccc cgccccactt	974
His Pro Trp Leu Lys His *	
290 295	
tccctttcttc aaaggacaaa gtgccctcaa agggaattga attttttttt tacacactta	1034
atcttagcgg attacttcag atgttttttaa aaagtatatt aagatgcctt ttcactgtag	1094
tatttaaata tctgttacag gtttccaagg tggacttgaa cagatggcct tatattacca	1154
aaacttttat attctagttg tttttgtact ttttttgcac acaagccgaa cgtttgtgct	1214
tcccgctgcat gcagtcaaag actcagcaca ggttttagag gaaatagtca aacatgaact	1274
aggaagccag gtgagtctcc tttctccagt ggaagagccg ggaccttccc cctgcacccc	1334
cgacatccag ggacgggggtg tgaggaagac gctgcctccc aatggcctgg acgggatgtt	1394
tccaagctct tgttccccta acgtctcaac aggcgctcac tgaagtgtat gaatattttt	1454
taaaaagggtt tttgcagtaa gctagtcttc cctctgctt tctcgaaagc ttactgagcc	1514
ctgggccccca agcacggggcc gggcatagat ttctcttccc acaagctgcc gcttttctgg	1574
gcaccttgaa gcatcagggc gtgaaatcaa actagatgtg ggcagggaga gtgttgctta	1634
cctgccctgc tggggcaggg tttctgaaa ctgggttaat tctttataga aatgtgaaca	1694
ctgaatttat tttaaaaaat aataataaaa atttaaaaaa attaaaaata aaaaaaaaaa	1754
a	1755

<210> 537

<211> 3716

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> (87)..(3452)

<400> 537

gaattcttag ttgttttctt tagaagaaca tttctaggga ataatacaag aagatttagg	60
aatcattgaa gttataaaatc tttgga atg agc aaa ctc aga atg gtg cta ctt	113
Met Ser Lys Leu Arg Met Val Leu Leu	
1 5	
gaa gac tct gga tct gct gac ttc aga aga cat ttt gtc aac ttg agt	161
Glu Asp Ser Gly Ser Ala Asp Phe Arg Arg His Phe Val Asn Leu Ser	
10 15 20 25	
ccc ttc acc att act gtg gtc tta ctt ctc agt gcc tgt ttt gtc acc	209
Pro Phe Thr Ile Thr Val Val Leu Leu Leu Ser Ala Cys Phe Val Thr	
26 31 36 41	
agt tct ctt gga gga aca gac aag gag ctg agg cta gtg gat ggt gaa	257
Ser Ser Leu Gly Gly Thr Asp Lys Glu Leu Arg Leu Val Asp Gly Glu	
42 47 52 57	
aac aag tgt agc ggg aga gtg gaa gtg aaa gtc cag gag gag tgg gga	305
Asn Lys Cys Ser Gly Arg Val Glu Val Lys Val Gln Glu Glu Trp Gly	
58 63 68 73	
acg gtg tgt aat aat ggc tgg agc atg gaa gcg gtc tct gtg att tgt	353
Thr Val Cys Asn Asn Gly Trp Ser Met Glu Ala Val Ser Val Ile Cys	
74 79 84 89	
aac cag ctg gga tgt cca act gct atc aaa gcc cct gga tgg gct aat	401
Asn Gln Leu Gly Cys Pro Thr Ala Ile Lys Ala Pro Gly Trp Ala Asn	
90 95 100 105	
tcc agt gca ggt tct gga cgc att tgg atg gat cat gtt tct tgt cgt	449
Ser Ser Ala Gly Ser Gly Arg Ile Trp Met Asp His Val Ser Cys Arg	
106 111 116 121	
ggg aat gag tca gct ctt tgg gat tgc aaa cat gat gga tgg gga aag	497
Gly Asn Glu Ser Ala Leu Trp Asp Cys Lys His Asp Gly Trp Gly Lys	
122 127 132 137	
cat agt aac tgt act cac caa caa gat gct gga gtg acc tgc tca gat	545
His Ser Asn Cys Thr His Gln Gln Asp Ala Gly Val Thr Cys Ser Asp	
138 143 148 153	
gga tcc aat ttg gaa atg agg ctg acg cgt gga ggg aat atg tgt tct	593
Gly Ser Asn Leu Glu Met Arg Leu Thr Arg Gly Gly Asn Met Cys Ser	
154 159 164 169	
gga aga ata gag atc aaa ttc caa gga cgg tgg gga aca gtg tgt gat	641
Gly Arg Ile Glu Ile Lys Phe Gln Gly Arg Trp Gly Thr Val Cys Asp	
170 175 180 185	
gat aac ttc aac ata gat cat gca tct gtc att tgt aga caa ctt gaa	689
Asp Asn Phe Asn Ile Asp His Ala Ser Val Ile Cys Arg Gln Leu Glu	

186	191	196	201	
tgt gga agt gct gtc agt ttc tct ggt tca tct aat ttt gga gaa ggc				737
Cys Gly Ser Ala Val Ser Phe Ser Gly Ser Ser Asn Phe Gly Glu Gly				
202	207	212	217	
tct gga cca atc tgg ttt gat gat ctt ata tgc aac gga aat gag tca				785
Ser Gly Pro Ile Trp Phe Asp Asp Leu Ile Cys Asn Gly Asn Glu Ser				
218	223	228	233	
gct ctc tgg aac tgc aaa cat caa gga tgg gga aag cat aac tgt gat				833
Ala Leu Trp Asn Cys Lys His Gln Gly Trp Gly Lys His Asn Cys Asp				
234	239	244	249	
cat gct gag gat gct gga gtg att tgc tca aag gga gca gat ctg agc				881
His Ala Glu Asp Ala Gly Val Ile Cys Ser Lys Gly Ala Asp Leu Ser				
250	255	260	265	
ctg aga ctg gta gat gga gtc act gaa tgt tca gga aga tta gaa gtg				929
Leu Arg Leu Val Asp Gly Val Thr Glu Cys Ser Gly Arg Leu Glu Val				
266	271	276	281	
aga ttc caa gga gaa tgg ggg aca ata tgt gat gac ggc tgg gac agt				977
Arg Phe Gln Gly Glu Trp Gly Thr Ile Cys Asp Asp Gly Trp Asp Ser				
282	287	292	297	
tac gat gct gct gtg gca tgc aag caa ctg gga tgt cca act gcc gtc				1025
Tyr Asp Ala Ala Val Ala Cys Lys Gln Leu Gly Cys Pro Thr Ala Val				
298	303	308	313	
aca gcc att ggt cga gtt aac gcc agt aag gga ttt gga cac atc tgg				1073
Thr Ala Ile Gly Arg Val Asn Ala Ser Lys Gly Phe Gly His Ile Trp				
314	319	324	329	
ctt gac agc gtt tct tgc cag gga cat gaa cct gct gtc tgg caa tgt				1121
Leu Asp Ser Val Ser Cys Gln Gly His Glu Pro Ala Val Trp Gln Cys				
330	335	340	345	
aaa cac cat gaa tgg gga aag cat tat tgc aat cac aat gaa gat gct				1169
Lys His His Glu Trp Gly Lys His Tyr Cys Asn His Asn Glu Asp Ala				
346	351	356	361	
ggc gtg aca tgt tct gat gga tca gat ctg gag cta aga ctt aga ggt				1217
Gly Val Thr Cys Ser Asp Gly Ser Asp Leu Glu Leu Arg Leu Arg Gly				
362	367	372	377	
gga ggc agc cgc tgt gct ggg aca gtt gag gtg gag att cag aga ctg				1265
Gly Gly Ser Arg Cys Ala Gly Thr Val Glu Val Glu Ile Gln Arg Leu				
378	383	388	393	
tta ggg aag gtg tgt gac aga ggc tgg gga ctg aaa gaa gct gat gtg				1313
Leu Gly Lys Val Cys Asp Arg Gly Trp Gly Leu Lys Glu Ala Asp Val				
394	399	404	409	
gtt tgc agg cag ctg gga tgt gga tct gca ctc aaa aca tct tat caa				1361
Val Cys Arg Gln Leu Gly Cys Gly Ser Ala Leu Lys Thr Ser Tyr Gln				
410	415	420	425	

gtg tac tcc aaa atc cag gca aca aac aca tgg ctg ttt cta agt agc	1409
Val Tyr Ser Lys Ile Gln Ala Thr Asn Thr Trp Leu Phe Leu Ser Ser	
426 431 436 441	
tgt aac gga aat gaa act tct ctt tgg gac tgc aag aac tgg caa tgg	1457
Cys Asn Gly Asn Glu Thr Ser Leu Trp Asp Cys Lys Asn Trp Gln Trp	
442 447 452 457	
ggg gga ctt acc tgt gat cac tat gaa gaa gcc aaa att acc tgc tca	1505
Gly Gly Leu Thr Cys Asp His Tyr Glu Glu Ala Lys Ile Thr Cys Ser	
458 463 468 473	
gcc cac agg gaa ccc aga ctg gtt gga ggg gac att ccc tgt tct gga	1553
Ala His Arg Glu Pro Arg Leu Val Gly Gly Asp Ile Pro Cys Ser Gly	
474 479 484 489	
cgt gtt gaa gtg aag cat ggt gac acg tgg ggc tcc atc tgt gat tcg	1601
Arg Val Glu Val Lys His Gly Asp Thr Trp Gly Ser Ile Cys Asp Ser	
490 495 500 505	
gac ttc tct ctg gaa gct gcc agc gtt cta tgc agg gaa tta cag tgt	1649
Asp Phe Ser Leu Glu Ala Ala Ser Val Leu Cys Arg Glu Leu Gln Cys	
506 511 516 521	
ggc aca gtt gtc tct atc ctg ggg gga gct cac ttt gga gag gga aat	1697
Gly Thr Val Val Ser Ile Leu Gly Gly Ala His Phe Gly Glu Gly Asn	
522 527 532 537	
gga cag atc tgg gct gaa gaa ttc cag tgt gag gga cat gag tcc cat	1745
Gly Gln Ile Trp Ala Glu Glu Phe Gln Cys Glu Gly His Glu Ser His	
538 543 548 553	
ctt tca ctc tgc cca gta gca ccc cgc cca gaa gga act tgt agc cac	1793
Leu Ser Leu Cys Pro Val Ala Pro Arg Pro Glu Gly Thr Cys Ser His	
554 559 564 569	
agc agg gat gtt gga gta gtc tgc tca aga tac aca gaa att cgc ttg	1841
Ser Arg Asp Val Gly Val Val Cys Ser Arg Tyr Thr Glu Ile Arg Leu	
570 575 580 585	
gtg aat ggc aag acc ccg tgt gag ggc aga gtg gag ctc aaa acg ctt	1889
Val Asn Gly Lys Thr Pro Cys Glu Gly Arg Val Glu Leu Lys Thr Leu	
586 591 596 601	
ggg gcc tgg gga tcc ctc tgt aac tct cac tgg gac ata gaa gat gcc	1937
Gly Ala Trp Gly Ser Leu Cys Asn Ser His Trp Asp Ile Glu Asp Ala	
602 607 612 617	
cat gtt ctt tgc cag cag ctt aaa tgt gga gtt gcc ctt tct acc cca	1985
His Val Leu Cys Gln Gln Leu Lys Cys Gly Val Ala Leu Ser Thr Pro	
618 623 628 633	
gga gga gca cgt ttt gga aaa gga aat ggt cag atc tgg agg cat atg	2033
Gly Gly Ala Arg Phe Gly Lys Gly Asn Gly Gln Ile Trp Arg His Met	
634 639 644 649	

ttt cac tgc act ggg act gag cag cac atg gga gat tgt cct gta act	2081
Phe His Cys Thr Gly Thr Glu Gln His Met Gly Asp Cys Pro Val Thr	
650 655 660 665	
gct cta ggt gct tca tta tgt cct tca gag caa gtg gcc tct gta atc	2129
Ala Leu Gly Ala Ser Leu Cys Pro Ser Glu Gln Val Ala Ser Val Ile	
666 671 676 681	
tgc tca gga aac cag tcc caa aca ctg tcc tgc tgc aat tca tgc tct	2177
Cys Ser Gly Asn Gln Ser Gln Thr Leu Ser Ser Cys Asn Ser Ser Ser	
682 687 692 697	
ttg ggc cca aca agg cct acc att cca gaa gaa agt gct gtg gcc tgc	2225
Leu Gly Pro Thr Arg Pro Thr Ile Pro Glu Glu Ser Ala Val Ala Cys	
698 703 708 713	
ata gag agt ggt caa ctt cgc ctg gta aat gga gga ggt cgc tgt gct	2273
Ile Glu Ser Gly Gln Leu Arg Leu Val Asn Gly Gly Gly Arg Cys Ala	
714 719 724 729	
ggg aga gta gag atc tat cat gag ggc tcc tgg ggc acc atc tgt gat	2321
Gly Arg Val Glu Ile Tyr His Glu Gly Ser Trp Gly Thr Ile Cys Asp	
730 735 740 745	
gac agc tgg gac ctg agt gat gcc cac gtg gtt tgc aga cag ctg ggc	2369
Asp Ser Trp Asp Leu Ser Asp Ala His Val Val Cys Arg Gln Leu Gly	
746 751 756 761	
tgt gga gag gcc att aat gcc act ggt tct gct cat ttt ggg gaa gga	2417
Cys Gly Glu Ala Ile Asn Ala Thr Gly Ser Ala His Phe Gly Glu Gly	
762 767 772 777	
aca ggg ccc atc tgg ctg gat gag atg aaa tgc aat gga aaa gaa tcc	2465
Thr Gly Pro Ile Trp Leu Asp Glu Met Lys Cys Asn Gly Lys Glu Ser	
778 783 788 793	
cgc att tgg cag tgc cat tca cac ggc tgg ggg cag caa aat tgc agg	2513
Arg Ile Trp Gln Cys His Ser His Gly Trp Gly Gln Gln Asn Cys Arg	
794 799 804 809	
cac aag gag gat gcg gga gtt atc tgc tca gaa ttc atg tct ctg aga	2561
His Lys Glu Asp Ala Gly Val Ile Cys Ser Glu Phe Met Ser Leu Arg	
810 815 820 825	
ctg acc agt gaa gcc agc aga gag gcc tgt gca ggg cgt ctg gaa gtt	2609
Leu Thr Ser Glu Ala Ser Arg Glu Ala Cys Ala Gly Arg Leu Glu Val	
826 831 836 841	
ttt tac aat gga gct tgg ggc act gtt ggc aag agt agc atg tct gaa	2657
Phe Tyr Asn Gly Ala Trp Gly Thr Val Gly Lys Ser Ser Met Ser Glu	
842 847 852 857	
acc act gtg ggt gtg gtg tgc agg cag ctg ggc tgt gca gac aaa ggg	2705
Thr Thr Val Gly Val Val Cys Arg Gln Leu Gly Cys Ala Asp Lys Gly	
858 863 868 873	
aaa atc aac cct gca tct tta gac aag gcc atg tcc att ccc atg tgg	2753

Lys Ile Asn Pro Ala Ser Leu Asp Lys Ala Met Ser Ile Pro Met Trp	
874 879 884 889	
gtg gac aat gtt cag tgt cca aaa gga cct gac acg ctg tgg cag tgc	2801
Val Asp Asn Val Gln Cys Pro Lys Gly Pro Asp Thr Leu Trp Gln Cys	
890 895 900 905	
cca tca tct cca tgg gag aag aga ctg gcc agc ccc tcg gag gag acc	2849
Pro Ser Ser Pro Trp Glu Lys Arg Leu Ala Ser Pro Ser Glu Glu Thr	
906 911 916 921	
tgg atc aca tgt gac aac aag ata aga ctt cag gaa gga ccc act tcc	2897
Trp Ile Thr Cys Asp Asn Lys Ile Arg Leu Gln Glu Gly Pro Thr Ser	
922 927 932 937	
tgt tct gga cgt gtg gag atc tgg cat gga ggt tcc tgg ggg aca gtg	2945
Cys Ser Gly Arg Val Glu Ile Trp His Gly Gly Ser Trp Gly Thr Val	
938 943 948 953	
tgt gat gac tct tgg gac ttg gac gat gct cag gtg gtg tgt caa caa	2993
Cys Asp Asp Ser Trp Asp Leu Asp Asp Ala Gln Val Val Cys Gln Gln	
954 959 964 969	
ctt ggc tgt ggt cca gct ttg aaa gca ttc aaa gaa gca gag ttt ggt	3041
Leu Gly Cys Gly Pro Ala Leu Lys Ala Phe Lys Glu Ala Glu Phe Gly	
970 975 980 985	
cag ggg act gga ccg ata tgg ctc aat gaa gtg aag tgc aaa ggg aat	3089
Gln Gly Thr Gly Pro Ile Trp Leu Asn Glu Val Lys Cys Lys Gly Asn	
986 991 996 1001	
gag tct tcc ttg tgg gat tgt cct gcc aga cgc tgg ggc cat agt gag	3137
Glu Ser Ser Leu Trp Asp Cys Pro Ala Arg Arg Trp Gly His Ser Glu	
1002 1007 1012 1017	
tgt ggg cac aag gaa gac gct gca gtg aat tgc aca gat att tca gtg	3185
Cys Gly His Lys Glu Asp Ala Ala Val Asn Cys Thr Asp Ile Ser Val	
1018 1023 1028 1033	
cag aaa acc cca caa aaa gcc aca aca ggt cgc tca tcc cgt cag tca	3233
Gln Lys Thr Pro Gln Lys Ala Thr Thr Gly Arg Ser Ser Arg Gln Ser	
1034 1039 1044 1049	
tcc ttt att gca gtc ggg atc ctt ggg gtt gtt ctg ttg gcc att ttc	3281
Ser Phe Ile Ala Val Gly Ile Leu Gly Val Val Leu Leu Ala Ile Phe	
1050 1055 1060 1065	
gtc gca tta ttc ttc ttg act aaa aag cga aga cag aga cag cgg ctt	3329
Val Ala Leu Phe Phe Leu Thr Lys Lys Arg Arg Gln Arg Gln Arg Leu	
1066 1071 1076 1081	
gca gtt tcc tca aga gga gag aac tta gtc cac caa att caa tac cgg	3377
Ala Val Ser Ser Arg Gly Glu Asn Leu Val His Gln Ile Gln Tyr Arg	
1082 1087 1092 1097	
gag atg aat tct tgc ctg aat gca gat gat ctg gac cta atg aat tcc	3425
Glu Met Asn Ser Cys Leu Asn Ala Asp Asp Leu Asp Leu Met Asn Ser	

1098	1103	1108	1113	
tca gga ggc cat tct gag cca cac tga aaagg aaaatgggaa tttataaccc				3477
Ser Gly Gly His Ser Glu Pro His *				
1114	1119			
agtgagttca gcctttaaga taccttgatg aagacctgga ctattgaatg gagcagaaat				3537
tcacctctct cactgactat tacagttgca tttttatgga gttcttcttc tctaggatt				3597
cctaagactg ctgctgaatt tataaaaaatt aagtttgtga atgtgactac ttagtggtgt				3657
atatgagact ttcaagggaa ttaaataaat aaataagaat gttattgaaa aaaaaaaaaa				3716

<210> 538
 <211> 3811
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (87)..(3551)

<400> 538	
gaattcttag ttgttttctt tagaagaaca tttctaggga ataatacaag aagatttagg	60
aatcattgaa gttataaatc tttgga atg agc aaa ctc aga atg gtg cta ctt	113
Met Ser Lys Leu Arg Met Val Leu Leu	
1 5	
gaa gac tct gga tct gct gac ttc aga aga cat ttt gtc aac ctg agt	161
Glu Asp Ser Gly Ser Ala Asp Phe Arg Arg His Phe Val Asn Leu Ser	
10 15 20 25	
ccc ttc acc att act gtg gtc tta ctt ctc agt gcc tgt ttt gtc acc	209
Pro Phe Thr Ile Thr Val Val Leu Leu Leu Ser Ala Cys Phe Val Thr	
26 31 36 41	
agt tct ctt gga gga aca gac aag gag ctg agg cta gtg gat ggt gaa	257
Ser Ser Leu Gly Gly Thr Asp Lys Glu Leu Arg Leu Val Asp Gly Glu	
42 47 52 57	
aac aag tgt agc ggg aga gtg gaa gtg aaa gtc cag gag gag tgg gga	305
Asn Lys Cys Ser Gly Arg Val Glu Val Lys Val Gln Glu Glu Trp Gly	
58 63 68 73	
acg gtg tgt aat aat ggc tgg agc atg gaa gcg gtc tct gtg att tgt	353
Thr Val Cys Asn Asn Gly Trp Ser Met Glu Ala Val Ser Val Ile Cys	
74 79 84 89	
aac cag ctg gga tgt cca act gct atc aaa gcc cct gga tgg gct aat	401
Asn Gln Leu Gly Cys Pro Thr Ala Ile Lys Ala Pro Gly Trp Ala Asn	
90 95 100 105	

tcc agt gca ggt tct gga cgc att tgg atg gat cat gtt tct tgt cgt	449
Ser Ser Ala Gly Ser Gly Arg Ile Trp Met Asp His Val Ser Cys Arg	
106 111 116 121	
ggg aat gag tca gct ctt tgg gat tgc aaa cat gat gga tgg gga aag	497
Gly Asn Glu Ser Ala Leu Trp Asp Cys Lys His Asp Gly Trp Gly Lys	
122 127 132 137	
cat agt aac tgt act cac caa caa gat gct gga gtg acc tgc tca gat	545
His Ser Asn Cys Thr His Gln Gln Asp Ala Gly Val Thr Cys Ser Asp	
138 143 148 153	
gga tcc aat ttg gaa atg agg ctg acg cgt gga ggg aat atg tgt tct	593
Gly Ser Asn Leu Glu Met Arg Leu Thr Arg Gly Gly Asn Met Cys Ser	
154 159 164 169	
gga aga ata gag atc aaa ttc caa gga cgg tgg gga aca gtg tgt gat	641
Gly Arg Ile Glu Ile Lys Phe Gln Gly Arg Trp Gly Thr Val Cys Asp	
170 175 180 185	
gat aac ttc aac ata gat cat gca tct gtc att tgt aga caa ctt gaa	689
Asp Asn Phe Asn Ile Asp His Ala Ser Val Ile Cys Arg Gln Leu Glu	
186 191 196 201	
tgt gga agt gct gtc agt ttc tct ggt tca tct aat ttt gga gaa ggc	737
Cys Gly Ser Ala Val Ser Phe Ser Gly Ser Ser Asn Phe Gly Glu Gly	
202 207 212 217	
tct gga cca atc tgg ttt gat gat ctt ata tgc aac gga aat gag tca	785
Ser Gly Pro Ile Trp Phe Asp Asp Leu Ile Cys Asn Gly Asn Glu Ser	
218 223 228 233	
gct ctc tgg aac tgc aaa cat caa gga tgg gga aag cat aac tgt gat	833
Ala Leu Trp Asn Cys Lys His Gln Gly Trp Gly Lys His Asn Cys Asp	
234 239 244 249	
cat gct gag gat gct gga gtg att tgc tca aag gga gca gat ctg agc	881
His Ala Glu Asp Ala Gly Val Ile Cys Ser Lys Gly Ala Asp Leu Ser	
250 255 260 265	
ctg aga ctg gta gat gga gtc act gaa tgt tca gga aga tta gaa gtg	929
Leu Arg Leu Val Asp Gly Val Thr Glu Cys Ser Gly Arg Leu Glu Val	
266 271 276 281	
aga ttc caa gga gaa tgg ggg aca ata tgt gat gac ggc tgg gac agt	977
Arg Phe Gln Gly Glu Trp Gly Thr Ile Cys Asp Asp Gly Trp Asp Ser	
282 287 292 297	
tac gat gct gct gtg gca tgc aag caa ctg gga tgt cca act gcc gtc	1025
Tyr Asp Ala Ala Val Ala Cys Lys Gln Leu Gly Cys Pro Thr Ala Val	
298 303 308 313	
aca gcc att ggt cga gtt aac gcc agt aag gga ttt gga cac atc tgg	1073
Thr Ala Ile Gly Arg Val Asn Ala Ser Lys Gly Phe Gly His Ile Trp	
314 319 324 329	
ctt gac agc gtt tct tgc cag gga cat gaa cct gct gtc tgg caa tgt	1121

Leu Asp Ser Val Ser Cys Gln Gly His Glu Pro Ala Val Trp Gln Cys	
330 335 340 345	
aaa cac cat gaa tgg gga aag cat tat tgc aat cac aat gaa gat gct	1169
Lys His His Glu Trp Gly Lys His Tyr Cys Asn His Asn Glu Asp Ala	
346 351 356 361	
ggc gtg aca tgt tct gat gga tca gat ctg gag cta aga ctt aga ggt	1217
Gly Val Thr Cys Ser Asp Gly Ser Asp Leu Glu Leu Arg Leu Arg Gly	
362 367 372 377	
gga ggc agc cgc tgt gct ggg aca gtt gag gtg gag att cag aga ctg	1265
Gly Gly Ser Arg Cys Ala Gly Thr Val Glu Val Glu Ile Gln Arg Leu	
378 383 388 393	
tta ggg aag gtg tgt gac aga ggc tgg gga ctg aaa gaa gct gat gtg	1313
Leu Gly Lys Val Cys Asp Arg Gly Trp Gly Leu Lys Glu Ala Asp Val	
394 399 404 409	
gtt tgc agg cag ctg gga tgt gga tct gca ctc aaa aca tct tat caa	1361
Val Cys Arg Gln Leu Gly Cys Gly Ser Ala Leu Lys Thr Ser Tyr Gln	
410 415 420 425	
gtg tac tcc aaa atc cag gca aca aac aca tgg ctg ttt cta agt agc	1409
Val Tyr Ser Lys Ile Gln Ala Thr Asn Thr Trp Leu Phe Leu Ser Ser	
426 431 436 441	
tgt aac gga aat gaa act tct ctt tgg gac tgc aag aac tgg caa tgg	1457
Cys Asn Gly Asn Glu Thr Ser Leu Trp Asp Cys Lys Asn Trp Gln Trp	
442 447 452 457	
ggc gga ctt acc tgt gat cac tat gaa gaa gcc aaa att acc tgc tca	1505
Gly Gly Leu Thr Cys Asp His Tyr Glu Glu Ala Lys Ile Thr Cys Ser	
458 463 468 473	
gcc cac agg gaa ccc aga ctg gtt gga ggg gac att ccc tgt tct gga	1553
Ala His Arg Glu Pro Arg Leu Val Gly Gly Asp Ile Pro Cys Ser Gly	
474 479 484 489	
cgt gtt gaa gtg aag cat ggt gac acg tgg ggc tcc atc tgt gat tcg	1601
Arg Val Glu Val Lys His Gly Asp Thr Trp Gly Ser Ile Cys Asp Ser	
490 495 500 505	
gac ttc tct ctg gaa gct gcc agc gtt cta tgc agg gaa tta cag tgt	1649
Asp Phe Ser Leu Glu Ala Ala Ser Val Leu Cys Arg Glu Leu Gln Cys	
506 511 516 521	
ggc aca gtt gtc tct atc ctg ggg gga gct cac ttt gga gag gga aat	1697
Gly Thr Val Val Ser Ile Leu Gly Gly Ala His Phe Gly Glu Gly Asn	
522 527 532 537	
gga cag atc tgg gct gaa gaa ttc cag tgt gag gga cat gag tcc cat	1745
Gly Gln Ile Trp Ala Glu Glu Phe Gln Cys Glu Gly His Glu Ser His	
538 543 548 553	
ctt tca ctc tgc cca gta gca ccc cgc cca gaa gga act tgt agc cac	1793
Leu Ser Leu Cys Pro Val Ala Pro Arg Pro Glu Gly Thr Cys Ser His	

554	559	564	569	
agc agg gat gtt gga gta gtc tgc tca agt aag acc cag aaa aca tct				1841
Ser Arg Asp Val Gly	Val Val Cys Ser Ser	Lys Thr Gln Lys Thr Ser		
570	575	580	585	
tta att ggt tct tat act gtg aaa ggg aca ggg tta ggg agt cat agc				1889
Leu Ile Gly Ser Tyr Thr	Val Lys Gly Thr	Gly Leu Gly Ser His Ser		
586	591	596	601	
tgt ctt ttt cta aag ccc tgt ctc ctt cca gga tac aca gaa att cgc				1937
Cys Leu Phe Leu Lys Pro	Cys Leu Leu Pro	Gly Tyr Thr Glu Ile Arg		
602	607	612	617	
ttg gtg aat ggc aag acc ccg tgt gag ggc aga gtg gag ctc aaa acg				1985
Leu Val Asn Gly Lys Thr	Pro Cys Glu Gly Arg	Val Glu Leu Lys Thr		
618	623	628	633	
ctt ggt gcc tgg gga tcc ctc tgt aac tct cac tgg gac ata gaa gat				2033
Leu Gly Ala Trp Gly Ser	Leu Cys Asn Ser	His Trp Asp Ile Glu Asp		
634	639	644	649	
gcc cat gtt ctt tgc cag cag ctt aaa tgt gga gtt gcc ctt tct acc				2081
Ala His Val Leu Cys Gln	Gln Leu Lys Cys Gly	Val Ala Leu Ser Thr		
650	655	660	665	
cca gga gga gca cgt ttt gga aaa gga aat ggt cag atc tgg agg cat				2129
Pro Gly Gly Ala Arg Phe	Gly Lys Gly Asn Gly	Gln Ile Trp Arg His		
666	671	676	681	
atg ttt cac tgc act ggg act gag cag cac atg gga gat tgt cct gta				2177
Met Phe His Cys Thr Gly	Thr Glu Gln His Met	Gly Asp Cys Pro Val		
682	687	692	697	
act gct cta ggt gct tca tta tgt cct tca gag caa gtg gcc tct gta				2225
Thr Ala Leu Gly Ala Ser	Leu Cys Pro Ser	Glu Gln Val Ala Ser Val		
698	703	708	713	
atc tgc tca gga aac cag tcc caa aca ctg tcc tcg tgc aat tca tcg				2273
Ile Cys Ser Gly Asn Gln	Ser Gln Thr Leu Ser	Ser Ser Cys Asn Ser Ser		
714	719	724	729	
tct ttg ggc cca aca agg cct acc att cca gaa gaa agt gct gtg gcc				2321
Ser Leu Gly Pro Thr Arg	Pro Thr Ile Pro	Glu Glu Ser Ala Val Ala		
730	735	740	745	
tgc ata gag agt ggt caa ctt cgc ctg gta aat gga gga ggt cgc tgt				2369
Cys Ile Glu Ser Gly Gln	Leu Arg Leu Val Asn	Gly Gly Gly Arg Cys		
746	751	756	761	
gct ggg aga gta gag atc tat cat gag ggc tcc tgg ggc acc atc tgt				2417
Ala Gly Arg Val Glu Ile	Tyr His Glu Gly Ser	Trp Gly Thr Ile Cys		
762	767	772	777	
gat gac agc tgg gac ctg agt gat gcc cac gtg gtt tgc aga cag ctg				2465
Asp Asp Ser Trp Asp Leu	Ser Asp Ala His Val	Val Cys Arg Gln Leu		
778	783	788	793	

ggc tgt gga gag gcc att aat gcc act ggt tct gct cat ttt ggg gaa	2513
Gly Cys Gly Glu Ala Ile Asn Ala Thr Gly Ser Ala His Phe Gly Glu	
794 799 804 809	
gga aca ggg ccc atc tgg ctg gat gag atg aaa tgc aat gga aaa gaa	2561
Gly Thr Gly Pro Ile Trp Leu Asp Glu Met Lys Cys Asn Gly Lys Glu	
810 815 820 825	
tcc cgc att tgg cag tgc cat tca cac gcc tgg ggg cag caa aat tgc	2609
Ser Arg Ile Trp Gln Cys His Ser His Gly Trp Gly Gln Gln Asn Cys	
826 831 836 841	
agg cac aag gag gat gcg gga gtt atc tgc tca gaa ttc atg tct ctg	2657
Arg His Lys Glu Asp Ala Gly Val Ile Cys Ser Glu Phe Met Ser Leu	
842 847 852 857	
aga ctg acc agt gaa gcc agc aga gag gcc tgt gca ggg cgt ctg gaa	2705
Arg Leu Thr Ser Glu Ala Ser Arg Glu Ala Cys Ala Gly Arg Leu Glu	
858 863 868 873	
gtt ttt tac aat gga gct tgg ggc act gtt ggc aag agt agc atg tct	2753
Val Phe Tyr Asn Gly Ala Trp Gly Thr Val Gly Lys Ser Ser Met Ser	
874 879 884 889	
gaa acc act gtg ggt gtg gtg tgc agg cag ctg ggc tgt gca gac aaa	2801
Glu Thr Thr Val Gly Val Val Cys Arg Gln Leu Gly Cys Ala Asp Lys	
890 895 900 905	
ggg aaa atc aac cct gca tct tta gac aag gcc atg tcc att ccc atg	2849
Gly Lys Ile Asn Pro Ala Ser Leu Asp Lys Ala Met Ser Ile Pro Met	
906 911 916 921	
tgg gtg gac aat gtt cag tgt cca aaa gga cct gac acg ctg tgg cag	2897
Trp Val Asp Asn Val Gln Cys Pro Lys Gly Pro Asp Thr Leu Trp Gln	
922 927 932 937	
tgc cca tca tct cca tgg gag aag aga ctg gcc agc ccc tgc gag gag	2945
Cys Pro Ser Ser Pro Trp Glu Lys Arg Leu Ala Ser Pro Ser Glu Glu	
938 943 948 953	
acc tgg atc aca tgt gac aac aag ata aga ctt cag gaa gga ccc act	2993
Thr Trp Ile Thr Cys Asp Asn Lys Ile Arg Leu Gln Glu Gly Pro Thr	
954 959 964 969	
tcc tgt tct gga cgt gtg gag atc tgg cat gga ggt tcc tgg ggg aca	3041
Ser Cys Ser Gly Arg Val Glu Ile Trp His Gly Gly Ser Trp Gly Thr	
970 975 980 985	
gtg tgt gat gac tct tgg gac ttg gac gat gct cag gtg gtg tgt caa	3089
Val Cys Asp Asp Ser Trp Asp Leu Asp Asp Ala Gln Val Val Cys Gln	
986 991 996 1001	
caa ctt ggc tgt ggt cca gct ttg aaa gca ttc aaa gaa gca gag ttt	3137
Gln Leu Gly Cys Gly Pro Ala Leu Lys Ala Phe Lys Glu Ala Glu Phe	
1002 1007 1012 1017	

```

ggt cag ggg act gga ccg ata tgg ctc aat gaa gtg aag tgc aaa ggg      3185
Gly Gln Gly Thr Gly Pro Ile Trp Leu Asn Glu Val Lys Cys Lys Gly
1018                1023                1028                1033

aat gag tct tcc ttg tgg gat tgt cct gcc aga cgc tgg ggc cat agt      3233
Asn Glu Ser Ser Leu Trp Asp Cys Pro Ala Arg Arg Trp Gly His Ser
1034                1039                1044                1049

gag tgt ggg cac aag gaa gac gct gca gtg aat tgc aca gat att tca      3281
Glu Cys Gly His Lys Glu Asp Ala Ala Val Asn Cys Thr Asp Ile Ser
1050                1055                1060                1065

gtg cag aaa acc cca caa aaa gcc aca aca ggt cgc tca tcc cgt cag      3329
Val Gln Lys Thr Pro Gln Lys Ala Thr Thr Gly Arg Ser Ser Arg Gln
1066                1071                1076                1081

tca tcc ttt att gca gtc ggg atc ctt ggg gtt gtt ctg ttg gcc att      3377
Ser Ser Phe Ile Ala Val Gly Ile Leu Gly Val Val Leu Leu Ala Ile
1082                1087                1092                1097

ttc gtc gca tta ttc ttc ttg act aaa aag cga aga cag aga cag cgg      3425
Phe Val Ala Leu Phe Phe Leu Thr Lys Lys Arg Arg Gln Arg Gln Arg
1098                1103                1108                1113

ctt gca gtt tcc tca aga gga gag aac tta gtc cac caa att caa tac      3473
Leu Ala Val Ser Ser Arg Gly Glu Asn Leu Val His Gln Ile Gln Tyr
1114                1119                1124                1129

cgg gag atg aat tct tgc ctg aat gca gat gat ctg gac cta atg aat      3521
Arg Glu Met Asn Ser Cys Leu Asn Ala Asp Asp Leu Asp Leu Met Asn
1130                1135                1140                1145

tcc tca gga ggc cat tct gag cca cac tga a aaggaaaatg ggaatttata      3572
Ser Ser Gly Gly His Ser Glu Pro His *
1146                1151

accagtgag ttcagccttt aagatacctt gatgaagacc tggactattg aatggagcag      3632

aaattcacct ctctcactga ctattacagt tgcattttta tggagttctt cttctcctag      3692

gattcctaag actgctgctg aatttataaa aattaagttt gtgaatgtga ctacttagtg      3752

gtgtatatga gactttcaag ggaattaaat aaataaataa gaatgttaaa aaaaaaaaaa      3811

```

```

<210> 539
<211> 1865
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (218) .. (1120)

<400> 539

```

atttcgggt cgacgatctc gtccgggagg ggccgcggga accggcgccc cacggagctg	60
ctgctgtcag accaaccacc ggccccatc atcactgcgc cgcgctttca ggcgccgaga	120
actaccgttc cgggcatgcc atgaaattgg cctcggcgct gaggcgggggt ccggccctcc	180
accgcctccc gccgcgcgcg aatcgcggtc gcgagcc atg gag gag gag gca tgc	235
Met Glu Glu Glu Ala Ser	
1	
tcc ccg ggg ctg ggc tgc agc aag ccg cac ctg gag aag ctg acc ctg	283
Ser Pro Gly Leu Gly Cys Ser Lys Pro His Leu Glu Lys Leu Thr Leu	
7 12 17 22	
ggc atc acg cgc atc cta gaa tct tcc cca ggt gtg act gag gtg acc	331
Gly Ile Thr Arg Ile Leu Glu Ser Ser Pro Gly Val Thr Glu Val Thr	
23 28 33 38	
atc ata gaa aag cct cct gct gaa cgt cat atg att tct tcc tgg gaa	379
Ile Ile Glu Lys Pro Pro Ala Glu Arg His Met Ile Ser Ser Trp Glu	
39 44 49 54	
caa aag aat aac tgt gtg atg cct gaa gat gtg aag aac ttt tac ctg	427
Gln Lys Asn Asn Cys Val Met Pro Glu Asp Val Lys Asn Phe Tyr Leu	
55 60 65 70	
atg acc aat ggc ttc cac atg aca tgg agt gtg aag ctg gat gag cac	475
Met Thr Asn Gly Phe His Met Thr Trp Ser Val Lys Leu Asp Glu His	
71 76 81 86	
atc att cca ctg gga agc atg gca att aac agc atc tca aaa ctg act	523
Ile Ile Pro Leu Gly Ser Met Ala Ile Asn Ser Ile Ser Lys Leu Thr	
87 92 97 102	
cag ctc acc cag tct tcc atg tat tca ctt cct aat gca ccc act ctg	571
Gln Leu Thr Gln Ser Ser Met Tyr Ser Leu Pro Asn Ala Pro Thr Leu	
103 108 113 118	
gca gac ctg gag gac gat aca cat gaa gcc agt gat gat cag cca gag	619
Ala Asp Leu Glu Asp Asp Thr His Glu Ala Ser Asp Asp Gln Pro Glu	
119 124 129 134	
aag cct cac ttt gac tct cgc agt gtg ata ttt gag ctg gat tca tgc	667
Lys Pro His Phe Asp Ser Arg Ser Val Ile Phe Glu Leu Asp Ser Cys	
135 140 145 150	
aat ggc agt ggg aaa gtt tgc ctt gtc tac aaa agt ggg aaa cca gca	715
Asn Gly Ser Gly Lys Val Cys Leu Val Tyr Lys Ser Gly Lys Pro Ala	
151 156 161 166	
tta gca gaa gac act gag atc tgg ttc ctg gac aga gcg tta tac tgg	763
Leu Ala Glu Asp Thr Glu Ile Trp Phe Leu Asp Arg Ala Leu Tyr Trp	
167 172 177 182	
cat ttt ctc aca gac acc ttt act gcc tat tac cgc ctg ctc atc acc	811
His Phe Leu Thr Asp Thr Phe Thr Ala Tyr Tyr Arg Leu Leu Ile Thr	
183 188 193 198	

cac ctg ggc ctg ccc cag tgg caa tat gcc ttc acc agc tat ggc att	859
His Leu Gly Leu Pro Gln Trp Gln Tyr Ala Phe Thr Ser Tyr Gly Ile	
199 204 209 214	
agc cca cag gcc aag caa tgg ttc agc atg tat aaa cct atc acc tac	907
Ser Pro Gln Ala Lys Gln Trp Phe Ser Met Tyr Lys Pro Ile Thr Tyr	
215 220 225 230	
aac aca aac ctg ctc aca gaa gag acc gac tcc ttt gtg aat aag cta	955
Asn Thr Asn Leu Leu Thr Glu Glu Thr Asp Ser Phe Val Asn Lys Leu	
231 236 241 246	
gat ccc agc aaa gtg ttt aag agc aag aac aag atc gta atc cca aaa	1003
Asp Pro Ser Lys Val Phe Lys Ser Lys Asn Lys Ile Val Ile Pro Lys	
247 252 257 262	
aag aaa ggg cct gtg cag cct gca ggt ggc cag aaa ggg ccc tca gga	1051
Lys Lys Gly Pro Val Gln Pro Ala Gly Gly Gln Lys Gly Pro Ser Gly	
263 268 273 278	
ccc tcc ggt ccc tcc act tcc tcc act tct aaa tcc tcc tct ggc tct	1099
Pro Ser Gly Pro Ser Thr Ser Ser Thr Ser Lys Ser Ser Ser Gly Ser	
279 284 289 294	
gga aac ccc acc cgg aag tga gc acccctccct ccaactccct accagctcca	1152
Gly Asn Pro Thr Arg Lys *	
295 300	
gagtgggtggt ttccatgcac agatggccct aggggtgacc tccagttttg cgtgtggacc	1212
gtaggcctct ttctagttga atgacaaaaa ttgtaaggct tttagtccca ccgacattag	1272
ccaggctcgt agtgaggcct ccagagcagg ttgtgctgtc ccctgcctct ggaagcaatg	1332
gggaatttgg aatcttgtgt aagtgcccaa ataagtctga gtgctttcct cttcttcaac	1392
actcaaccct caatccotta gcactgattg attagagagg tccccaaaag aaaccactgg	1452
ttttgaccca tgaagcatta gaactgcatt gttcattcag gagccactag tcacatatga	1512
ctattttaat ttaaagtaaa ttgtatgaaa aattcatttc ttcaattgca ttagccacat	1572
tttgagtatt catgtggctg gtagattctg tattagcaca aagatatgga acatttccat	1632
caccacagaa agttctgttg gacagcactg cattagaata ttttcatact gctcttcctc	1692
aattaatttt tgttgtaaat gttgatgtct tcattggatg ggtcataatg ttccatgaaa	1752
cctctcaagt acacaattgt atgttctttg tatcccttac cacaaatc tcgctctgct	1812
catttctttt gcagcttcct ataaagtttg tcttctcat caaaaaaaaaaaa aaa	1865

<210> 540

<211> 1736
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (218)..(991)

<400> 540

```

atttcgggt cgacgatctc gtccgggagg ggccgcggga accggcgccc cacggagctg      60
ctgctgtcag accaaccacc ggcccccatc atcactgcgc cgcgctttca ggccgccgaga    120
actaccgttc ccggcatgcc atgaaattgg cctcggcgct gagggcgggt ccggccctcc      180
accgctccc gccgcgcgcg aatcgcggtc gcgagcc atg gag gag gag gca tcg      235
                               Met Glu Glu Glu Ala Ser
                               1

tcc ccg ggg ctg ggc tgc agc aag ccg cac ctg gag aag ctg acc ctg      283
Ser Pro Gly Leu Gly Cys Ser Lys Pro His Leu Glu Lys Leu Thr Leu
  7              12              17              22

ggc atc acg cgc atc cta gaa tct tcc cca ggt gtg act gag gtg acc      331
Gly Ile Thr Arg Ile Leu Glu Ser Ser Pro Gly Val Thr Glu Val Thr
 23              28              33              38

atc ata gaa aag cct cct gct gaa cgt cat atg att tct tcc tgg gaa      379
Ile Ile Glu Lys Pro Pro Ala Glu Arg His Met Ile Ser Ser Trp Glu
 39              44              49              54

caa aag aat aac tgt gtg atg cct gaa gat gtg aag aac ttt tac ctg      427
Gln Lys Asn Asn Cys Val Met Pro Glu Asp Val Lys Asn Phe Tyr Leu
 55              60              65              70

atg acc aat ggc ttc cac atg aca tgg agt gtg aag ctg gat gcc agt      475
Met Thr Asn Gly Phe His Met Thr Trp Ser Val Lys Leu Asp Ala Ser
 71              76              81              86

gat gat cag cca gag aag cct cac ttt gac tct cgc agt gtg ata ttt      523
Asp Asp Gln Pro Glu Lys Pro His Phe Asp Ser Arg Ser Val Ile Phe
 87              92              97             102

gag ctg gat tca tgc aat ggc agt ggg aaa gtt tgc ctt gtc tac aaa      571
Glu Leu Asp Ser Cys Asn Gly Ser Gly Lys Val Cys Leu Val Tyr Lys
103             108             113             118

agt ggg aaa cca gca tta gca gaa gac act gag atc tgg ttc ctg gac      619
Ser Gly Lys Pro Ala Leu Ala Glu Asp Thr Glu Ile Trp Phe Leu Asp
119             124             129             134

aga gcg tta tac tgg cat ttt ctc aca gac acc ttt act gcc tat tac      667
Arg Ala Leu Tyr Trp His Phe Leu Thr Asp Thr Phe Thr Ala Tyr Tyr
135             140             145 /             150

cgc ctg ctc atc acc cac ctg ggc ctg ccc cag tgg caa tat gcc ttc      715
Arg Leu Leu Ile Thr His Leu Gly Leu Pro Gln Trp Gln Tyr Ala Phe

```

151	156	161	166	
acc agc tat ggc att agc cca cag gcc aag caa tgg ttc agc atg tat				763
Thr Ser Tyr Gly Ile Ser Pro Gln Ala Lys Gln Trp Phe Ser Met Tyr				
167	172	177	182	
aaa cct atc acc tac aac aca aac ctg ctc aca gaa gag acc gac tcc				811
Lys Pro Ile Thr Tyr Asn Thr Asn Leu Leu Thr Glu Glu Thr Asp Ser				
183	188	193	198	
ttt gtg aat aag cta gat ccc agc aaa gtg ttt aag agc aag aac aag				859
Phe Val Asn Lys Leu Asp Pro Ser Lys Val Phe Lys Ser Lys Asn Lys				
199	204	209	214	
atc gta atc cca aaa aag aaa ggg cct gtg cag cct gca ggt ggc cag				907
Ile Val Ile Pro Lys Lys Lys Gly Pro Val Gln Pro Ala Gly Gly Gln				
215	220	225	230	
aaa ggg ccc tca gga ccc tcc ggt ccc tcc act tcc tcc act tct aaa				955
Lys Gly Pro Ser Gly Pro Ser Gly Pro Ser Thr Ser Ser Thr Ser Lys				
231	236	241	246	
tcc tcc tct ggc tct gga aac ccc acc cgg aag tga gcac cctccctcc				1005
Ser Ser Ser Gly Ser Gly Asn Pro Thr Arg Lys *				
247	252	257		
aactccctac cagctccaga gtggtggttt ccatgcacag atggccctag gggtgacctc				1065
cagttttgcg tgtggaccgt aggctcttt ctagttgaat gacccaaatt gtaaggcttt				1125
tagtcccacc gacattagcc aggctcgtag tgaggcctcc agagcagggt gtgctgtccc				1185
ctgcctctgg aagcaatggg gaatttgga tcttgtgtaa gtgccaaat aagtctgagt				1245
gctttcctct tcttcaacac tcaaccctca atcccttagc actgattgat tagagaggtc				1305
ccccaaagaa accactgggt ttgacctatg aagcattaga actgcattgt tcattcagga				1365
gccactagtc acatatgact atttaaattt aaagtaaatt gtatgaaaaa ttcatttctt				1425
caattgcatt agccacattt tgagtattca tgtggctggg agattctgta ttagcacaaa				1485
gatatggaac atttccatca ccacagaaag ttctgttgga cagcactgca ttagaatatt				1545
ttcatactgc tcttctcaa ttaatttttg ttgttaatgt tgatgtcttc attggatggg				1605
tcataatggt ccatgaaacc tctcaagtac acaattgtat gttctttgta tcccttacca				1665
caaatatctc gctctgctca tttcttttgc agcttctat aaagtttgtc ttcctcatca				1725
aaaaaaaaa a				1736

<210> 541

<211> 563

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (185)..(460)

<400> 541

```
gcacgagctg gcgccgtccg cgatccgcag ggctgcccg ttaggcttag gcccggcccg      60
ctggcaaagc cgagccgcag cattttatctt cgttcgtggt ttccgcacag gctggagttt    120
cgtgggttgg gtcgtacttg ggacctcggc gaagaggacc cgtttatttt tttttctttc    180
caaa atg gca gcc tcc agt cgc gca caa gtg tta tct ctg tac cgg gcg      229
  Met Ala Ala Ser Ser Arg Ala Gln Val Leu Ser Leu Tyr Arg Ala
    1             5             10
atg ctg aga gag agc aag cgt ttc agc gcc tac aat tac aga aca tat      277
Met Leu Arg Glu Ser Lys Arg Phe Ser Ala Tyr Asn Tyr Arg Thr Tyr
  16             21             26             31
gct gtc agg agg ata aga gat gcc ttc aga gaa aat aaa aat gta aag      325
Ala Val Arg Arg Ile Arg Asp Ala Phe Arg Glu Asn Lys Asn Val Lys
  32             37             42             47
gat cct gta gaa att caa acc cta gtg aat aaa gcc aag aga gac ctt      373
Asp Pro Val Glu Ile Gln Thr Leu Val Asn Lys Ala Lys Arg Asp Leu
  48             53             58             63
gga gta att cgt cga cag gtc cac att ggc caa ctg tat tca act gac      421
Gly Val Ile Arg Arg Gln Val His Ile Gly Gln Leu Tyr Ser Thr Asp
  64             69             74             79
aag ctg atc att gag aat cga gac atg ccc agg acc tag caagccgggg      470
Lys Leu Ile Ile Glu Asn Arg Asp Met Pro Arg Thr *
  80             85             90
accagccacc agtggcggcc agggaccacc ttcagcatcc actctctggt tgagctgggg    530
gctcccaaaa ccagcttaca atagcctttt gcg                                  563
```

<210> 542
<211> 2100
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (33)..(1835)

<400> 542

```
gcacgagcgg gtccggggagc gcggcggaga cg atg cct gag atc aga gtc acg      53
  Met Pro Glu Ile Arg Val Thr
```

ccc ttg ggg gcc ggc cag gac gtg ggc cga agc tgc atc ctg gtc tcc	101
Pro Leu Gly Ala Gly Gln Asp Val Gly Arg Ser Cys Ile Leu Val Ser	
8 13 18 23	
att gcg ggc aag aat gtc atg ctg gac tgt gga atg cac atg ggc ttc	149
Ile Ala Gly Lys Asn Val Met Leu Asp Cys Gly Met His Met Gly Phe	
24 29 34 39	
aat gac gac cga cgc ttc cct gac ttc tcc tac atc acc cag aac ggc	197
Asn Asp Asp Arg Arg Phe Pro Asp Phe Ser Tyr Ile Thr Gln Asn Gly	
40 45 50 55	
cgc cta aca gac ttc ctg gac tgt gtg atc att agc cac ttc cac ctg	245
Arg Leu Thr Asp Phe Leu Asp Cys Val Ile Ile Ser His Phe His Leu	
56 61 66 71	
gac cac tgc ggg gca ctc ccc tac ttc agc gag atg gtg ggc tac gac	293
Asp His Cys Gly Ala Leu Pro Tyr Phe Ser Glu Met Val Gly Tyr Asp	
72 77 82 87	
ggc ccc atc tac atg act cac ccc acc cag gcc atc tgc ccc atc ttg	341
Gly Pro Ile Tyr Met Thr His Pro Thr Gln Ala Ile Cys Pro Ile Leu	
88 93 98 103	
ctg gag gac tac cgc aag atc gcc gta gac aag aag ggc gag gcc aac	389
Leu Glu Asp Tyr Arg Lys Ile Ala Val Asp Lys Lys Gly Glu Ala Asn	
104 109 114 119	
ttc ttc acc tcc cag atg atc aaa gac tgc atg aag aag gtg gtg gct	437
Phe Phe Thr Ser Gln Met Ile Lys Asp Cys Met Lys Lys Val Val Ala	
120 125 130 135	
gtc cac ctc cac cag acg gtc cag gta gat gat gag ctg gag atc aag	485
Val His Leu His Gln Thr Val Gln Val Asp Asp Glu Leu Glu Ile Lys	
136 141 146 151	
gcc tac tat gca ggc cac gtg ctg ggg gca gcc atg ttc cag att aaa	533
Ala Tyr Tyr Ala Gly His Val Leu Gly Ala Ala Met Phe Gln Ile Lys	
152 157 162 167	
gtg ggc tca gag tct gtg gtc tac acg ggt gat tat aac atg acc cca	581
Val Gly Ser Glu Ser Val Val Tyr Thr Gly Asp Tyr Asn Met Thr Pro	
168 173 178 183	
gac cga cac tta gga gct gcc tgg att gac aag tgc cgc ccc aac ctg	629
Asp Arg His Leu Gly Ala Ala Trp Ile Asp Lys Cys Arg Pro Asn Leu	
184 189 194 199	
ctc atc aca gag tcc acg tac gcc acg acc atc cgt gac tcc aag cgc	677
Leu Ile Thr Glu Ser Thr Tyr Ala Thr Thr Ile Arg Asp Ser Lys Arg	
200 205 210 215	
tgc cgg gag cga gac ttc ctg aag aaa gtc cac gag acc gtg gag cgt	725
Cys Arg Glu Arg Asp Phe Leu Lys Lys Val His Glu Thr Val Glu Arg	
216 221 226 231	

ggt ggg aag gtg ctg ata cct gtg ttc gcg ctg ggc cgc gcc cag gag	773
Gly Gly Lys Val Leu Ile Pro Val Phe Ala Leu Gly Arg Ala Gln Glu	
232 237 242 247	
ctc tgc atc ctc ctg gag acc ttc tgg gag cgc atg aac ctg aag gtg	821
Leu Cys Ile Leu Leu Glu Thr Phe Trp Glu Arg Met Asn Leu Lys Val	
248 253 258 263	
ccc atc tac ttc tcc acg ggg ctg acc gag aag gcc aac cac tac tac	869
Pro Ile Tyr Phe Ser Thr Gly Leu Thr Glu Lys Ala Asn His Tyr Tyr	
264 269 274 279	
aag ctg ttc atc ccc tgg acc aac cag aag atc cgc aag act ttc gtg	917
Lys Leu Phe Ile Pro Trp Thr Asn Gln Lys Ile Arg Lys Thr Phe Val	
280 285 290 295	
cag agg aac atg ttt gag ttc aag cac atc aag gcc ttc gac cgg gct	965
Gln Arg Asn Met Phe Glu Phe Lys His Ile Lys Ala Phe Asp Arg Ala	
296 301 306 311	
ttt gct gac aac cca gga ccg atg gtt gtg ttt gcc acg cca gga atg	1013
Phe Ala Asp Asn Pro Gly Pro Met Val Val Phe Ala Thr Pro Gly Met	
312 317 322 327	
ctg cac gct ggg cag tcc ctg cag atc ttc cgg aaa tgg gcc gga aac	1061
Leu His Ala Gly Gln Ser Leu Gln Ile Phe Arg Lys Trp Ala Gly Asn	
328 333 338 343	
gaa aag aac atg gtc atc atg ccc ggc tac tgc gtg cag ggc acc gtc	1109
Glu Lys Asn Met Val Ile Met Pro Gly Tyr Cys Val Gln Gly Thr Val	
344 349 354 359	
ggc cac aag atc ctc agc ggg cag cgg aag ctc gag atg gag ggg cgg	1157
Gly His Lys Ile Leu Ser Gly Gln Arg Lys Leu Glu Met Glu Gly Arg	
360 365 370 375	
cag gtg ctg gag gtc aag atg cag gtg gag tac atg tca ttc agc gca	1205
Gln Val Leu Glu Val Lys Met Gln Val Glu Tyr Met Ser Phe Ser Ala	
376 381 386 391	
cac gcg gac gcc aag ggc atc atg cag ctg gtg ggc cag gca gag ccg	1253
His Ala Asp Ala Lys Gly Ile Met Gln Leu Val Gly Gln Ala Glu Pro	
392 397 402 407	
gag agc gtg ctg ctg gtg cat ggc gag gcc aag aag atg gag ttc ctg	1301
Glu Ser Val Leu Leu Val His Gly Glu Ala Lys Lys Met Glu Phe Leu	
408 413 418 423	
aag cag aag atc gag cag gag ctc cgg gtc aac tgc tac atg ccg gcc	1349
Lys Gln Lys Ile Glu Gln Glu Leu Arg Val Asn Cys Tyr Met Pro Ala	
424 429 434 439	
aat ggc gag acg gtg acg ctg ccc aca agc ccc agc atc ccc gta ggc	1397
Asn Gly Glu Thr Val Thr Leu Pro Thr Ser Pro Ser Ile Pro Val Gly	
440 445 450 455	

atc tcg ctg ggg ctg ctg aag cgg gag atg gcg cag ggg ctg ctc cct	1445
Ile Ser Leu Gly Leu Leu Lys Arg Glu Met Ala Gln Gly Leu Leu Pro	
456 461 466 471	
gag gcc aag aag cct cgg ctc ctg cac ggc acc ctg atc atg aag gac	1493
Glu Ala Lys Lys Pro Arg Leu Leu His Gly Thr Leu Ile Met Lys Asp	
472 477 482 487	
agc aac ttc cgg ctg gtg tcc tca gag caa gcc ctc aaa gag ctg ggt	1541
Ser Asn Phe Arg Leu Val Ser Ser Glu Gln Ala Leu Lys Glu Leu Gly	
488 493 498 503	
ctg gct gag cac cag ctg cgc ttc acc tgc cgc gtg cac ctg cat gac	1589
Leu Ala Glu His Gln Leu Arg Phe Thr Cys Arg Val His Leu His Asp	
504 509 514 519	
aca cgc aag gag cag gag acg gca ttg cgc gtc tac agc cac ctc aag	1637
Thr Arg Lys Glu Gln Glu Thr Ala Leu Arg Val Tyr Ser His Leu Lys	
520 525 530 535	
agc gtc ctg aag gac cac tgt gtg cag cac ctc cca gac ggc tct gtg	1685
Ser Val Leu Lys Asp His Cys Val Gln His Leu Pro Asp Gly Ser Val	
536 541 546 551	
act gtg gag tcc gtc ctc ctc cag gcc gcc gcc cct tct gag gac cca	1733
Thr Val Glu Ser Val Leu Leu Gln Ala Ala Ala Pro Ser Glu Asp Pro	
552 557 562 567	
ggc acc aag gtg ctg ctg gtc tcc tgg acc tac cag gac gag gag ctg	1781
Gly Thr Lys Val Leu Leu Val Ser Trp Thr Tyr Gln Asp Glu Glu Leu	
568 573 578 583	
ggg agc ttc ctc aca tct ctg ctg aag aag ggc ctc ccc cag gcc ccc	1829
Gly Ser Phe Leu Thr Ser Leu Leu Lys Lys Gly Leu Pro Gln Ala Pro	
584 589 594 599	
agc tga ggccggcaac tcaccagcc gccacctctg ccctctccca gctggacaga	1885
Ser *	
600	
ccctgggcct gcacttcagg actgtgggtg ccctgggtga acagaccctg caggtcccat	1945
ccctggggac agaggccttg tgtcacctgc ctgcccaggc agctgtttgc agctgaagaa	2005
acaaactggt ctccaggctg tcttgccctt attcctggtt agggcagggtg gtcctagaca	2065
gcagtttcca gtaaaagctg aacaaaaaaa aaaaa	2100

<210> 543

<211> 657

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (40)..(453)

<400> 543

```
ggccagtgaa ttgaatttag gtgacactat agaagagct   atg acg tcg cat gca   54
                                         Met Thr Ser His Ala
                                         1

cgc gta cgt aag ctt gga tcc tct aga gcg gcc cta cta cta cta aat   102
Arg Val Arg Lys Leu Gly Ser Ser Arg Ala Ala Leu Leu Leu Leu Asn
  6                      11                      16                      21

tcg cgg ccg cgt cga cca aaa atg gcg gta gtt ggt gtg tcc tcg gtt   150
Ser Arg Pro Arg Arg Pro Lys Met Ala Val Val Gly Val Ser Ser Val
  22                      27                      32                      37

tct cgg ctg ctg ggt cgg tcc cgc cca cag ctg ggg cgg cct atg tcg   198
Ser Arg Leu Leu Gly Arg Ser Arg Pro Gln Leu Gly Arg Pro Met Ser
  38                      43                      48                      53

agt ggc gcc cat ggc gaa gag ggc tca gct cgc atg tgg aag act ctc   246
Ser Gly Ala His Gly Glu Glu Gly Ser Ala Arg Met Trp Lys Thr Leu
  54                      59                      64                      69

acc ttc ttc gtc gcg ctc ccc ggg gtg gca gtc agc atg ctg aat gtg   294
Thr Phe Phe Val Ala Leu Pro Gly Val Ala Val Ser Met Leu Asn Val
  70                      75                      80                      85

tac ctg aag tcg cac cac gga gag cac gag aga ccc gag ttc atc gcc   342
Tyr Leu Lys Ser His His Gly Glu His Glu Arg Pro Glu Phe Ile Ala
  86                      91                      96                      101

tac ccc cat ctc cgc atc agg acc aag ccg ttt ccc tgg gga gat ggt   390
Tyr Pro His Leu Arg Ile Arg Thr Lys Pro Phe Pro Trp Gly Asp Gly
  102                      107                      112                      117

aac cat act cta ttc cat aac cct cat gtg aat cca ctt cca act ggc   438
Asn His Thr Leu Phe His Asn Pro His Val Asn Pro Leu Pro Thr Gly
  118                      123                      128                      133

tac gaa gat gaa taa agagaatctg gaccactacc cgggcaccag ggaccacagc   493
Tyr Glu Asp Glu *
134

actggttttg accgttactc tgcacatgga ccagaaaaag tatatgggac cttaagctca   553

ccttcttttac ttgtatcaaa tgatgactgg tatactggtc tcccatccct ttgcttggtg   613

caggagatgg cttaaataaa taacttaaac ttaaaaaaaaa aaaa   657
```

<210> 544

<211> 1505

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> (72)..(1208)

<400> 544

atttggccct cgaggccaag aattcggcac gagattgaac tcgagttgga agaggcgagt	60
ccgggtctcaa a atg gag gta aaa ccg ccg ccc ggt cgc ccc cag ccc gac	110
Met Glu Val Lys Pro Pro Pro Gly Arg Pro Gln Pro Asp	
1 5 10	
tcc ggc cgt cgc cgt cgc cgc cgg ggg gag gag ggc cat gat cca aag	158
Ser Gly Arg Arg Arg Arg Arg Arg Gly Glu Glu Gly His Asp Pro Lys	
14 19 24 29	
gaa cca gag cag ttg aga aaa ctg ttt att ggt ggt ctg agc ttt gaa	206
Glu Pro Glu Gln Leu Arg Lys Leu Phe Ile Gly Gly Leu Ser Phe Glu	
30 35 40 45	
act aca gat gat agt tta cga gaa cat ttt gag aaa tgg ggc aca ctc	254
Thr Thr Asp Asp Ser Leu Arg Glu His Phe Glu Lys Trp Gly Thr Leu	
46 51 56 61	
aca gat tgt gtg gta atg aga gac ccc caa aca aaa cgt tcc agg ggc	302
Thr Asp Cys Val Val Met Arg Asp Pro Gln Thr Lys Arg Ser Arg Gly	
62 67 72 77	
ttt ggt ttt gtg act tat tct tgt gtt gaa gag gtg gat gca gca atg	350
Phe Gly Phe Val Thr Tyr Ser Cys Val Glu Glu Val Asp Ala Ala Met	
78 83 88 93	
tgt gct cga cca cac aag gtt gat ggg cgt gta gtg gaa cca aag aga	398
Cys Ala Arg Pro His Lys Val Asp Gly Arg Val Val Glu Pro Lys Arg	
94 99 104 109	
gct gtt tct aga gag gat tct gta aag cct ggt gcc cat cta aca gtg	446
Ala Val Ser Arg Glu Asp Ser Val Lys Pro Gly Ala His Leu Thr Val	
110 115 120 125	
aag aaa att ttt gtt ggt ggt att aaa gaa gat aca gaa gaa tat aat	494
Lys Lys Ile Phe Val Gly Gly Ile Lys Glu Asp Thr Glu Glu Tyr Asn	
126 131 136 141	
ttg aga gac tac ttt gaa aag tat ggc aag att gaa acc ata gaa gtt	542
Leu Arg Asp Tyr Phe Glu Lys Tyr Gly Lys Ile Glu Thr Ile Glu Val	
142 147 152 157	
atg gaa gac agg cag agt gga aaa aag aga gga ttt gct ttt gta act	590
Met Glu Asp Arg Gln Ser Gly Lys Lys Arg Gly Phe Ala Phe Val Thr	
158 163 168 173	
ttt gat gat cat gat aca gtt gat aaa att gtt gtt cag aaa tac cac	638
Phe Asp Asp His Asp Thr Val Asp Lys Ile Val Val Gln Lys Tyr His	
174 179 184 189	
act att aat ggg cat aat tgt gaa gtg aaa aag gcc ctt tct aaa caa	686

Thr	Ile	Asn	Gly	His	Asn	Cys	Glu	Val	Lys	Lys	Ala	Leu	Ser	Lys	Gln
190					195					200					205

gag	atg	cag	tct	gct	gga	tca	cag	aga	ggt	cgt	gga	ggt	gga	tct	ggc	734
Glu	Met	Gln	Ser	Ala	Gly	Ser	Gln	Arg	Gly	Arg	Gly	Gly	Gly	Ser	Gly	
206					211					216					221	

aat	ttt	atg	ggt	cgc	gga	ggg	aac	ttt	gga	ggt	ggt	gga	ggt	aat	ttt	782
Asn	Phe	Met	Gly	Arg	Gly	Gly	Asn	Phe	Gly	Gly	Gly	Gly	Gly	Asn	Phe	
222					227					232					237	

ggc	cgt	ggt	gga	aac	ttt	ggt	gga	aga	gga	ggc	tat	ggt	ggt	gga	ggt	830
Gly	Arg	Gly	Gly	Asn	Phe	Gly	Gly	Arg	Gly	Gly	Tyr	Gly	Gly	Gly	Gly	
238					243					248					253	

ggt	ggc	agc	aga	ggt	agt	tat	gga	gga	ggt	gat	ggt	gga	tat	aat	gga	878
Gly	Gly	Ser	Arg	Gly	Ser	Tyr	Gly	Gly	Gly	Asp	Gly	Gly	Tyr	Asn	Gly	
254					259					264					269	

ttt	gga	ggt	gat	ggt	ggc	aac	tat	ggc	ggt	ggt	cct	ggt	tat	agt	agt	926
Phe	Gly	Gly	Asp	Gly	Gly	Asn	Tyr	Gly	Gly	Gly	Pro	Gly	Tyr	Ser	Ser	
270					275					280					285	

aga	ggg	ggc	tat	ggt	ggt	ggt	gga	cca	gga	tat	gga	aac	caa	ggt	ggt	974
Arg	Gly	Gly	Tyr	Gly	Gly	Gly	Gly	Pro	Gly	Tyr	Gly	Asn	Gln	Gly	Gly	
286					291					296					301	

gga	tat	ggt	gga	ggt	gga	gga	tat	gat	ggt	tac	aat	gaa	gga	gga	aat	1022
Gly	Tyr	Gly	Gly	Gly	Gly	Gly	Tyr	Asp	Gly	Tyr	Asn	Glu	Gly	Gly	Asn	
302					307					312					317	

ttt	ggc	ggt	ggt	aac	tat	ggt	ggt	ggt	ggg	aac	tat	aat	gat	ttt	gga	1070
Phe	Gly	Gly	Gly	Asn	Tyr	Gly	Gly	Gly	Gly	Asn	Tyr	Asn	Asp	Phe	Gly	
318					323					328					333	

aat	tat	agt	gga	caa	cag	caa	tca	aat	tat	gga	ccc	atg	aaa	ggg	ggc	1118
Asn	Tyr	Ser	Gly	Gln	Gln	Gln	Ser	Asn	Tyr	Gly	Pro	Met	Lys	Gly	Gly	
334					339					344					349	

agt	ttt	ggt	gga	aga	agc	tcg	ggc	agt	ccc	tat	ggt	ggt	ggt	tat	gga	1166
Ser	Phe	Gly	Gly	Arg	Ser	Ser	Gly	Ser	Pro	Tyr	Gly	Gly	Gly	Tyr	Gly	
350					355					360					365	

tct	ggt	ggt	gga	agt	ggt	gga	tat	ggt	agc	aga	agg	ttc	taa	aaacagc		1215
Ser	Gly	Gly	Gly	Ser	Gly	Gly	Tyr	Gly	Ser	Arg	Arg	Phe	*			
366					371					376						

agaaaagggc	tacagttctt	agcaggagag	agagcgagga	gttgtcagga	aagctgcagg		1275
------------	------------	------------	------------	------------	------------	--	------

ttacttttgag	acagtcgtcc	caaatgcatt	agaggaactg	taaaaatctg	ccacagaagg		1335
-------------	------------	------------	------------	------------	------------	--	------

aacgatgadc	catagtcaga	aaagttactg	cagcttaaac	aggaaccctt	cttgttcagg		1395
------------	------------	------------	------------	------------	------------	--	------

actgtcatag	ccacagtttg	caaaagtgcg	gctattgatt	aatgcatgta	gtgtcaatta		1455
------------	------------	------------	------------	------------	------------	--	------

gatgtcaatc	ctgaggcttt	tatctgttgt	gcttgccctt	tcctttcctt			1505
------------	------------	------------	------------	------------	--	--	------

<210> 545
 <211> 1440
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (168)..(542)

<400> 545

```

atttggccct cgaggccaag aattcggcac gaggggtcatg aatcatgtga cgggtggcttg      60
aggaggaacc tgtctttaa gctgtccctg aagtgcacgc ggagagaacc aggcagccca      120
gaaacccag gcgtggagat tgatcctgcg agagaagggg gttcatc  atg gcg gat      176
                                     Met Ala Asp
                                     1

gac cta aag cga ttc ttg tat aaa aag tta cca agt gtt gaa ggg ctc      224
Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val Glu Gly Leu
  4                      9                      14                      19

cat gcc att gtt gtg tca gat aga gat gga gta cct gtt att aaa gtg      272
His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val Ile Lys Val
  20                      25                      30                      35

gca aat gac aat gct cca gag cat gct ttg cga cct ggt ttc tta tcc      320
Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly Phe Leu Ser
  36                      41                      46                      51

act ttt gcc ctt gca aca gac caa gga agc aaa ctt gga ctt tcc aaa      368
Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly Leu Ser Lys
  52                      57                      62                      67

aat aaa agt atc atc tgt tac tat aac acc tac cag gtg gtt caa ttt      416
Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val Val Gln Phe
  68                      73                      78                      83

aat cgt tta cct ttg gtg gtg agt ttc ata gcc agc agc agt gcc aat      464
Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser Ser Ala Asn
  84                      89                      94                      99

aca gga cta att gtc agc cta gaa aag gaa ctt gct cca ttg ttt gaa      512
Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro Leu Phe Glu
  100                      105                      110                      115

gaa ctg aga caa gtt gtg gaa gtt tct taa t ctgacagtgg tttcagtgtg      563
Glu Leu Arg Gln Val Val Glu Val Ser *
  116                      121

taccttatct tcattataac aacacaatat caatccagca atctttagac tacaataata      623
cttttatcca tgtgtcaag aaagggcccc tttttccaac ttatactaaa gagctagcat      683

```


atagatgtaa tttatagata gatcagttgc tatatcttct ggtgtagggc ctttcttatt	743
tagtgagatc tagggatacc acagaaatgg ttcagtttat cacagctccc atggagttag	803
tctggtcacc agatatggat gagagattct attcagtgga tcagaatcaa actggtacat	863
tgatccactt gagccgttaa gtgctgcaa ttgtacaata tgcccaggct tgcagaataa	923
agccaacttt ttattgtgaa taataataag gacatatttt tcttcagatt atgttttatt	983
tctttgcatt gagtgaggaa cataaaatgg cttggtaaaa gtaataaaat cagtacaatc	1043
actaactttc ctttgtacat attatcttgc agtatagatg aatattacta atcagtttga	1103
ttattctcag aggggtgctgc tctttaatga aaatgaaaat tatagctaata gttttttcct	1163
caaactctgc tttctgtaac caatcagttg tttaatgttt gtgtgttctt cataaaattt	1223
aaatacaatt cgttattctg tttccaatgt tagtatgtat gtaaacaatga tagtacagcc	1283
atctttttca tatgtgagta aaaataaaat agtattttta aaaatatagt ttgagcactg	1343
tataggtcct tttttgttc agactttttc caaaaatcta aacataatta atatactctt	1403
tcagccacat gaataaataa tgagtgtttc ttgtaaa.	1440

<210> 546
 <211> 1288
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (95) .. (928)

<400> 546	
accggcccgg aattcccggg tcgaccacg cgtccgcgcg gggcctgggg aaggggcggg	60
cgcggggacc cgatgcgcgg gagcggaggg cgag	112
atg gct tcg gcg gga ggc	
Met Ala Ser Ala Gly Gly	
1	
gaa gac tgc gag agc ccc gcg ccg gag gcc gac cgt ccg cac cag cgg	160
Glu Asp Cys Glu Ser Pro Ala Pro Glu Ala Asp Arg Pro His Gln Arg	
7 12 17 22	
ccc ttc ctg ata ggg gtg agc ggc ggc act gcc agc ggg aag tcg acc	208
Pro Phe Leu Ile Gly Val Ser Gly Gly Thr Ala Ser Gly Lys Ser Thr	
23 28 33 38	
gtg tgt gag aag atc atg gag ttg ctg gga cag aac gag gtg gaa cag	256
Val Cys Glu Lys Ile Met Glu Leu Leu Gly Gln Asn Glu Val Glu Gln	
39 44 49 54	

cgg cag cgg aag gtg gtc atc ctg agc cag gac agg ttc tac aag gtc	304
Arg Gln Arg Lys Val Val Ile Leu Ser Gln Asp Arg Phe Tyr Lys Val	
55 60 65 70	
ctg acg gca gag cag aag gcc aag gcc ttg aaa gga cag tac aat ttt	352
Leu Thr Ala Glu Gln Lys Ala Lys Ala Leu Lys Gly Gln Tyr Asn Phe	
71 76 81 86	
gac cat cca gat gcc ttt gat aat gat ttg atg cac agg act ctg aag	400
Asp His Pro Asp Ala Phe Asp Asn Asp Leu Met His Arg Thr Leu Lys	
87 92 97 102	
aac atc gtg gag ggc aaa acg gtg gag gtg ccg acc tat gat ttt gtg	448
Asn Ile Val Glu Gly Lys Thr Val Glu Val Pro Thr Tyr Asp Phe Val	
103 108 113 118	
aca cac tca agg tta cca gag acc acg gtg gtc tac cct gcg gac gtg	496
Thr His Ser Arg Leu Pro Glu Thr Thr Val Tyr Pro Ala Asp Val	
119 124 129 134	
gtt ctg ttt gag ggc atc ttg gtg ttc tac agc cag gag atc cgg gac	544
Val Leu Phe Glu Gly Ile Leu Val Phe Tyr Ser Gln Glu Ile Arg Asp	
135 140 145 150	
atg ttc cac ctg cgc ctc ttc gtg gac acc gac tcc gac gtc agg ctg	592
Met Phe His Leu Arg Leu Phe Val Asp Thr Asp Ser Asp Val Arg Leu	
151 156 161 166	
tct cga aga gtt ctc cgg gac gtg cgc cga ggg agg gac ctg gag cag	640
Ser Arg Arg Val Leu Arg Asp Val Arg Arg Gly Arg Asp Leu Glu Gln	
167 172 177 182	
att ctg acg cag tac acc acc ttc gtg aag ccg gcc ttc gag gag ttc	688
Ile Leu Thr Gln Tyr Thr Thr Phe Val Lys Pro Ala Phe Glu Glu Phe	
183 188 193 198	
tgc ctg ccg aca aag aag tat gcc gat gtg atc atc cca cga gga gtg	736
Cys Leu Pro Thr Lys Lys Tyr Ala Asp Val Ile Ile Pro Arg Gly Val	
199 204 209 214	
gac aat atg gtt gcc atc aac ctg atc gtg cag cac atc cag gac att	784
Asp Asn Met Val Ala Ile Asn Leu Ile Val Gln His Ile Gln Asp Ile	
215 220 225 230	
ctg aat ggt gac atc tgc aaa tgg cac cga gga ggg tcc aat ggg cgg	832
Leu Asn Gly Asp Ile Cys Lys Trp His Arg Gly Gly Ser Asn Gly Arg	
231 236 241 246	
agc tac aag cgg acc ttt tct gag cca ggg gac cac cct ggg atg ctg	880
Ser Tyr Lys Arg Thr Phe Ser Glu Pro Gly Asp His Pro Gly Met Leu	
247 252 257 262	
acc tct ggc aaa cgg tca cat ttg gag tcc agc agc aga ccc cac tga	928
Thr Ser Gly Lys Arg Ser His Leu Glu Ser Ser Ser Arg Pro His *	
263 268 273 278	
ggggctgccg agcctcaggg caggtctccc gcccgcatg tgtgttcagg aactgagcct	988

ggggacgccc acccacacccc actgctatgt ggagctcaca gcctcacatg tgaacacccg 1048
 tgtctggggtt gcctgggggtg atcctccctc ctgcgtgggtg gctgtctctg gaaagcatcc 1108
 cttgccgctg ccacgggcag cccagcccc cgtcctgcca ggctcaccca cagtagtgat 1168
 gcagacgtga cgtgggggaa gggggctgag cctgtgggt gggttctgac aactgtaacg 1228
 gttttgtcga gcttaggccc ctttggaggg agaatcaata aataacaaac accaactaaa 1288

<210> 547
 <211> 2670
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (107)..(634)

<400> 547
 gcacgagctt cccttgagt cataggtccc gggttggtaga gggtttgagt ccgcacgccc 60
 acagctgaag gctgagggg actaagagca gaatatatct ttagaa atg agt tgc 115
 Met Ser Cys
 1
 aca att gag aag gca ctt gcc gac gct aaa gct ctt gtt gaa aga tta 163
 Thr Ile Glu Lys Ala Leu Ala Asp Ala Lys Ala Leu Val Glu Arg Leu
 4 9 14 19
 aga gat cat gac gat gca gca gaa tot ctg att gag caa acc aca gct 211
 Arg Asp His Asp Asp Ala Ala Glu Ser Leu Ile Glu Gln Thr Thr Ala
 20 25 30 35
 ctc aac aag cga gta gaa gcc atg aaa cag tat cag gaa gaa att caa 259
 Leu Asn Lys Arg Val Glu Ala Met Lys Gln Tyr Gln Glu Glu Ile Gln
 36 41 46 51
 gaa ctt aat gaa gtc gcg aga cat cgg cca cgg tcc acg tta gtt atg 307
 Glu Leu Asn Glu Val Ala Arg His Arg Pro Arg Ser Thr Leu Val Met
 52 57 62 67
 gga atc cag caa gaa aac aga caa atc aga gag ttg caa caa gaa aac 355
 Gly Ile Gln Gln Glu Asn Arg Gln Ile Arg Glu Leu Gln Gln Glu Asn
 68 73 78 83
 aaa gaa tta cgt aca tct ctg gaa gaa cat cag tcg gcc ttg gaa ctt 403
 Lys Glu Leu Arg Thr Ser Leu Glu Glu His Gln Ser Ala Leu Glu Leu
 84 89 94 99
 ata atg agc aag tac cga gaa caa atg ttt aga ttg cta atg gct agc 451
 Ile Met Ser Lys Tyr Arg Glu Gln Met Phe Arg Leu Leu Met Ala Ser
 100 105 110 115

aaa aaa gat gat ccg ggt ata ata atg aag tta aaa gag cag cac tcc	499
Lys Lys Asp Asp Pro Gly Ile Ile Met Lys Leu Lys Glu Gln His Ser	
116 121 126 131	
aag gaa ctg caa gca cat gtt gac cag ata act gaa atg gca gca gta	547
Lys Glu Leu Gln Ala His Val Asp Gln Ile Thr Glu Met Ala Ala Val	
132 137 142 147	
atg agg aag cca ttg aaa ttg acg agc aac agg gtt gca agg aac aag	595
Met Arg Lys Pro Leu Lys Leu Thr Ser Asn Arg Val Ala Arg Asn Lys	
148 153 158 163	
aac gaa tat ttc aac ttg aac aag aaa aca aag gct tga gagagatcct	644
Asn Glu Tyr Phe Asn Leu Asn Lys Lys Thr Lys Ala *	
164 169 174	
tcaaataact cgagaatcat ttttgaacct aaggaaagat gatgcgtcgg aaagtacttc	704
tttgtcagca ttagtgacca acagtgattt gagtctgagg aagagctgaa gagtttctga	764
gtctgtgagc ttcttacatg gctccaaatg gtcaaataag tgaatgaatg aatggacaga	824
aaattcaatc ctttattttt ttctctgtaa atatgtacag tgcacgggct atgagatagc	884
aacaaaaaat gcatagttaa tgggtcataga ctttattcca aaacataatt ggaaaaataga	944
aactgagcca ttgccaaatg gtaaagaaat gaaaagtttt cacagtgact actgaatata	1004
ccaagagctt ttggcagtac tgctggcttt ctgggtgatt aattaggtaa acttgaatat	1064
tcccagtaaa tgtttgagaa tgcataaaat tataccaatt taaaaatata aatttttgcc	1124
actgttttgt gaacggagga tttgtacgct aaatttcatc cttatttggc gtcaaagttg	1184
atgcaaagtt tatgtaccat gagacttcta gtgattgcct actttcacat ttatttaa	1244
ttttgtgaaa gaaaatacag ttttaaaggc tataggaatg tggtatatgt accttaaaca	1304
gataatttaa ttttagcaat ttatcataac tgatacttag ctaacaattg tccataactt	1364
gtttaagtgt aagaaatacc atttcaggaa tgaaaaagaa ggaatactac tttctaagaa	1424
agaagatctt ataatagaca tatttagtag gttaaactac tcctttgaaa gaataagttt	1484
tggttcaaag tcaataatga agacgagatt tgttttctc ttctctggct gatttttaag	1544
gatattatgt agttcattta gttaacagaa ttgaaatggt tgatatggca agataggtat	1604
ggtaatttca aagtgaattg ggaattcctc tgggtcatag aacccttttt ttttccctt	1664
aagtattctt gagatacaaa aaaaaaaggt aaatacaatt tcaaaaaaaa aagttccgga	1724
tctgttttta agctccatct ggtcctcata acctgcaaga ttttctttaa aacctttcag	1784
ctgaaagtgg gggtaaaggt ggagtaatct gtggatttgt ttctgttgct ttttaaatg	1844

tcaaataatat aatatgtaat ttttttaaaa accaccagat acagaaatgt gctttaacat	1904
cagttgaaac cttaaattttc ttatgttgtg gtgattgtat taaaaaggga taaaagaaga	1964
gtgtcaaaca tgggttaaata tattgtactc atttatgttg aatacgtatt aaaattaaga	2024
caagtggaaa attatacttt gagtatataa tttgttaaat attactttat atggtaat	2084
tatgtataat ttcatatatt ggtaaaatc aaaactacac ttgagaat	2144
agtttggggt gaatggggtg gatgagactg attgaataga aaagggctaa tggcccaa	2204
attatataga tttctttttt tcagtcagag gccttatttg atattttata aataaatgac	2264
agtttttatt tttaaacttt ttattgtttt tgggaaagta ttccttaatt taatgacaca	2324
ttcattcaga tacttcttat ccctgcta	2384
agattaagtc tgaggcagtt cattgaggca gctctactat aaaagcttac ttgataaata	2444
attat	2504
taaggcttc atgtttaaag acatttactt tgttatttag tgacacattt ccac	2564
ttttttttt tttttgggtg ttgttaaaca gaaccttaag tttatgtttg aggtatgtac	2624
tgcataggaa cctat	2670

<210> 548
 <211> 1764
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (365)..(916)

<400> 548	
atccgcttcg ccggaacaat cctgtgagtt tatgatct gctatacaga tgaggataac	60
agaagttgac taacttgccc aagtcacaag tttgtaaaga tggatctggg atttaaacc	120
agtgagtgat ggattggaac tgagaccgaa atataatgga attttacatt gcttgactac	180
catttgga	240
tgaggttta tctgggggac totactttt cttttacaat gccatcaagt catataaac	300
agaaggaaga gctgaacgtt tagaggcaac agaatacctt gtctcagctg ctgaagctg	360
agcc atg acc ctc tgc att aca aac cca tta tgg gta aca aaa act cgc	409
Met Thr Leu Cys Ile Thr Asn Pro Leu Trp Val Thr Lys Thr Arg	
1 5 10	

ctt atg tta cag tat gat gct gtt gtt aac tcc cca cac cga caa tat	457
Leu Met Leu Gln Tyr Asp Ala Val Val Asn Ser Pro His Arg Gln Tyr	
16 21 26 31	
aaa gga atg ttt gat aca ctt gtg aaa ata tat aag tat gaa ggt gtg	505
Lys Gly Met Phe Asp Thr Leu Val Lys Ile Tyr Lys Tyr Glu Gly Val	
32 37 42 47	
cgt gga tta tat aag gga ttt gtt cct ggg ctg ttt gga aca tcg cat	553
Arg Gly Leu Tyr Lys Gly Phe Val Pro Gly Leu Phe Gly Thr Ser His	
48 53 58 63	
ggt gcc ctt cag ttt atg gca tat gaa ttg ctg aag ttg aag tac aac	601
Gly Ala Leu Gln Phe Met Ala Tyr Glu Leu Leu Lys Leu Lys Tyr Asn	
64 69 74 79	
cag cat atc aat aga tta cca gaa gcc cag ttg agc aca gta gaa tat	649
Gln His Ile Asn Arg Leu Pro Glu Ala Gln Leu Ser Thr Val Glu Tyr	
80 85 90 95	
ata tct gtt gca gca cta tcc aaa ata ttt gct gtc gca gca aca tac	697
Ile Ser Val Ala Ala Leu Ser Lys Ile Phe Ala Val Ala Ala Thr Tyr	
96 101 106 111	
cca tat caa gtc gta aga gct cgt ctt cag gat caa cac atg ttt tac	745
Pro Tyr Gln Val Val Arg Ala Arg Leu Gln Asp Gln His Met Phe Tyr	
112 117 122 127	
agt ggt gta ata gat gta atc aca aag aca tgg agg aaa gaa ggc gtc	793
Ser Gly Val Ile Asp Val Ile Thr Lys Thr Trp Arg Lys Glu Gly Val	
128 133 138 143	
ggt gga ttt tac aag gga att gct cct aat ttg att aga gtg act cca	841
Gly Gly Phe Tyr Lys Gly Ile Ala Pro Asn Leu Ile Arg Val Thr Pro	
144 149 154 159	
gcc tgc tgt att acc ttt gtg gta tat gaa aac gtc tca cat ttt tta	889
Ala Cys Cys Ile Thr Phe Val Val Tyr Glu Asn Val Ser His Phe Leu	
160 165 170 175	
ctt gac ctt aga gaa aag aga aag taa gctca aagaggacaa ttccagtata	941
Leu Asp Leu Arg Glu Lys Arg Lys *	
176 181	
tctgcccaag gcagcaacaa gctcttttgt gtttaaggca taaaagaaga attctgcata	1001
gaaacatggc tcatattcga aattgctcta tagtcattag aagccagaga actgctaagt	1061
ctcctgcaat gtttttctgc tttttgcctt ccccatatat atggaacttg gctacctctg	1121
cctgaaatgg ctgccatcaa cacaatgtta aaactgacac gaagtataga gtttcacaga	1181
tttctacgtt ttattggtgg aagctgattt gcaacatttg ctaaattggat tagatgaatg	1241
tacttctttt tgtgagctta cttgcctgga ttgctttaaa attaaccttt gtgcaatacc	1301
aagaaaatag ctctttaaaa gaatgtcttt gtatgtctca aggtaaatta aggatttact	1361

```

gaataagggtg ttgaccaaatt ccagaccatt ttatttttatt tttttattta tttatttttt 1421
gagatggagt cttgctttgt cgcccaggct ggagtgcagt ggctgatct cagctcactg 1481
caacctccac ctcccgggtt cagccattc tctgctca gcctcctgag tagctgggac 1541
tacaggcacc tgccaccacg cctggctaac ttttttttat attttgagta gaaatggggg 1601
ttcaccatgt tagccaggat gggctcaatc tctgacctt gtgatccgcc tgccttggcc 1661
tcccaaagtg ctgggattac aggcgtgagc cactgcgcct ggccagacca ttttagaatt 1721
gggaaattgt agtgagaaaa aatgcactgt aaatatgctt tat 1764

```

```

<210> 549
<211> 2482
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (50)..(2164)

```

```

<400> 549
aaggatcctt aattaaatta atcccccccc ccccccgagg gagtaacgac atg gcg 55
Met Ala
1

cgc gag ctg cgg gcg ctg ctg ctg tgg ggc cgc cgc ctg cgg cct ttg 103
Arg Glu Leu Arg Ala Leu Leu Leu Trp Gly Arg Arg Leu Arg Pro Leu
3 8 13 18

ctg cgg gcg ccg gcg ctg gcg gcc gtg ccg gga gga aaa cca att ctg 151
Leu Arg Ala Pro Ala Leu Ala Ala Val Pro Gly Gly Lys Pro Ile Leu
19 24 29 34

tgt cct cgg agg acc aca gcc cag ttg ggc ccc agg cga aac cca gcc 199
Cys Pro Arg Arg Thr Thr Ala Gln Leu Gly Pro Arg Arg Asn Pro Ala
35 40 45 50

tgg agc ttg cag gca gga cga ctg ttc agc acg cag acc gcc gag gac 247
Trp Ser Leu Gln Ala Gly Arg Leu Phe Ser Thr Gln Thr Ala Glu Asp
51 56 61 66

aag gag gaa ccc ctg cac tcg att atc agc agc aca gag agc gtg cag 295
Lys Glu Glu Pro Leu His Ser Ile Ile Ser Ser Thr Glu Ser Val Gln
67 72 77 82

ggg tcc act tcc aaa cat gag ttc cag gcc gag aca aag aag ctt ttg 343
Gly Ser Thr Ser Lys His Glu Phe Gln Ala Glu Thr Lys Lys Leu Leu
83 88 93 98

gac att gtt gcc cgg tcc ctg tac tca gaa aaa gag gtg ttt ata cgg 391

```

Asp	Ile	Val	Ala	Arg	Ser	Leu	Tyr	Ser	Glu	Lys	Glu	Val	Phe	Ile	Arg		
99					104					109					114		
gag	ctg	atc	tcc	aat	gcc	agc	gat	gcc	ttg	gaa	aaa	ctg	cgt	cac	aaa	439	
Glu	Leu	Ile	Ser	Asn	Ala	Ser	Asp	Ala	Leu	Glu	Lys	Leu	Arg	His	Lys		
115					120					125					130		
ctg	gtg	tct	gac	ggc	caa	gca	ctg	cca	gaa	atg	gag	att	cac	ttg	cag	487	
Leu	Val	Ser	Asp	Gly	Gln	Ala	Leu	Pro	Glu	Met	Glu	Ile	His	Leu	Gln		
131					136					141					146		
acc	aat	gcc	gag	aaa	ggc	acc	atc	acc	atc	cag	gat	act	ggg	atc	ggg	535	
Thr	Asn	Ala	Glu	Lys	Gly	Thr	Ile	Thr	Ile	Gln	Asp	Thr	Gly	Ile	Gly		
147					152					157					162		
atg	aca	cag	gaa	gag	ctg	gtg	tcc	aac	ctg	ggg	acg	att	gcc	aga	tcg	583	
Met	Thr	Gln	Glu	Glu	Leu	Val	Ser	Asn	Leu	Gly	Thr	Ile	Ala	Arg	Ser		
163					168					173					178		
ggg	tca	aag	gcc	ttc	ctg	gat	gct	ctg	cag	aac	cag	gct	gag	gcc	agc	631	
Gly	Ser	Lys	Ala	Phe	Leu	Asp	Ala	Leu	Gln	Asn	Gln	Ala	Glu	Ala	Ser		
179					184					189					194		
agc	aag	atc	atc	ggc	cag	ttt	gga	gtg	ggg	ttc	tac	tca	gct	ttc	atg	679	
Ser	Lys	Ile	Ile	Gly	Gln	Phe	Gly	Val	Gly	Phe	Tyr	Ser	Ala	Phe	Met		
195					200					205					210		
gtg	gct	gac	aga	gtg	gag	gtc	tat	tcc	cgc	tcg	gca	gcc	ccg	ggg	agc	727	
Val	Ala	Asp	Arg	Val	Glu	Val	Tyr	Ser	Arg	Ser	Ala	Ala	Pro	Gly	Ser		
211					216					221					226		
ctg	ggg	tac	cag	tgg	ctt	tca	gat	ggg	tct	gga	gtg	ttt	gaa	atc	gcc	775	
Leu	Gly	Tyr	Gln	Trp	Leu	Ser	Asp	Gly	Ser	Gly	Val	Phe	Glu	Ile	Ala		
227					232					237					242		
gaa	gct	tcg	gga	gtt	aga	acc	ggg	aca	aaa	atc	atc	atc	cac	ctg	aaa	823	
Glu	Ala	Ser	Gly	Val	Arg	Thr	Gly	Thr	Lys	Ile	Ile	Ile	His	Leu	Lys		
243					248					253					258		
tcc	gac	tgc	aag	gag	ttt	tcc	agc	gag	gcc	cgg	gtg	cga	gat	gtg	gta	871	
Ser	Asp	Cys	Lys	Glu	Phe	Ser	Ser	Glu	Ala	Arg	Val	Arg	Asp	Val	Val		
259					264					269					274		
acg	aag	tac	agc	aac	ttc	gtc	agc	ttc	ccc	ttg	tac	ttg	aat	gga	agg	919	
Thr	Lys	Tyr	Ser	Asn	Phe	Val	Ser	Phe	Pro	Leu	Tyr	Leu	Asn	Gly	Arg		
275					280					285					290		
cgg	atg	aac	acc	ttg	cag	gcc	atc	tgg	atg	atg	gac	ccc	aag	gat	gtc	967	
Arg	Met	Asn	Thr	Leu	Gln	Ala	Ile	Trp	Met	Met	Asp	Pro	Lys	Asp	Val		
291					296					301					306		
cgt	gag	tgg	caa	cat	gag	gag	ttc	tac	cgc	tac	gtc	gcg	cag	gct	cac	1015	
Arg	Glu	Trp	Gln	His	Glu	Glu	Phe	Tyr	Arg	Tyr	Val	Ala	Gln	Ala	His		
307					312					317					322		
gac	aag	ccc	cgc	tac	acc	ctg	cac	tat	aag	acg	gac	gca	ccg	ctc	aac	1063	
Asp	Lys	Pro	Arg	Tyr	Thr	Leu	His	Tyr	Lys	Thr	Asp	Ala	Pro	Leu	Asn		

323	328	333	338	
atc cgc agc atc ttc tac gtg ccc gac atg aaa ccg tcc atg ttt gat				1111
Ile Arg Ser Ile Phe Tyr Val Pro Asp Met Lys Pro Ser Met Phe Asp				
339	344	349	354	
gtg agc cgg gag ctg ggc tcc agc gtt gca ctg tac agc cgc aaa gtc				1159
Val Ser Arg Glu Leu Gly Ser Ser Val Ala Leu Tyr Ser Arg Lys Val				
355	360	365	370	
ctc atc cag acc aag gcc acg gac atc ctg ccc aag tgg ctg cgc ttc				1207
Leu Ile Gln Thr Lys Ala Thr Asp Ile Leu Pro Lys Trp Leu Arg Phe				
371	376	381	386	
atc cga ggt gtg gtg gac agt gag gac att ccc ctg aac ctc agc cgg				1255
Ile Arg Gly Val Val Asp Ser Glu Asp Ile Pro Leu Asn Leu Ser Arg				
387	392	397	402	
gag ctg ctg cag gag agc gca ctc atc agg aaa ctc cgg gac gtt tta				1303
Glu Leu Leu Gln Glu Ser Ala Leu Ile Arg Lys Leu Arg Asp Val Leu				
403	408	413	418	
cag cag agg ctg atc aaa ttc ttc att gac cag agt aaa aaa gat gct				1351
Gln Gln Arg Leu Ile Lys Phe Phe Ile Asp Gln Ser Lys Lys Asp Ala				
419	424	429	434	
gag aag tat gca aag ttt ttt gaa gat tac ggc ctg ttc atg cgg gag				1399
Glu Lys Tyr Ala Lys Phe Phe Glu Asp Tyr Gly Leu Phe Met Arg Glu				
435	440	445	450	
ggc att gtg acc gcc acc gag cag gag gtc aag gag gac ata gca aag				1447
Gly Ile Val Thr Ala Thr Glu Gln Glu Val Lys Glu Asp Ile Ala Lys				
451	456	461	466	
ctg ctg cgc tac gag tcc tcc ggc ctg ccc tcc ggg cag cta acc agc				1495
Leu Leu Arg Tyr Glu Ser Ser Ala Leu Pro Ser Gly Gln Leu Thr Ser				
467	472	477	482	
ctc tca gaa tac gcc agc cgc atg cgg gcc ggc acc cgc aac atc tac				1543
Leu Ser Glu Tyr Ala Ser Arg Met Arg Ala Gly Thr Arg Asn Ile Tyr				
483	488	493	498	
tac ctg tgc gcc ccc aac cgt cac ctg gca gag cac tca ccc tac tat				1591
Tyr Leu Cys Ala Pro Asn Arg His Leu Ala Glu His Ser Pro Tyr Tyr				
499	504	509	514	
gag gcc atg aag aag aaa gac aca gag gtt ctc ttc tgc ttt gag cag				1639
Glu Ala Met Lys Lys Lys Asp Thr Glu Val Leu Phe Cys Phe Glu Gln				
515	520	525	530	
ttt gat gag ctc acc ctg ctg cac ctt cgt gag ttt gac aag aag aag				1687
Phe Asp Glu Leu Thr Leu Leu His Leu Arg Glu Phe Asp Lys Lys Lys				
531	536	541	546	
ctg atc tct gtg gag acg gac ata gtc gtg gat cac tac aag gag gag				1735
Leu Ile Ser Val Glu Thr Asp Ile Val Val Asp His Tyr Lys Glu Glu				
547	552	557	562	

aag ttt gag gac agg tcc cca gcc gcc gag tgc cta tca gag aag gag	1783
Lys Phe Glu Asp Arg Ser Pro Ala Ala Glu Cys Leu Ser Glu Lys Glu	
563 568 573 578	
acg gag gag ctc atg gcc tgg atg aga aat gtg ctg ggg tog cgt gtc	1831
Thr Glu Glu Leu Met Ala Trp Met Arg Asn Val Leu Gly Ser Arg Val	
579 584 589 594	
acc aac gtg aag gtg acc ctc cga ctg gac acc cac cct gcc atg gtc	1879
Thr Asn Val Lys Val Thr Leu Arg Leu Asp Thr His Pro Ala Met Val	
595 600 605 610	
acc gtg ctg gag atg ggg gct gcc cgc cac ttc ctg cgc atg cag cag	1927
Thr Val Leu Glu Met Gly Ala Ala Arg His Phe Leu Arg Met Gln Gln	
611 616 621 626	
ctg gcc aag acc cag gag gag cgc gca cag ctc ctg cag ccc acg ctg	1975
Leu Ala Lys Thr Gln Glu Glu Arg Ala Gln Leu Leu Gln Pro Thr Leu	
627 632 637 642	
gag atc aac ccc agg cac gcg ctc atc aag aag ctg aat cag ctg cgc	2023
Glu Ile Asn Pro Arg His Ala Leu Ile Lys Lys Leu Asn Gln Leu Arg	
643 648 653 658	
gca agc gag cct ggc ctg gct cag ctg ctg gtg gat cag ata tac gag	2071
Ala Ser Glu Pro Gly Leu Ala Gln Leu Leu Val Asp Gln Ile Tyr Glu	
659 664 669 674	
aac gcc atg att gct gct gga ctt gtt gac gac cct agg gcc atg gtg	2119
Asn Ala Met Ile Ala Ala Gly Leu Val Asp Asp Pro Arg Ala Met Val	
675 680 685 690	
ggc cgc ttg aat gag ctg ctt gtc aag gcc ctg gag cga cac tga cag	2167
Gly Arg Leu Asn Glu Leu Leu Val Lys Ala Leu Glu Arg His *	
691 696 701	
ccagggggcc agaaggactg acaccacaga tgacagcccc acctccttga gctttattta	2227
cctaaattta aaggatatttc ttaacccgag tgttgtgttg gctttttttc tgggtcctgt	2287
ggcaggatgg gtcctctctc cctgcagttc aactggtgtg gggaggggct gctcacttca	2347
gcacaccct cactggatag tggtcactga tggcttgggc tgcaggcaag tgggcacagg	2407
gtctggctga gcctacctga gctcctccct cgtgccgaac tggtcgtcga gggccaaatt	2467
ccatatagt cccgt	2482

<210> 550
 <211> 1187
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (64)..(759)

<220>
 <221> misc_feature
 <222> (1)...(1187)
 <223> n = a,t,c or g

<400> 550

aatacaagct acttggttctt tttgcaggat cccatcgatt cgaattcggc acgagcgcga	60
acc atg gcc ggc atg gtg gac ttc cag gat gag gag cag gtc aag tcc	108
Met Ala Gly Met Val Asp Phe Gln Asp Glu Glu Gln Val Lys Ser	
1 5 10	
ttt ttg gag aac atg gag gtg gag tgc aac tac cac tgc tac cac gag	156
Phe Leu Glu Asn Met Glu Val Glu Cys Asn Tyr His Cys Tyr His Glu	
16 21 26 31	
aag gac ccg gac ggt tgc tat cgg ctg gtg gac tat ttg gaa ggg atc	204
Lys Asp Pro Asp Gly Cys Tyr Arg Leu Val Asp Tyr Leu Glu Gly Ile	
32 37 42 47	
cgg aag aat ttt gat gag gct gcc aag gtg ttg aag ttt aac tgt gaa	252
Arg Lys Asn Phe Asp Glu Ala Ala Lys Val Leu Lys Phe Asn Cys Glu	
48 53 58 63	
gag aac cag cac agt gat agc tgc tac aaa ctg ggg gcc tac tat gtg	300
Glu Asn Gln His Ser Asp Ser Cys Tyr Lys Leu Gly Ala Tyr Tyr Val	
64 69 74 79	
act gga aaa ggt ggt ctg acc cag gac ctg aaa gct gcc gcc agg tgc	348
Thr Gly Lys Gly Gly Leu Thr Gln Asp Leu Lys Ala Ala Ala Arg Cys	
80 85 90 95	
ttt ttg atg gcg tgt gag aag cct gga aag aag tca ata gca gca tgt	396
Phe Leu Met Ala Cys Glu Lys Pro Gly Lys Lys Ser Ile Ala Ala Cys	
96 101 106 111	
cac aac gtt ggc ctc ctg gca cat gat gga cag gtt aat gag gat ggc	444
His Asn Val Gly Leu Leu Ala His Asp Gly Gln Val Asn Glu Asp Gly	
112 117 122 127	
cag cct gac ttg gga aag gcc agg gac tac tac aca agg gcc tgt gat	492
Gln Pro Asp Leu Gly Lys Ala Arg Asp Tyr Tyr Thr Arg Ala Cys Asp	
128 133 138 143	
ggg ggc tat act tcc agt tgc ttc aac ctc agt gcc atg ttc ctg cag	540
Gly Gly Tyr Thr Ser Ser Cys Phe Asn Leu Ser Ala Met Phe Leu Gln	
144 149 154 159	
ggg gcc cca ggc ttt ccc aag gac atg gac ctg gca tgt aaa tac tcc	588
Gly Ala Pro Gly Phe Pro Lys Asp Met Asp Leu Ala Cys Lys Tyr Ser	
160 165 170 175	
atg aaa gcc tgt gac ctg ggt cat atc tgg gcc tgt gcc aat gcc agt	636

[illegible]

```
<220>  
<221> CDS  
<222> (67)..(510)
```

tccagc	atg gcc tgg tct cct ctc ctc ctc act ctc ctc gct cac tgc	108
	Met Ala Trp Ser Pro Leu Leu Leu Thr Leu Leu Ala His Cys	
	1 5 10	
aca ggg tcc tgg gcc cag tct gtg ctg acg cag ccg ccc tca gtg tct	156	
Thr Gly Ser Trp Ala Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser		
15 20 25 30		
ggg gcc cca ggg cag agg gtc acc atc tcc tgc act ggg agc agc tcc	204	
Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser		
31 36 41 46		

[illegible]

```
<210> 552
<211> 3582
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (392)..(2647)

<220>
<221> misc_feature
<222> (1)..(3582)
<223> n = a,t,c or g
```

<400>	552						
cgagactcaa	gaaaatcctg	agatcagtac	gaccgtgcga	aagtncgta	tgcacctacg		60
cgtdccggcaa	gacctcatct	gctggtgtac	ctcatccttt	tagcccctct	ttgatgtttg		120
ctgcaaacgt	caccagctc	ctggggcaca	ctggactccc	agatgagctt	gtcctggatt		180
tgcaggggagc	ctggctccct	aaaccttttg	gccagatccc	cacaggggaa	ttgtgcaggt		240
gcgccctccc	cagatcccca	gctggtattg	gaatcacacc	aactgtcaca	catggggagg		300

gcagctgcac ccagccaccc tctgacttct ctctgccac agattggcca tctgcaagct	360
tcccttctcc gtggagagca ggaagacagt c atg gga cct cag gga gcc agg	412
Met Gly Pro Gln Gly Ala Arg	
1 5	
aga cag gct ttc ttg gca ttt ggg gat gtc act gtg gat ttc acc cag	460
Arg Gln Ala Phe Leu Ala Phe Gly Asp Val Thr Val Asp Phe Thr Gln	
8 13 18 23	
aag gaa tgg agg ctg ctg agc cct gct cag agg gcc ctg tac agg gag	508
Lys Glu Trp Arg Leu Leu Ser Pro Ala Gln Arg Ala Leu Tyr Arg Glu	
24 29 34 39	
gtg aca ctg gag aac tac agc cac ctg gtc tca cta gga att ctc cat	556
Val Thr Leu Glu Asn Tyr Ser His Leu Val Ser Leu Gly Ile Leu His	
40 45 50 55	
tct aaa cca gaa ctc atc agg cgg cta gag caa ggg gaa gtg ccc tgg	604
Ser Lys Pro Glu Leu Ile Arg Arg Leu Glu Gln Gly Glu Val Pro Trp	
56 61 66 71	
gga gaa gag aga aga cgc cgg cca ggc ccc tgt gca gga ata tat gca	652
Gly Glu Glu Arg Arg Arg Arg Pro Gly Pro Cys Ala Gly Ile Tyr Ala	
72 77 82 87	
gaa cat gtc ctg cgg ccc aag aat ctt gga ctt gca cat cag agg caa	700
Glu His Val Leu Arg Pro Lys Asn Leu Gly Leu Ala His Gln Arg Gln	
88 93 98 103	
cag caa cta caa ttt tct gat caa agc ttc cag agt gac aca gct gaa	748
Gln Gln Leu Gln Phe Ser Asp Gln Ser Phe Gln Ser Asp Thr Ala Glu	
104 109 114 119	
ggt caa gag aaa gaa aaa agc act aag ccc atg gca ttt tcc agc cca	796
Gly Gln Glu Lys Glu Lys Ser Thr Lys Pro Met Ala Phe Ser Ser Pro	
120 125 130 135	
ccc cta aga cat gca gta agc tca agg agg agg aac agt gta gtg gaa	844
Pro Leu Arg His Ala Val Ser Ser Arg Arg Arg Asn Ser Val Val Glu	
136 141 146 151	
ata gag tct agt caa ggc cag agg gaa aat cct aca gaa ata gac aaa	892
Ile Glu Ser Ser Gln Gly Gln Arg Glu Asn Pro Thr Glu Ile Asp Lys	
152 157 162 167	
gta ttg aaa gga ata gaa aat tca aga tgg gga gca ttc aag tgt gca	940
Val Leu Lys Gly Ile Glu Asn Ser Arg Trp Gly Ala Phe Lys Cys Ala	
168 173 178 183	
gag cgt ggg caa gac ttc agc cgg aag atg atg gta atc ata cac aaa	988
Glu Arg Gly Gln Asp Phe Ser Arg Lys Met Met Val Ile Ile His Lys	
184 189 194 199	
aaa gca cat tcc agg cag aaa ctt ttt aca tgc agg gag tgt cac cag	1036
Lys Ala His Ser Arg Gln Lys Leu Phe Thr Cys Arg Glu Cys His Gln	
200 205 210 215	

ggc ttt aga gat gag tca gca ttg ctc ttg cac cag aac aca cac aca	1084
Gly Phe Arg Asp Glu Ser Ala Leu Leu Leu His Gln Asn Thr His Thr	
216 221 226 231	
gga gag aag tcc tat gtg tgc agt gtg tgt ggg cga ggc ttc agc ctc	1132
Gly Glu Lys Ser Tyr Val Cys Ser Val Cys Gly Arg Gly Phe Ser Leu	
232 237 242 247	
aag gcc aac ctc ctc aga cac cag agg aca cac tca gga gag aag cct	1180
Lys Ala Asn Leu Leu Arg His Gln Arg Thr His Ser Gly Glu Lys Pro	
248 253 258 263	
ttt ctg tgc aag gtg tgt gga cga ggc tat acc agt aag tca tac ctc	1228
Phe Leu Cys Lys Val Cys Gly Arg Gly Tyr Thr Ser Lys Ser Tyr Leu	
264 269 274 279	
act gtg cat gag aga aca cac aca gga gag aag cct tat gaa tgc cag	1276
Thr Val His Glu Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Gln	
280 285 290 295	
gag tgt ggg cga agg ttt aac gat aag tcc tca tac aac aag cac ttg	1324
Glu Cys Gly Arg Arg Phe Asn Asp Lys Ser Ser Tyr Asn Lys His Leu	
296 301 306 311	
aag gcg cat tca ggg gag aag cct ttt gtg tgc aag gag tgt ggg cga	1372
Lys Ala His Ser Gly Glu Lys Pro Phe Val Cys Lys Glu Cys Gly Arg	
312 317 322 327	
ggc tat act aat aag tca tac ttc gtt gtg cac aag aga ata cac tca	1420
Gly Tyr Thr Asn Lys Ser Tyr Phe Val Val His Lys Arg Ile His Ser	
328 333 338 343	
gga gag aag cct tac aga tgc cag gag tgt ggc cga ggc ttt agc aat	1468
Gly Glu Lys Pro Tyr Arg Cys Gln Glu Cys Gly Arg Gly Phe Ser Asn	
344 349 354 359	
aag tca cac ctt atc aca cac cag agg aca cac tca ggg gag aag ccc	1516
Lys Ser His Leu Ile Thr His Gln Arg Thr His Ser Gly Glu Lys Pro	
360 365 370 375	
ttt gcg tgc agg cag tgt aag caa agt ttt agc gtg aaa gga agt ctc	1564
Phe Ala Cys Arg Gln Cys Lys Gln Ser Phe Ser Val Lys Gly Ser Leu	
376 381 386 391	
ctc aga cac cag aga aca cac tca ggg gag aag cct ttt gtg tgc aag	1612
Leu Arg His Gln Arg Thr His Ser Gly Glu Lys Pro Phe Val Cys Lys	
392 397 402 407	
gat tgt gag cga agc ttt agc caa aag tca act ctt gtc tac cac cag	1660
Asp Cys Glu Arg Ser Phe Ser Gln Lys Ser Thr Leu Val Tyr His Gln	
408 413 418 423	
aga aca cac tca ggg gag aaa cct ttt gtt tgt aga gaa tgt ggg caa	1708
Arg Thr His Ser Gly Glu Lys Pro Phe Val Cys Arg Glu Cys Gly Gln	
424 429 434 439	

gga ttt att cag aag tca acc ctt gtg aaa cat cag atc aca cac tca	1756
Gly Phe Ile Gln Lys Ser Thr Leu Val Lys His Gln Ile Thr His Ser	
440 445 450 455	
gag gag aag cct ttt gtg tgc aag gac tgt gga cga ggc ttt atc caa	1804
Glu Glu Lys Pro Phe Val Cys Lys Asp Cys Gly Arg Gly Phe Ile Gln	
456 461 466 471	
aag tca acc ttc gct tta cac cag agg aca cac tca gag gag aag cct	1852
Lys Ser Thr Phe Ala Leu His Gln Arg Thr His Ser Glu Glu Lys Pro	
472 477 482 487	
tat gga tgt cgg gag tgt ggg cgt agg ttt cgg gat aag tcc tcc tat	1900
Tyr Gly Cys Arg Glu Cys Gly Arg Arg Phe Arg Asp Lys Ser Ser Tyr	
488 493 498 503	
aac aag cac ctg agg gca cac ttg ggt gag aaa cgt ttt ttc tgc agg	1948
Asn Lys His Leu Arg Ala His Leu Gly Glu Lys Arg Phe Phe Cys Arg	
504 509 514 519	
gat tgt ggg cga ggc ttt acc ttg aag cca aat ctc acc ata cat cag	1996
Asp Cys Gly Arg Gly Phe Thr Leu Lys Pro Asn Leu Thr Ile His Gln	
520 525 530 535	
agg aca cac tca gga gag aag ccc ttc atg tgc aag cag tgt gag aaa	2044
Arg Thr His Ser Gly Glu Lys Pro Phe Met Cys Lys Gln Cys Glu Lys	
536 541 546 551	
agt ttt agt ttg aag gca aat ctt ctt aga cat cag tgg aca cac tgc	2092
Ser Phe Ser Leu Lys Ala Asn Leu Leu Arg His Gln Trp Thr His Ser	
552 557 562 567	
ggg gaa agg cca ttt aat tgc aag gat tgc ggg cga ggc ttc atc cta	2140
Gly Glu Arg Pro Phe Asn Cys Lys Asp Cys Gly Arg Gly Phe Ile Leu	
568 573 578 583	
aaa tca act ctc ctc ttc cac cag aag aca cac tca ggg gag aag cct	2188
Lys Ser Thr Leu Leu Phe His Gln Lys Thr His Ser Gly Glu Lys Pro	
584 589 594 599	
ttc atc tgt agt gaa tgt ggg caa gga ttt atc tgg aag tca aat ctt	2236
Phe Ile Cys Ser Glu Cys Gly Gln Gly Phe Ile Trp Lys Ser Asn Leu	
600 605 610 615	
gtg aaa cac cag ctt gca cat tct ggc aag cag cct ttt gta tgc aag	2284
Val Lys His Gln Leu Ala His Ser Gly Lys Gln Pro Phe Val Cys Lys	
616 621 626 631	
gag tgt ggg cga ggc ttc aac tgg aag gga aat ctc ctc aca cac cag	2332
Glu Cys Gly Arg Gly Phe Asn Trp Lys Gly Asn Leu Leu Thr His Gln	
632 637 642 647	
agg aca cac tca ggg gag aag ccc ttc gtg tgt aat gtg tgt ggg caa	2380
Arg Thr His Ser Gly Glu Lys Pro Phe Val Cys Asn Val Cys Gly Gln	
648 653 658 663	
ggc ttc agc tgg aag aga agt ctc acc aga cac cac tgg cgg ata cac	2428

Gly Phe Ser Trp Lys Arg Ser Leu Thr Arg His His Trp Arg Ile His	
664 669 674 679	
tca aag gag aag cct ttt gtt tgc cag gag tgt aag cga ggc tat acc	2476
Ser Lys Glu Lys Pro Phe Val Cys Gln Glu Cys Lys Arg Gly Tyr Thr	
680 685 690 695	
agt aag tca gac ctc act gtg cat gaa aga ata cac aca gga gag agg	2524
Ser Lys Ser Asp Leu Thr Val His Glu Arg Ile His Thr Gly Glu Arg	
696 701 706 711	
cct tat gaa tgc caa gag tgt gga cga aag ttt agc aat aag tca tac	2572
Pro Tyr Glu Cys Gln Glu Cys Gly Arg Lys Phe Ser Asn Lys Ser Tyr	
712 717 722 727	
tac agt aag cac tta aag aga cac tta cgt gag aag cgt ttt tgt aca	2620
Tyr Ser Lys His Leu Lys Arg His Leu Arg Glu Lys Arg Phe Cys Thr	
728 733 738 743	
ggg agt gtg ggt gag gct tca tct tga agtta tatctcacca tccatcagag	2672
Gly Ser Val Gly Glu Ala Ser Ser *	
744 749	
gacacactca ggagagtaac tttgctttgt tacaagcttt agttgaggct gcataacttg	2732
ttcgtgaaga tataacagag gcagacagaa tccagagggc tacagagaac ctgaattcaa	2792
cccatgtgtc cccaagagat tcagagaaaa gaggtcaatg tttagggaaac agagatgcc	2852
gttgagggga gggcattacc tgggctattg gggaaatgtg gtctctttcc tactgagcac	2912
atattcttgt tgtattttgt ccaggctgtg ctttctaagg actgctctta gccagtgact	2972
gcagagcagg gataccaagg caggcctgtt acactctccc caacctcctt ggactgcaaa	3032
caatctagga cacctccacc aaacctctc ttgcactttc cctctggctt cctcccagc	3092
cttccttggt ttggatgttt tgtcccctcc ttaatttatg ttgaaactct acataaactg	3152
tttactgttg aaacagtgtg agtattagga ggtgggacct ttgggaagtg attaagtcaa	3212
gtcacgaaga tagagctttg cgaatgggat cagggtgcct tatgaaaagg cttgatagag	3272
ggagtttgtc ctgtggccct tctattttct gctctgtgag gacacaatgc tctcccttc	3332
caaaagatgc agcatgaagg catcatcttg gaaacagaca tgagccctca acagacaact	3392
gcacctactg atgttttgat gttgaacttc ccagcctcca gaactctggg aaaataaagt	3452
cctctttata catttcctag tcagtgggat tttattataa cagctcaaat agactaagta	3512
actgctcccc tcatcattct ctcacagtca tatctggaaa taaaatctct gtatatgcaa	3572
aaaaaaaaa	3582

<210> 553
 <211> 548
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (268) .. (426)

<400> 553
 agcgtgagat tctacgaaga taatacccca ccaaacccaa aaaaagagat ctctcgagga 60
 tccgaattcg cggccgcgctc gacggggggtt cgattctgct gactccagtg gcccagagagg 120
 cgccgctttct tccgctttct cgtcaggctc ctgcaacccc aggcattgaac caagggtttct 180
 gaactactgg gcgggagcca acgtctcttc tttctccgc tctggcggag gctttgtcgc 240
 tgccggctgg gcccagggt gtcccc atg gcg ggg ccg cgg gtg gag gtc 291
 Met Ala Gly Pro Arg Val Glu Val
 1 5
 gat ggc agc atc atg gaa ggg ggc ggc cag atc ctg aga gtc tct acg 339
 Asp Gly Ser Ile Met Glu Gly Gly Gly Gln Ile Leu Arg Val Ser Thr
 9 14 19 24
 gcc ttg agc tgt ctg cta ggc ctg ccc ttg cgg gtg cag aag atc cga 387
 Ala Leu Ser Cys Leu Leu Gly Leu Pro Leu Arg Val Gln Lys Ile Arg
 25 30 35 40
 gcc ggc cgg agc acg cca ggc ctg agt att atg acc tga aggcctcaac 436
 Ala Gly Arg Ser Thr Pro Gly Leu Ser Ile Met Thr *
 41 46 51
 atttatctgg actggaatg attcgagatt tgtgtgatgg gcaactggag ggggcagaaa 496
 ttggctcaac agaaataacc ttacaccag agaagatcaa aggtggaatc ca 548

<210> 554
 <211> 3845
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (408) .. (2120)

<400> 554
 ccgtgagcac agcttccgct cctccaatcc gccagagggc gcagcggccg gcctctccct 60
 tcccgggggtt cttcgcgccg ggccccttcc gcgtgggtga gtgaatgtga gagtcagcgc 120
 tcgcgcgcgc cgcgcgcgcc gcctccgctg ttcggcgctc tgctttaggc ggtggggggc 180

```

gggcgcgcgc gtaaaagcat agagacgggc attgagctct tgggctagag cgtcgccgag 240
tcggagccgg agcctgagcc gcgcgtgtg tctccgctgc gtccgccgag gcccccgagt 300
gtcaggggaca aaagcctccg cctgctcccg cagccggggc tcatctgccg ccgccgccgc 360
gctgaggaga gttcgccgcc gtcgccgcc gtgaggatct gagagcc atg tgc gcc 416
Met Ser Ala
1
agc agc ctc ttg gag cag aga cca aaa ggt caa gga aac aaa gta caa 464
Ser Ser Leu Leu Glu Gln Arg Pro Lys Gly Gln Gly Asn Lys Val Gln
4 9 14 19
aat gga tct gta cat caa aag gat gga tta aac gat gat gat ttt gaa 512
Asn Gly Ser Val His Gln Lys Asp Gly Leu Asn Asp Asp Asp Phe Glu
20 25 30 35
cct tac ttg agt cca cag gca agg ccc aat aat gca tat act gcc atg 560
Pro Tyr Leu Ser Pro Gln Ala Arg Pro Asn Asn Ala Tyr Thr Ala Met
36 41 46 51
tca gat tcc tac tta ccc agt tac tac agt ccc tcc att ggc ttc tcc 608
Ser Asp Ser Tyr Leu Pro Ser Tyr Tyr Ser Pro Ser Ile Gly Phe Ser
52 57 62 67
tat tct ttg ggt gaa gct gct tgg tct acg ggg ggt gac aca gcc atg 656
Tyr Ser Leu Gly Glu Ala Ala Trp Ser Thr Gly Gly Asp Thr Ala Met
68 73 78 83
ccc tac tta act tct tat gga cag ctg agc aac gga gag ccc cac ttc 704
Pro Tyr Leu Thr Ser Tyr Gly Gln Leu Ser Asn Gly Glu Pro His Phe
84 89 94 99
cta cca gat gca atg ttt ggg caa cca gga gcc cta ggt agc act cca 752
Leu Pro Asp Ala Met Phe Gly Gln Pro Gly Ala Leu Gly Ser Thr Pro
100 105 110 115
ttt ctt ggt cag cat ggt ttt aat ttc ttt ccc agt ggg att gac ttc 800
Phe Leu Gly Gln His Gly Phe Asn Phe Phe Pro Ser Gly Ile Asp Phe
116 121 126 131
tca gca tgg gga aat aac agt tct cag gga cag tct act cag agc tct 848
Ser Ala Trp Gly Asn Asn Ser Ser Gln Gly Gln Ser Thr Gln Ser Ser
132 137 142 147
gga tat agt agc aat tat gct tat gca cct agc tcc tta ggt gga gcc 896
Gly Tyr Ser Ser Asn Tyr Ala Tyr Ala Pro Ser Ser Leu Gly Gly Ala
148 153 158 163
atg att gat gga cag tca gct ttt gcc aat gag acc ctc aat aag gct 944
Met Ile Asp Gly Gln Ser Ala Phe Ala Asn Glu Thr Leu Asn Lys Ala
164 169 174 179
cct ggc atg aat act ata gac caa ggg atg gca gca ctg aag ttg ggt 992
Pro Gly Met Asn Thr Ile Asp Gln Gly Met Ala Ala Leu Lys Leu Gly

```

180	185	190	195	
agc aca gaa gtt gca agc aat gtt cca aaa gtt gta ggt tct gct gtt				1040
Ser Thr Glu Val Ala Ser Asn Val Pro Lys Val Val Gly Ser Ala Val				
196	201	206	211	
ggg agc ggg tcc att act agt aac atc gtg gct tcc aat agt ttg cct				1088
Gly Ser Gly Ser Ile Thr Ser Asn Ile Val Ala Ser Asn Ser Leu Pro				
212	217	222	227	
cca gcc acc att gct cct cca aaa cca gca tct tgg gct gat att gct				1136
Pro Ala Thr Ile Ala Pro Pro Lys Pro Ala Ser Trp Ala Asp Ile Ala				
228	233	238	243	
agc aag cct gca aaa cag caa cct aaa ctg aag acc aag aat ggc att				1184
Ser Lys Pro Ala Lys Gln Gln Pro Lys Leu Lys Thr Lys Asn Gly Ile				
244	249	254	259	
gca ggg tca agt ctt ccg cca ccc ccg ata aag cat aac atg gat att				1232
Ala Gly Ser Ser Leu Pro Pro Pro Pro Ile Lys His Asn Met Asp Ile				
260	265	270	275	
gga act tgg gat aac aag ggt ccc gtt gca aaa gcc ccc tca cag gct				1280
Gly Thr Trp Asp Asn Lys Gly Pro Val Ala Lys Ala Pro Ser Gln Ala				
276	281	286	291	
ttg gtt cag aat ata ggt cag cca acc cag ggg tct cct cag cct gta				1328
Leu Val Gln Asn Ile Gly Gln Pro Thr Gln Gly Ser Pro Gln Pro Val				
292	297	302	307	
ggg cag cag gct aac aat agc cca cca gtg gct cag gca tca gta ggg				1376
Gly Gln Gln Ala Asn Asn Ser Pro Pro Val Ala Gln Ala Ser Val Gly				
308	313	318	323	
caa cag aca cag cca ttg cct cca cct cca cca cag cct gcc cag ctt				1424
Gln Gln Thr Gln Pro Leu Pro Pro Pro Pro Pro Gln Pro Ala Gln Leu				
324	329	334	339	
tca gtc cag caa cag gca gct cag cca acc cgc tgg gta gca cct cgg				1472
Ser Val Gln Gln Gln Ala Ala Gln Pro Thr Arg Trp Val Ala Pro Arg				
340	345	350	355	
aac cgt ggc agt ggg ttc ggt cat aat ggg gtg gat ggt aat gga gta				1520
Asn Arg Gly Ser Gly Phe Gly His Asn Gly Val Asp Gly Asn Gly Val				
356	361	366	371	
gga cag tct cag gct ggt tct gga tct act cct tca gaa ccc cac cca				1568
Gly Gln Ser Gln Ala Gly Ser Gly Ser Thr Pro Ser Glu Pro His Pro				
372	377	382	387	
gtg ttg gag aag ctt ccg tcc att aat aac tat aac ccc aaa gat ttt				1616
Val Leu Glu Lys Leu Arg Ser Ile Asn Asn Tyr Asn Pro Lys Asp Phe				
388	393	398	403	
gac tgg aat ctg aaa cat ggc cgg gtt ttc atc att aag agc tac tct				1664
Asp Trp Asn Leu Lys His Gly Arg Val Phe Ile Ile Lys Ser Tyr Ser				
404	409	414	419	

gag gac gat att cac cgt tcc att aag tat aat att tgg tgc agc aca	1712
Glu Asp Asp Ile His Arg Ser Ile Lys Tyr Asn Ile Trp Cys Ser Thr	
420 425 430 435	
gag cat ggt aac aag aga ctg gat gct gct tat cgt tcc atg aac ggg	1760
Glu His Gly Asn Lys Arg Leu Asp Ala Ala Tyr Arg Ser Met Asn Gly	
436 441 446 451	
aaa ggc ccc gtt tac tta ctt ttc agt gtc aac ggc agt gga cac ttc	1808
Lys Gly Pro Val Tyr Leu Leu Phe Ser Val Asn Gly Ser Gly His Phe	
452 457 462 467	
tgt ggc gtg gca gaa atg aaa tct gct gtg gac tac aac aca tgt gca	1856
Cys Gly Val Ala Glu Met Lys Ser Ala Val Asp Tyr Asn Thr Cys Ala	
468 473 478 483	
ggt gtg tgg tcc cag gac aaa tgg aag ggt cgt ttt gat gtc agg tgg	1904
Gly Val Trp Ser Gln Asp Lys Trp Lys Gly Arg Phe Asp Val Arg Trp	
484 489 494 499	
att ttt gtg aag gac gtt ccc aat agc caa ctg cga cac att cgc cta	1952
Ile Phe Val Lys Asp Val Pro Asn Ser Gln Leu Arg His Ile Arg Leu	
500 505 510 515	
gag aac aac gag aat aaa cca gtg acc aac tct agg gac act cag gaa	2000
Glu Asn Asn Glu Asn Lys Pro Val Thr Asn Ser Arg Asp Thr Gln Glu	
516 521 526 531	
gtg cct ctg gaa aag gct aag cag gtg ttg aaa att ata gcc agc tac	2048
Val Pro Leu Glu Lys Ala Lys Gln Val Leu Lys Ile Ile Ala Ser Tyr	
532 537 542 547	
aag cac acc act tcc att ttt gat gac ttc tca cac tat gag aaa cgc	2096
Lys His Thr Thr Ser Ile Phe Asp Asp Phe Ser His Tyr Glu Lys Arg	
548 553 558 563	
cca aga gga aga aga aag tgt taa aaaggaacgt caaggtcgtg ggaaataaaaa	2150
Pro Arg Gly Arg Arg Lys Cys *	
564 569	
ggcagttcta cacagactgc agcaacgggt gcactctgcat atcctaagag gaaaaaatga	2210
ccttcaagag aattaggact tttttcttaa tttcactgac ttcagagacg attgcagact	2270
tgcagtttaa gtattggaat ttcacaaaag acataggact taactggaaa atgaaaaaaaa	2330
aaagaaaaag aaaaaactaa ccaaaaaatc cctctaggtg gtttagggga aaaatgtccc	2390
ttttattttg gctttggttg ggatttcaga gcataatgct atgttttttt gtctttttac	2450
tatgtttttc ggatttttaa gtccgtaagt gcatacagtt ttctctaatt tttaaaccct	2510
ttcctcctcc cattttgaca tttgcacttg gagaacactt gagttgtgaa ggttttgggc	2570
atccacccca gaaagtggga atttgatttt atccttccga actggaagaa catttttatg	2630

aagaatTTTT gtctaggaga atataacagt gttacccaag gttgtgtctt taagggtggt 2690
tcattttctc tgaccttttg ttactcaaag taaagtacta ggagtcctaa gaaatgttct 2750
gttcttgtac attatactga ttaagtcagg attaatttga tttcaaagct gagaacagtg 2810
gtaaaaactc gtttacagaa atgcatttct gtaaacgagt ttttaccact gttctcagct 2870
ttgaaatcaa attaatcctg acttaatcag tataatgtac aagaacagaa catttcttag 2930
gactcctagt actttacttt gagtaacaaa aggtcagaga aaatgaacca cccttaaaga 2990
cacaaccttg ggtaacactg ttatattctc ctagacaaaa attcttcata aaaatgttct 3050
tccagttcgg aaggataaaa tcaaattccc actttctggg gtggatgcc aaaaccttca 3110
caactcaagt gttctccaag tgcaaatgtc aaaatgggag gaggaaaggg tttaaaaatt 3170
agagaaaact gtatgcactt acggacttaa aaatccgaaa aacatagtaa aaagacaaaa 3230
aaacatagca ttatgtcttg aaatcacaa caaagccaaa ataaaaggga catttttcac 3290
ctaaactacc tagagggatt ttttgtttag tttttcttt ttcttttttt tttcattttc 3350
cagttaagtc ctatgtcttt tgtgaaattc caatacttaa actgcaagtc tgcaatcgtc 3410
tctgaagtca gtgaaattaa gaaaaaagtc ctaattctct tgaaggatcat tttttcctct 3470
taggatatgc agatgcaacc gttgctgcag tctgtgtaga actgcctttt atttcccacg 3530
accttgacgt tcttacagag gtaagaaaaa aattgaaatg gttaaaaatt atctgaacat 3590
gctttatgaa tttaaaaact tcacagaata actcaacaga aatttaatta tttagaatta 3650
ttagaaaatt aattatttta agtagaacat tccccacaaa gaaaaactgg cttttacttt 3710
gttttaaaca cttaaacacc ttaatgcaaa attacttttg acttgaaaat tcattacatg 3770
ctttcctatt atactgttta gattaatact tagttgtcag gccccccaaa aatatgggcc 3830
taatggaagt acccc 3845

<210> 555
<211> 4352
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (77)..(1978)

<400> 555
gaaccgctcc ggaatttccg ggtcgacgat ttcgtgaaga ggctgagggg ggcgggtgctg 60

ccgccgcggc gctgtc	atg gag cta gcg cag gaa gcg cgg gaa ctg ggt	109
	Met Glu Leu Ala Gln Glu Ala Arg Glu Leu Gly	
	1 5	
tgc tgg gcg gtc gaa gag atg ggg gtg ccc gtg gcg gcc cgg gcc ccg	157	
Cys Trp Ala Val Glu Glu Met Gly Val Pro Val Ala Ala Arg Ala Pro		
12 17 22 27		
gaa tcg acg ctg cgc agg ctg tgt ctg ggc cag ggg gct gac atc tgg	205	
Glu Ser Thr Leu Arg Arg Leu Cys Leu Gly Gln Gly Ala Asp Ile Trp		
28 33 38 43		
gcc tac atc ttg cag cat gtg cac agt cag agg act gtc aag aag atc	253	
Ala Tyr Ile Leu Gln His Val His Ser Gln Arg Thr Val Lys Lys Ile		
44 49 54 59		
cgg gga aac cta ctc tgg tat ggc cac cag gac agt cca cag gtc cgt	301	
Arg Gly Asn Leu Leu Trp Tyr Gly His Gln Asp Ser Pro Gln Val Arg		
60 65 70 75		
cgg aag tta gag ctg gaa gct gct gtg acc cgc ctg cgg gca gaa atc	349	
Arg Lys Leu Glu Leu Glu Ala Ala Val Thr Arg Leu Arg Ala Glu Ile		
76 81 86 91		
cag gaa ctc gac cag agc ctg gag ctg atg gag cga gac act gag gct	397	
Gln Glu Leu Asp Gln Ser Leu Glu Leu Met Glu Arg Asp Thr Glu Ala		
92 97 102 107		
cag gac acg gcc atg gag cag gca cgt cag cac act caa gac acc cag	445	
Gln Asp Thr Ala Met Glu Gln Ala Arg Gln His Thr Gln Asp Thr Gln		
108 113 118 123		
cgt cga gct ctc ctc ctc cgg gcc caa gct ggg gcc atg cga aga cag	493	
Arg Arg Ala Leu Leu Leu Arg Ala Gln Ala Gly Ala Met Arg Arg Gln		
124 129 134 139		
cag cat acg ctc cga gat ccc atg cag cgg ctg cag aat caa ctg agg	541	
Gln His Thr Leu Arg Asp Pro Met Gln Arg Leu Gln Asn Gln Leu Arg		
140 145 150 155		
cgc ctg cag gac atg gag agg aaa gcc aaa gta gat gtg acc ttt gga	589	
Arg Leu Gln Asp Met Glu Arg Lys Ala Lys Val Asp Val Thr Phe Gly		
156 161 166 171		
tcc ctc acg tcg gca gct ctg ggc ctg gag ccc gtg gtc ctg cgt gat	637	
Ser Leu Thr Ser Ala Ala Leu Gly Leu Glu Pro Val Val Leu Arg Asp		
172 177 182 187		
gtc cga aca gcc tgc acc ctc cgg gcc cag ttc ctg cag aac ctc ctg	685	
Val Arg Thr Ala Cys Thr Leu Arg Ala Gln Phe Leu Gln Asn Leu Leu		
188 193 198 203		
ctt ccc cag gcc aag agg ggc agc ctc cca acc cct cat gat gac cac	733	
Leu Pro Gln Ala Lys Arg Gly Ser Leu Pro Thr Pro His Asp Asp His		
204 209 214 219		
ttt ggc act tcg tac cag cag tgg ctg agc tca gtg gag acg ctg ctg	781	

Phe Gly Thr Ser Tyr Gln Gln Trp Leu Ser Ser Val Glu Thr Leu Leu	
220 225 230 235	
aca aac cac ccc cca ggc cac gtc ctg gct gcc ttg gag cac ctg gct	829
Thr Asn His Pro Pro Gly His Val Leu Ala Ala Leu Glu His Leu Ala	
236 241 246 251	
gca gag cgg gag gca gag gtt cgg tcc ctg tgc agt ggg gat ggg ctt	877
Ala Glu Arg Glu Ala Glu Val Arg Ser Leu Cys Ser Gly Asp Gly Leu	
252 257 262 267	
ggc gac aca gag ata tcc aga ccc cag gcc ccg gac cag tca gac tcc	925
Gly Asp Thr Glu Ile Ser Arg Pro Gln Ala Pro Asp Gln Ser Asp Ser	
268 273 278 283	
agc cag acc ctg ccg tcc atg gtt cat ctc atc cag gag ggc tgg cgg	973
Ser Gln Thr Leu Pro Ser Met Val His Leu Ile Gln Glu Gly Trp Arg	
284 289 294 299	
act gtg ggt gtg ctg gtc tcc cag cgg agc acc ctc ctg aag gag cgg	1021
Thr Val Gly Val Leu Val Ser Gln Arg Ser Thr Leu Leu Lys Glu Arg	
300 305 310 315	
caa gtc ttg acc cag cgc ctc cag ggc ctg gtg gag gag gtg gag aga	1069
Gln Val Leu Thr Gln Arg Leu Gln Gly Leu Val Glu Glu Val Glu Arg	
316 321 326 331	
cgc gtc ctg gga tcc agt gag agg cag gtg ctg ata ctg ggg ctt cgg	1117
Arg Val Leu Gly Ser Ser Glu Arg Gln Val Leu Ile Leu Gly Leu Arg	
332 337 342 347	
cgc tgt tgc ctg tgg acg gag ctc aag gcc ctg cac gat cag agc cag	1165
Arg Cys Cys Leu Trp Thr Glu Leu Lys Ala Leu His Asp Gln Ser Gln	
348 353 358 363	
gag ctg cag gat gca gct ggg cat cgg cag ctc ctg ctg agg gag cta	1213
Glu Leu Gln Asp Ala Ala Gly His Arg Gln Leu Leu Leu Arg Glu Leu	
364 369 374 379	
cag gcc aaa cag cag cgg atc ctg cac tgg cgc cag ctg gtg gag gag	1261
Gln Ala Lys Gln Gln Arg Ile Leu His Trp Arg Gln Leu Val Glu Glu	
380 385 390 395	
acc cag gaa cag gtc cgc ctg ctc atc aag gga aac tcg gcc agc aag	1309
Thr Gln Glu Gln Val Arg Leu Leu Ile Lys Gly Asn Ser Ala Ser Lys	
396 401 406 411	
acc cgc ctg tgc cgg agc ccg ggg gag gtg cta gct ctg gtc cag cga	1357
Thr Arg Leu Cys Arg Ser Pro Gly Glu Val Leu Ala Leu Val Gln Arg	
412 417 422 427	
aag gtg gtc cct aca ttt gag gca gtg gca cca cag agc cgg gag ctg	1405
Lys Val Val Pro Thr Phe Glu Ala Val Ala Pro Gln Ser Arg Glu Leu	
428 433 438 443	
ctg cgc tgt ctg gag gag gaa gtc cgg cat ttg ccc cac att ctg ttg	1453
Leu Arg Cys Leu Glu Glu Glu Val Arg His Leu Pro His Ile Leu Leu	

444	449	454	459	
ggc acg ctg ctg cgg cac agg ccg gga gag ttg aag ccc ctg ccc acg				1501
Gly Thr Leu Leu Arg His Arg Pro Gly Glu Leu Lys Pro Leu Pro Thr				
460	465	470	475	
gtc ctc cca tcc atc cac cag ctg cac ccc gcg tcc cca agg ggc tcc				1549
Val Leu Pro Ser Ile His Gln Leu His Pro Ala Ser Pro Arg Gly Ser				
476	481	486	491	
agc ttc ata gcg ctg agc cac aag ctg ggg ctg cct cca ggg aag gcc				1597
Ser Phe Ile Ala Leu Ser His Lys Leu Gly Leu Pro Pro Gly Lys Ala				
492	497	502	507	
tgc gag ctg ctc ctg ccg gcg gct gcc tct ctt cgc cag gac ctt ctg				1645
Ser Glu Leu Leu Leu Pro Ala Ala Ala Ser Leu Arg Gln Asp Leu Leu				
508	513	518	523	
ctc ctg cag gac cag ccg agc ctc tgg tgc tgg gat cta ctc cac atg				1693
Leu Leu Gln Asp Gln Arg Ser Leu Trp Cys Trp Asp Leu Leu His Met				
524	529	534	539	
aag acc agc ctg ccg cca ggc ctt ccc acc cag gag ctg ctg cag atc				1741
Lys Thr Ser Leu Pro Pro Gly Leu Pro Thr Gln Glu Leu Leu Gln Ile				
540	545	550	555	
cag gca tcc cag gaa aaa cag cag aaa gag aac ctg ggg cag gct ctg				1789
Gln Ala Ser Gln Glu Lys Gln Gln Lys Glu Asn Leu Gly Gln Ala Leu				
556	561	566	571	
aag agg ctg gag aag cta ctg aaa cag gca ctg gag cga atc cct gag				1837
Lys Arg Leu Glu Lys Leu Leu Lys Gln Ala Leu Glu Arg Ile Pro Glu				
572	577	582	587	
ctg cag ggg atc gtg ggg gac tgg tgg gag cag cca ggc cag gcc gcc				1885
Leu Gln Gly Ile Val Gly Asp Trp Trp Glu Gln Pro Gly Gln Ala Ala				
588	593	598	603	
ctc tct gag gag ctc tgc cag ggc ctg tcc ctg ccc cag tgg cgg ctg				1933
Leu Ser Glu Glu Leu Cys Gln Gly Leu Ser Leu Pro Gln Trp Arg Leu				
604	609	614	619	
cgc tgg gtt cag gcc cag ggg gcc ctg cag aag ctg tgc agc tga aga				1981
Arg Trp Val Gln Ala Gln Gly Ala Leu Gln Lys Leu Cys Ser *				
620	625	630		
gaggggttcaa acggaagccg agaacttgac actgttcacc ccaacacctc acctccccca				2041
ggacatttgg aagaaagcag cgccaggatt cctcggcagt cgtccccacc cgcaoctgca				2101
gtcccctcat gtgctgttct gctgccccac tcagctcctg gaccctgtcc tttcatcccg				2161
ctaaagcacc ccctaaaacc ccttcatcac tttcattctc agcaaaaagt aattgagcac				2221
ctcctctagg cgctggggag tccacactga acaaaagaaa cagaaaaccc tgtcttccag				2281
cagttgagtt ctagggcagg gagacagagt ttacaagata aggaaaatat atatgtagta				2341

tgctgcaagt taactgctgt gtgggaaatc cagcaggggg tgggatgtgt gatttgaatt	2401
gagggccaca ctgccaggt cgtgctccgt caaggggtga gcaggagcaa caggggtggc	2461
tgagtaaggg cttgcagctg gaggcaacag cacatgcaaa ggccctgagc caggatgtgc	2521
tgcaataagg gccactgagg gggacagtgt aggttggggg tgaggaatgt attaaaagat	2581
gagattgcct tctagtttgt atagtttctt tttttacatg taaatcagcc atttggaatt	2641
tatcctagca catggatcca attttgtctt attttacata tatcctagta gcacttactg	2701
aaattcccag tcagagtggc agttgcctct gagggaggt ggggtggcagg gatcaactga	2761
ggaggagaca cagaaatgtc ctagcctgat gggaaatgtg tgggtgtcaag accagcggcg	2821
gtgacgcagg tgtagagatt tgtcagagct catgtagttg tagtcttaag gcctgtgcat	2881
ttcactgcgt gggttactca atttataaag caaagccctt acacttttga gatgccacct	2941
ttttatgcac taaatttcca tgtttaattg gggtatatct ggcttctctc cagacctgct	3001
ttgtatttaa ctctccatgt gtcattccta cagtagctta atagaaaggc ttgtgacaca	3061
ttgtcatatc tgttcttggt ttcttttgggt tttttttttt ttttttttga gatgcagtct	3121
cattctgttg cccaagttgg agtgcagtgg catgatctca gctcactgca acctccgcct	3181
cccaggttca agccattctc atgcctcagc ttccccagta gctaggatta caggtacgca	3241
ccaccacgcc cagctcattt ttgtactttt agtagggacg gggtttcatc atgttggcca	3301
gactgggtctc gaactcctga cctcaagtga tctgcctgcc tcggcctccc aaagtgctgg	3361
gattacaggc atgagccacc gcgcctgacc acattgccat atctgaaatg gctggattct	3421
cttaggtgct tttctttttc tttctttctt tctttttttg agacagaatc tggctgtttc	3481
ccaggtgaa gtgcagtggc atgaactcag ctactgcaa cctctgcctc ctggattcaa	3541
acaattctca tgtctcagcc tcctgaatag ctgggattac aggcacccac caccatatct	3601
ggctaataatt tgtatttttt gtagagtcgg agctttacca tgttggtcag gctgctctcc	3661
aactcctggc ctcaagtgat tctatgcct ctgcctccca aatcttcacc tgctgggatt	3721
agtttcccct gtctcagtaa atttttttt ccaaactaag tgaacattag atttaatttg	3781
gctggcccca gaagaaaaac atgcacagat ggtagtttta ctgggtgttg agtaagtttt	3841
caaatttgga agtttggcag ctttatgata ttgaaccttg ctgtccatct ctcacacaac	3901
tcctctcttg gcctccagag tccctttact ctcccagctt tcctcctgcc cctggctgct	3961
gtttcccagc ctttccacat tggctttccc atgtagtcct tagtgtgtct gctcctcctc	4021

tctctcctca tcacagttcc cagccccac cttcaactga actcaacaaa atcttcaact 4081
tcatacagta gtcacattgt tagtaataac actggcattt ttattttgat aaaatagacc 4141
gtttaaattt ttgagattct accttatatt ttttgaatta tataactaaag caaataagta 4201
gtgatgtaat gtcattgggg accaagattt ttagtgtaaa tgaaaaaaga taacaaatat 4261
aaactcaagt aaacaccctg tagtctttca catgaattgg aaatatcaga ataaagtcat 4321
gattttttctc tttctaaaaa aaaaaaaaaa a 4352

<210> 556
<211> 1731
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (188)..(1108)

<400> 556
ttgaacccat cgacgcctgc aggtaccggg ccggaattcc cgggtcgacc cacgcgtccg 60
ctgggctgga ccgaaaccgg cgcgagcaaa ctgaggcccg agccttctcg ggaccggggg 120
gacgcctaac ccgcgagaaa ccttgcaaat tttcttctc ataattggga gaagactcac 180
tgggcga atg gca gca gta gat gac ttg caa ttt gaa gaa ttt ggc aat 229
Met Ala Ala Val Asp Asp Leu Gln Phe Glu Glu Phe Gly Asn
1 5 10
gca gcc act tct ctg aca gca aac cca gat gcc acc aca gta aac att 277
Ala Ala Thr Ser Leu Thr Ala Asn Pro Asp Ala Thr Thr Val Asn Ile
15 20 25 30
gag gat cct ggt gaa acc cca aaa cat cag cca gga tcc cca aga ggc 325
Glu Asp Pro Gly Glu Thr Pro Lys His Gln Pro Gly Ser Pro Arg Gly
31 36 41 46
tca gga aga gaa gaa gat gat gag tta ctg gga aat gat gac tct gac 373
Ser Gly Arg Glu Glu Asp Asp Glu Leu Leu Gly Asn Asp Asp Ser Asp
47 52 57 62
aaa act gag tta ctt gct gga cag aag aaa agc tcc ccc ttc tgg aca 421
Lys Thr Glu Leu Leu Ala Gly Gln Lys Lys Ser Ser Pro Phe Trp Thr
63 68 73 78
ttt gaa tac tac caa aca ttc ttt gat gtg gac acc tac cag gtc ttt 469
Phe Glu Tyr Tyr Gln Thr Phe Phe Asp Val Asp Thr Tyr Gln Val Phe
79 84 89 94
gac aga att aaa gga tct ctt ttg cca ata ccc ggg aaa aac ttt gtg 517
Asp Arg Ile Lys Gly Ser Leu Leu Pro Ile Pro Gly Lys Asn Phe Val

95	100	105	110	
agg tta tat atc cgc agc aat cca gat ctc tat ggc ccc ttt tgg ata				565
Arg Leu Tyr Ile Arg Ser Asn Pro Asp Leu Tyr Gly Pro Phe Trp Ile				
111	116	121	126	
tgt gcc acg ttg gtc ttt gcc ata gca att agt ggg aat ctt tcc aac				613
Cys Ala Thr Leu Val Phe Ala Ile Ala Ile Ser Gly Asn Leu Ser Asn				
127	132	137	142	
ttc ttg atc cat ctg gga gag aag acg tac cat tat gtg ccc gaa ttc				661
Phe Leu Ile His Leu Gly Glu Lys Thr Tyr His Tyr Val Pro Glu Phe				
143	148	153	158	
cga aaa gtg tcc ata gca gct acc atc atc tat gcc tat gcc tgg ctg				709
Arg Lys Val Ser Ile Ala Ala Thr Ile Ile Tyr Ala Tyr Ala Trp Leu				
159	164	169	174	
gtt cct ctt gca ctc tgg ggt ttc ctc atg tgg aga aac agc aaa gtt				757
Val Pro Leu Ala Leu Trp Gly Phe Leu Met Trp Arg Asn Ser Lys Val				
175	180	185	190	
atg aac atc gtc tcc tat tca ttt ctg gag att gtg tgt gtc tat gga				805
Met Asn Ile Val Ser Tyr Ser Phe Leu Glu Ile Val Cys Val Tyr Gly				
191	196	201	206	
tat tcc ctc ttc att tat atc ccc acc gca ata ctg tgg att atc ccc				853
Tyr Ser Leu Phe Ile Tyr Ile Pro Thr Ala Ile Leu Trp Ile Ile Pro				
207	212	217	222	
cag aaa gct gtt cgt tgg att cta gtc atg att gcc ctg ggc atc tca				901
Gln Lys Ala Val Arg Trp Ile Leu Val Met Ile Ala Leu Gly Ile Ser				
223	228	233	238	
gga tct ctc ttg gca atg aca ttt tgg cca gct gtt cgt gag gat aac				949
Gly Ser Leu Leu Ala Met Thr Phe Trp Pro Ala Val Arg Glu Asp Asn				
239	244	249	254	
cga cgc gtt gca ttg gcc aca att gtg aca att gtg ttg ctc cat atg				997
Arg Arg Val Ala Leu Ala Thr Ile Val Thr Ile Val Leu Leu His Met				
255	260	265	270	
ctg ctt tct gtg ggc tgc ttg gca tac ttt ttt gat gca cca gag atg				1045
Leu Leu Ser Val Gly Cys Leu Ala Tyr Phe Phe Asp Ala Pro Glu Met				
271	276	281	286	
gac cat ctc cca aca act aca gct act cca aac caa aca gtt gct gca				1093
Asp His Leu Pro Thr Thr Thr Ala Thr Pro Asn Gln Thr Val Ala Ala				
287	292	297	302	
gcc aag tcc agc taa tgaggaaaga ctcaacttgag ataccctctc cttgctgaag				1148
Ala Lys Ser Ser *				
303				
tttttcttga cttotccagt tctcttttgt tttttggagc atggttcttt gggaagtggc				1208
atccactgca ggaaagcaga atgagcagag ccagcagaac tgatggagtg gcacaaattc				1268

```

ccagtgtctg gatggtgcc aactggcgcc taatcacccg ttaacaagc agaaattaaa 1328
tgttgctcag cacatgtgtc tttcagctct tccttttcac ccatggatga tcattgcgag 1388
catgcgctga ttggactgaa atgccgggga ataggttagg catgctcagt gccgtccctt 1448
tgccaccaca gtcaaatgac atgcttcact gtggtacctt aatacctgaa atagaaccat 1508
ggaaaattct gatgtcctct ctctgaatta tgtacagact acctggggga tcctcttctc 1568
tccaaatgtt agccatcctg aagtagccga acagtagaaa ctttggtggg gattaaccgg 1628
gagcttgaaa atttgtcttt ggtaacctga tactggacag ctgaactgaa tggctgcaaa 1688
ataaatacct cacatgatgt ctgtgtctgc aaaaaaaaaa aaa 1731

```

```

<210> 557
<211> 1716
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (259)..(1377)

```

```

<400> 557
aaggatcctt attaaattaa tccccccccc cccccccccc cccgagagaa ctgccgcttg 60
ccgccattga cacgcacaga tagaacccaa agaaaggcaa agagtctctgc ccggcaccgg 120
cgccgcgtgg gccaaacctg cgcccgtgga ggggcgcgca gagggcaccg ggcgcgggga 180
gcaggcggcg cagcaccagc atttgtgtag tgccgggagg cactgtgtgc agcaagctga 240
gagggaaact gaagcaag atg tcg ggc cgg agt ggg aag aag aaa atg tcc 291
          Met Ser Gly Arg Ser Gly Lys Lys Lys Met Ser
          1              5

aag ctg tcc cgt tca gct agg gca ggt gtc atc ttt cca gtg ggg agg 339
Lys Leu Ser Arg Ser Ala Arg Ala Gly Val Ile Phe Pro Val Gly Arg
12              17              22              27

ctg atg cgt tat ctg aag aaa ggg acg ttc aag tac cgg atc agc gtg 387
Leu Met Arg Tyr Leu Lys Lys Gly Thr Phe Lys Tyr Arg Ile Ser Val
28              33              38              43

ggc gcc cct gtc tac atg gcg gca gtc att gag tac ctg gca gcg gaa 435
Gly Ala Pro Val Tyr Met Ala Ala Val Ile Glu Tyr Leu Ala Ala Glu
44              49              54              59

att cta gaa ttg gcc ggc aat gcc gcg agg gac aac aag aag gcc cgg 483
Ile Leu Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Ala Arg
60              65              70              75

```

ata gcc ccg aga cac atc ttg ctg gca gtt gcc aat gac gag gag ctc	531
Ile Ala Pro Arg His Ile Leu Leu Ala Val Ala Asn Asp Glu Glu Leu	
76 81 86 91	
aac cag ctg cta aaa gga gtg acc atc gcc agt gga ggc gtc ctg ccc	579
Asn Gln Leu Leu Lys Gly Val Thr Ile Ala Ser Gly Gly Val Leu Pro	
92 97 102 107	
aga att cac ccc gaa ctg ctg gcc aaa aag cga ggg acc aaa ggc aag	627
Arg Ile His Pro Glu Leu Leu Ala Lys Lys Arg Gly Thr Lys Gly Lys	
108 113 118 123	
tcg gaa acg atc ctc tcc cca ccc cca gag aaa aga ggc agg aag gcc	675
Ser Glu Thr Ile Leu Ser Pro Pro Pro Glu Lys Arg Gly Arg Lys Ala	
124 129 134 139	
acg tca ggc aag aag ggg ggg aag aaa tcc aag gct gcc aaa cca cgg	723
Thr Ser Gly Lys Lys Gly Gly Lys Lys Ser Lys Ala Ala Lys Pro Arg	
140 145 150 155	
acg tcc aaa aag tcc aaa cca aag gac agc gat aaa gaa gga act tca	771
Thr Ser Lys Lys Ser Lys Pro Lys Asp Ser Asp Lys Glu Gly Thr Ser	
156 161 166 171	
aat tcc acc tct gaa gat ggg cca ggg gat gga ttc acc att ctg tct	819
Asn Ser Thr Ser Glu Asp Gly Pro Gly Asp Gly Phe Thr Ile Leu Ser	
172 177 182 187	
tct aag agc ctt gtt ctg gga cag aag ctg tcc tta acc cag agt gac	867
Ser Lys Ser Leu Val Leu Gly Gln Lys Leu Ser Leu Thr Gln Ser Asp	
188 193 198 203	
atc agc cat att ggc tcc atg aga gtg gag ggc att gtc cac cca acc	915
Ile Ser His Ile Gly Ser Met Arg Val Glu Gly Ile Val His Pro Thr	
204 209 214 219	
aca gcc gaa att gac ctc aaa gaa gat ata ggt aaa gcc ttg gaa aag	963
Thr Ala Glu Ile Asp Leu Lys Glu Asp Ile Gly Lys Ala Leu Glu Lys	
220 225 230 235	
gct ggg gga aaa gag ttc ttg gaa acg gta aag gag ctt cgc aaa tcc	1011
Ala Gly Gly Lys Glu Phe Leu Glu Thr Val Lys Glu Leu Arg Lys Ser	
236 241 246 251	
caa ggc cct ttg gaa gtc gcc gaa gcc gcc gtc agc caa tcc agt gga	1059
Gln Gly Pro Leu Glu Val Ala Glu Ala Ala Val Ser Gln Ser Ser Gly	
252 257 262 267	
ctc gca gcc aaa ttt gtc atc cac tgt cac atc cct cag tgg ggc tcc	1107
Leu Ala Ala Lys Phe Val Ile His Cys His Ile Pro Gln Trp Gly Ser	
268 273 278 283	
gac aaa tgt gaa gaa cag ctt gaa gag acc atc aaa aac tgc ctg tca	1155
Asp Lys Cys Glu Glu Gln Leu Glu Glu Thr Ile Lys Asn Cys Leu Ser	
284 289 294 299	

gcg gcg gag gac aag aag cta aag tcc gtc gcg ttc ccg cct ttc ccc	1203
Ala Ala Glu Asp Lys Lys Leu Lys Ser Val Ala Phe Pro Pro Phe Pro	
300 305 310 315	
agc ggc aga aac tgc ttt ccc aaa cag act gcg gcc cag gtg acc ctc	1251
Ser Gly Arg Asn Cys Phe Pro Lys Gln Thr Ala Ala Gln Val Thr Leu	
316 321 326 331	
aaa gcc atc tca gcc cac ttt gat gac tcg agc gcg tcc tcg ctg aag	1299
Lys Ala Ile Ser Ala His Phe Asp Asp Ser Ser Ala Ser Ser Leu Lys	
332 337 342 347	
aac gtg tac ttc ctg ctc ttc gac agc gag agc atc gcc atc tac gtg	1347
Asn Val Tyr Phe Leu Leu Phe Asp Ser Glu Ser Ile Gly Ile Tyr Val	
348 353 358 363	
cag gag atg gcc aag ctc gac gcc aag tag c cgccgcactt tccagcaggg	1398
Gln Glu Met Ala Lys Leu Asp Ala Lys *	
364 369	
atcggaggac gacccgagtc ccaagagtgg ggttttgctt tttaaaagga gagaggaggg	1458
gtgatggcag gggagtggag ggtggccggg caggtcctgc cggcgcaggg agccctctgc	1518
ccttcacact ctctccaaa agagcctcca tctgtaagga agcaggtctc cgcgaggggt	1578
ttctttccat gtgttttctt cctgttggtt tagaactttt ttataaaaaac agacctcggt	1638
ttagatttat agcattgact ttacacaca ttcacacaag aaaaaaatcc tttcaaaatt	1698
cttaaaaaaa aaaaaaaa	1716

<210> 558
 <211> 918
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (187)..(846)

<400> 558	
atttggccct cgaggccaag aattcggcac gaggactaac acacctctaa catttcacct	60
ctagctcaga tgagagagag aatgggactt cttggtactg attgtttttc ccatgcctca	120
attggtttct tttagggagc tacaaattta cgggttcact ggtgattgat cttttcatcc	180
agcaca atg gac aga agt cta agg aac gtc ctt gtg gtt tcc ttt ggg	228
Met Asp Arg Ser Leu Arg Asn Val Leu Val Val Ser Phe Gly	
1 5 10	
ttc ctg ctt ctc ttt aca gcc tat gga ggt ctg cag agc ctg cag agc	276
Phe Leu Leu Leu Phe Thr Ala Tyr Gly Gly Leu Gln Ser Leu Gln Ser	

15	20	25	30	
agc ctg tac agc gag gag ggc ctg ggt gtc aca gcg ctc agc acc ctc				324
Ser Leu Tyr Ser Glu Glu Gly Leu Gly Val Thr Ala Leu Ser Thr Leu				
31	36	41	46	
tat gga ggc atg ctc ctg tcc tcc atg ttc ctc cca ccg ctc ctc atc				372
Tyr Gly Gly Met Leu Leu Ser Ser Met Phe Leu Pro Pro Leu Leu Ile				
47	52	57	62	
gag agg ctg ggc tgc aag ggg acc atc atc ctc tcc atg tgt ggc tac				420
Glu Arg Leu Gly Cys Lys Gly Thr Ile Ile Leu Ser Met Cys Gly Tyr				
63	68	73	78	
gtg gcc ttc tcc gtg ggc aac ttc ttc gcc agc tgg tac act ttg atc				468
Val Ala Phe Ser Val Gly Asn Phe Phe Ala Ser Trp Tyr Thr Leu Ile				
79	84	89	94	
ccc acc tcc ata ctg ctg gga ctc ggg gcc gcc ccg ctg tgg tct gca				516
Pro Thr Ser Ile Leu Leu Gly Leu Gly Ala Ala Pro Leu Trp Ser Ala				
95	100	105	110	
cag tgc aca tac ctc acg atc acg gga aac aca cat gca gag aag gcg				564
Gln Cys Thr Tyr Leu Thr Ile Thr Gly Asn Thr His Ala Glu Lys Ala				
111	116	121	126	
gga aag cgt ggc aaa gac atg gtg aac cag tat ttt ggc atc ttc ttc				612
Gly Lys Arg Gly Lys Asp Met Val Asn Gln Tyr Phe Gly Ile Phe Phe				
127	132	137	142	
ctc ata ttc cag tca tcc ggt gtg tgg ggc aac ttg atc tca tcc ctg				660
Leu Ile Phe Gln Ser Ser Gly Val Trp Gly Asn Leu Ile Ser Ser Leu				
143	148	153	158	
gta ttt ggc cag act ccc agc caa gag acc ctt cca gaa gag cag ctc				708
Val Phe Gly Gln Thr Pro Ser Gln Glu Thr Leu Pro Glu Glu Gln Leu				
159	164	169	174	
acg tcc tgt ggg gcc agt gac tgc ctg atg gcc acc aca acc acc aac				756
Thr Ser Cys Gly Ala Ser Asp Cys Leu Met Ala Thr Thr Thr Thr Asn				
175	180	185	190	
agc acc cag agg ccc tcc cag cag ctg gtc tac acc ctc ctg ggc atc				804
Ser Thr Gln Arg Pro Ser Gln Gln Leu Val Tyr Thr Leu Leu Gly Ile				
191	196	201	206	
tac act ggt acg agc tcc atc ggc cca ggg cag ggt ccc tag caaagca				853
Tyr Thr Gly Thr Ser Ser Ile Gly Pro Gly Gln Gly Pro *				
207	212	217		
gagccaagcc tccttctctgg gctgacaaag actgtctctc ccaatgtaaa aagtaatctc				913
tcttc				918

<210> 559
 <211> 2511
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (47)..(2233)

<400> 559

```

accggaccgg aattcccggg togacgattt cgttgcgggg acaaca  atg gcg ggg      55
                                     Met Ala Gly
                                     1

ttc tgg gtc ggg aca gca ccg ctg gtc gct gcc gga cgg cgt ggg cgg      103
Phe Trp Val Gly Thr Ala Pro Leu Val Ala Ala Gly Arg Arg Gly Arg
  4              9              14              19

tgg ccg ccg cag cag ctg atg ctg agc gcg gcg ctg cgg acc ctg aag      151
Trp Pro Pro Gln Gln Leu Met Leu Ser Ala Ala Leu Arg Thr Leu Lys
  20              25              30              35

cat gtt ctg tac tat tca aga cag tgc tta atg gtg tcc cgt aat ctt      199
His Val Leu Tyr Tyr Ser Arg Gln Cys Leu Met Val Ser Arg Asn Leu
  36              41              46              51

ggg tca gtg gga tat gat cct aat gaa aaa act ttt gat aaa att ctt      247
Gly Ser Val Gly Tyr Asp Pro Asn Glu Lys Thr Phe Asp Lys Ile Leu
  52              57              62              67

gtt gct aat aga gga gaa att gca tgt cgg gtt att aga act tgc aag      295
Val Ala Asn Arg Gly Glu Ile Ala Cys Arg Val Ile Arg Thr Cys Lys
  68              73              78              83

aag atg ggc att aag aca gtt gcc atc cac agt gat gtt gat gct agt      343
Lys Met Gly Ile Lys Thr Val Ala Ile His Ser Asp Val Asp Ala Ser
  84              89              94              99

tct gtt cat gtg aaa atg gcg gat gag gct gtc tgt gtt ggc cca gct      391
Ser Val His Val Lys Met Ala Asp Glu Ala Val Cys Val Gly Pro Ala
 100              105              110              115

ccc acc agt aaa agc tac ctc aac atg gat gcc atc atg gaa gcc att      439
Pro Thr Ser Lys Ser Tyr Leu Asn Met Asp Ala Ile Met Glu Ala Ile
 116              121              126              131

aag aaa acc agg gcc caa gct gta cat cca ggt tat gga ttc ctt tca      487
Lys Lys Thr Arg Ala Gln Ala Val His Pro Gly Tyr Gly Phe Leu Ser
 132              137              142              147

gaa aac aaa gaa ttt gcc aga tgt ttg gca gca gaa gat gtc gtt ttc      535
Glu Asn Lys Glu Phe Ala Arg Cys Leu Ala Ala Glu Asp Val Val Phe
 148              153              158              163

att gga cct gac aca cat gct att caa gcc atg ggc gac aag att gaa      583
Ile Gly Pro Asp Thr His Ala Ile Gln Ala Met Gly Asp Lys Ile Glu
 164              169              174              179

```

agc aaa tta tta gct aag aaa gca gag gtt aat aca atc cct ggc ttt	631
Ser Lys Leu Leu Ala Lys Lys Ala Glu Val Asn Thr Ile Pro Gly Phe	
180 185 190 195	
gat gga gta gtc aag gat gca gaa gaa gct gtc aga att gca agg gaa	679
Asp Gly Val Val Lys Asp Ala Glu Glu Ala Val Arg Ile Ala Arg Glu	
196 201 206 211	
att ggc tac cct gtc atg atc aag gcc tca gca ggt ggt ggt ggg aaa	727
Ile Gly Tyr Pro Val Met Ile Lys Ala Ser Ala Gly Gly Gly Gly Lys	
212 217 222 227	
ggc atg cgc att gct tgg gat gat gaa gag acc agg gat ggt ttt aga	775
Gly Met Arg Ile Ala Trp Asp Asp Glu Glu Thr Arg Asp Gly Phe Arg	
228 233 238 243	
ttg tca tct caa gaa gct gct tct agt ttt ggc gat gat aga cta cta	823
Leu Ser Ser Gln Glu Ala Ala Ser Ser Phe Gly Asp Asp Arg Leu Leu	
244 249 254 259	
ata gaa aaa ttt att gat aat cct cgt cat ata gaa atc cag gtt cta	871
Ile Glu Lys Phe Ile Asp Asn Pro Arg His Ile Glu Ile Gln Val Leu	
260 265 270 275	
ggg gat aaa cat ggg aat gct tta tgg ctt aat gaa aga gag tgc tca	919
Gly Asp Lys His Gly Asn Ala Leu Trp Leu Asn Glu Arg Glu Cys Ser	
276 281 286 291	
att cag aga aga aat cag aag gtg gtg gag gaa gca cca agc att ttt	967
Ile Gln Arg Arg Asn Gln Lys Val Val Glu Glu Ala Pro Ser Ile Phe	
292 297 302 307	
ttg gat gcg gag act cga aga gcg atg gga gaa caa gct gta gct ctt	1015
Leu Asp Ala Glu Thr Arg Arg Ala Met Gly Glu Gln Ala Val Ala Leu	
308 313 318 323	
gcc aga gca gta aaa tat tcc tct gct ggg acc gtg gag ttc ctt gtg	1063
Ala Arg Ala Val Lys Tyr Ser Ser Ala Gly Thr Val Glu Phe Leu Val	
324 329 334 339	
gac tct aag aag aat ttt tat ttc ttg gaa atg aat aca aga ctc cag	1111
Asp Ser Lys Lys Asn Phe Tyr Phe Leu Glu Met Asn Thr Arg Leu Gln	
340 345 350 355	
gtt gag cat cct gtc aca gaa tgc att act ggc ctg gac cta gtc cag	1159
Val Glu His Pro Val Thr Glu Cys Ile Thr Gly Leu Asp Leu Val Gln	
356 361 366 371	
gaa atg atc cgt gtt gct aag ggc tac cct ctc agg cac aaa caa gct	1207
Glu Met Ile Arg Val Ala Lys Gly Tyr Pro Leu Arg His Lys Gln Ala	
372 377 382 387	
gat att cgc atc aac ggc tgg gca gtt gaa tgt cgg gtt tat gct gag	1255
Asp Ile Arg Ile Asn Gly Trp Ala Val Glu Cys Arg Val Tyr Ala Glu	
388 393 398 403	

gac ccc tac aag tct ttt ggt tta cca tct att ggg aga ttg tct cag	1303
Asp Pro Tyr Lys Ser Phe Gly Leu Pro Ser Ile Gly Arg Leu Ser Gln	
404 409 414 419	
tac caa gaa ccg tta cat cta cct ggt gtc cga gtg gac agt ggc atc	1351
Tyr Gln Glu Pro Leu His Leu Pro Gly Val Arg Val Asp Ser Gly Ile	
420 425 430 435	
caa cca gga agt gat att agc att tat tat gat cct atg att tca aaa	1399
Gln Pro Gly Ser Asp Ile Ser Ile Tyr Tyr Asp Pro Met Ile Ser Lys	
436 441 446 451	
cta atc aca tat ggc tct gat aga act gag gca ctg aag aga atg gca	1447
Leu Ile Thr Tyr Gly Ser Asp Arg Thr Glu Ala Leu Lys Arg Met Ala	
452 457 462 467	
gat gca ctg gat aac tat gtt att cga ggt gtt aca cat aat att gca	1495
Asp Ala Leu Asp Asn Tyr Val Ile Arg Gly Val Thr His Asn Ile Ala	
468 473 478 483	
tta ctt cga gag gtg ata atc aac tca cgc ttt gta aaa gga gac atc	1543
Leu Leu Arg Glu Val Ile Ile Asn Ser Arg Phe Val Lys Gly Asp Ile	
484 489 494 499	
agc act aaa ttt ctc tcc gat gtg tat cct gat ggc ttc aaa gga cac	1591
Ser Thr Lys Phe Leu Ser Asp Val Tyr Pro Asp Gly Phe Lys Gly His	
500 505 510 515	
atg cta acc aag agt gag aag aac cag tta ttg gca ata gca tca tca	1639
Met Leu Thr Lys Ser Glu Lys Asn Gln Leu Leu Ala Ile Ala Ser Ser	
516 521 526 531	
ttg ttt gtg gca ttc cag tta aga gca caa cat ttt caa gaa aat tca	1687
Leu Phe Val Ala Phe Gln Leu Arg Ala Gln His Phe Gln Glu Asn Ser	
532 537 542 547	
aga atg cct gtt att aaa cca gac ata gcc aac tgg gag ctc tca gta	1735
Arg Met Pro Val Ile Lys Pro Asp Ile Ala Asn Trp Glu Leu Ser Val	
548 553 558 563	
aaa ttg cat gat aaa gtt cat acc gta gta gca tca aac aat ggg tca	1783
Lys Leu His Asp Lys Val His Thr Val Val Ala Ser Asn Asn Gly Ser	
564 569 574 579	
gtg ttc tcg gtg gaa gtt gat ggg tcg aaa cta aat gtg acc agc acg	1831
Val Phe Ser Val Glu Val Asp Gly Ser Lys Leu Asn Val Thr Ser Thr	
580 585 590 595	
tgg aac ctg gct tcg ccc tta ttg tct gtc agc gtt gat ggc act cag	1879
Trp Asn Leu Ala Ser Pro Leu Leu Ser Val Ser Val Asp Gly Thr Gln	
596 601 606 611	
agg act gtc cag tgt ctt tct cga gaa gca ggt gga aac atg agc att	1927
Arg Thr Val Gln Cys Leu Ser Arg Glu Ala Gly Gly Asn Met Ser Ile	
612 617 622 627	
cag ttt ctt ggt aca gtg tac aag gtg aat atc tta acc aga ctt gcc	1975

Gln Phe Leu Gly Thr Val Tyr Lys Val Asn Ile Leu Thr Arg Leu Ala	
628 633 638 643	
gca gaa ttg aac aaa ttt atg ctg gaa aaa gtg act gag gac aca agc	2023
Ala Glu Leu Asn Lys Phe Met Leu Glu Lys Val Thr Glu Asp Thr Ser	
644 649 654 659	
agt gtt ctg cgt tcc ccg atg ccc gga gtg gtg gtg gcc gtc tct gtc	2071
Ser Val Leu Arg Ser Pro Met Pro Gly Val Val Val Ala Val Ser Val	
660 665 670 675	
aag cct gga gac gcg gta gca gaa ggt caa gaa att tgt gtg att gaa	2119
Lys Pro Gly Asp Ala Val Ala Glu Gly Gln Glu Ile Cys Val Ile Glu	
676 681 686 691	
gcc atg aaa atg cag aat agt atg aca gct ggg aaa act ggc acg gtg	2167
Ala Met Lys Met Gln Asn Ser Met Thr Ala Gly Lys Thr Gly Thr Val	
692 697 702 707	
aaa tct gtg cac tgt caa gct gga gac aca gtt gga gaa ggg gat ctg	2215
Lys Ser Val His Cys Gln Ala Gly Asp Thr Val Gly Glu Gly Asp Leu	
708 713 718 723	
ctc gtg gag ctg gaa tga aggatt tataaccttt cagtcacac ccaatttaat	2269
Leu Val Glu Leu Glu *	
724 729	
tagccatttg catgatgctt tcacacacaa ttgattcaag cattatacag gaacacccct	2329
gtgcagctac gtttacgtcg tcattttattc cacagagtca agaccaatat tctgccaaaa	2389
aatcaccaat ggaaattttc attgatataa atacttgtac atatgatttg tactttctgct	2449
gtgagattcc ctagtgtcaa aattaaatca ataaaactga gcatttgtct aaaaaaaaaa	2509
aa	2511

<210> 560
 <211> 4478
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (339)..(3050)

<400> 560	
atttggccct cgaggcaaga attcggcacg aggattttat aataccggag ttttgctcta	60
tcactgtatc atggacagca agcttatgga acttattcct caaaaagtgg gacatgctga	120
aaatacaaac ctagcttgag tttagttatg tcocataaatg ttaactgatc cctgtggtca	180
gtagggagac agctggcatc cgtttccaac cagccaagga tattcggtcg actgtactga	240

ctgaccactt tgctcaggcc gcaagtgtcc ctcagaaaag cctgaggact tattaaggtc	300
atggaagggtt gccttggcag gaactotttt ctaatcac atg ttt ttg act tcc	353
Met Phe Leu Thr Ser	
1	
ctc tct agc cct aac cgg cag cca ttt gtt ctc ttt ggt aat cac tcc	401
Leu Ser Ser Pro Asn Arg Gln Pro Phe Val Leu Phe Gly Asn His Ser	
6 11 16 21	
aca cga gaa aac ctg aat gct ggc aac ttt aac ttc cct tct gaa gga	449
Thr Arg Glu Asn Leu Asn Ala Gly Asn Phe Asn Phe Pro Ser Glu Gly	
22 27 32 37	
cat ctg gta cga agc act ggt ccc ggc ggg agc ttt gcc aag cac atg	497
His Leu Val Arg Ser Thr Gly Pro Gly Gly Ser Phe Ala Lys His Met	
38 43 48 53	
gta gcc cag tgt gtc tca cca aag gga cct ctt gct tgt tcg aga aca	545
Val Ala Gln Cys Val Ser Pro Lys Gly Pro Leu Ala Cys Ser Arg Thr	
54 59 64 69	
tac ttt ttt gga gct act cat gtt cct tac ttg ggt ggt gac agc aag	593
Tyr Phe Phe Gly Ala Thr His Val Pro Tyr Leu Gly Gly Asp Ser Lys	
70 75 80 85	
ctg ccc aag aaa act gaa caa att agg cta ttg tcc cag ata tat gct	641
Leu Pro Lys Lys Thr Glu Gln Ile Arg Leu Leu Ser Gln Ile Tyr Ala	
86 91 96 101	
gct gtt att gag gct gtt ttg gct ggc att gca tgt tat gct aaa act	689
Ala Val Ile Glu Ala Val Leu Ala Gly Ile Ala Cys Tyr Ala Lys Thr	
102 107 112 117	
tcc agt cta aca aag gcc aag gag gta gca gag caa act ctg gga tct	737
Ser Ser Leu Thr Lys Ala Lys Glu Val Ala Glu Gln Thr Leu Gly Ser	
118 123 128 133	
ggg tta gat tcc ttt gag ttg att ccg ttt aag gca gcc ctg cgc tcc	785
Gly Leu Asp Ser Phe Glu Leu Ile Pro Phe Lys Ala Ala Leu Arg Ser	
134 139 144 149	
aag atg act ttt cat ata cat gct gtg aat aat cag gga aga att gta	833
Lys Met Thr Phe His Ile His Ala Val Asn Asn Gln Gly Arg Ile Val	
150 155 160 165	
ccg ctg gac agt gaa gat agc tta tcc ttt gtg aag acg gct tgt atg	881
Pro Leu Asp Ser Glu Asp Ser Leu Ser Phe Val Lys Thr Ala Cys Met	
166 171 176 181	
gcc gtc tat gac att cct gac tta ctg gga ggc aat ggt tgt tta gga	929
Ala Val Tyr Asp Ile Pro Asp Leu Leu Gly Gly Asn Gly Cys Leu Gly	
182 187 192 197	
tct gtg gtt ttc tct gaa tca ttt ttg act tct cag atc tta gtt aaa	977
Ser Val Val Phe Ser Glu Ser Phe Leu Thr Ser Gln Ile Leu Val Lys	

198	203	208	213	
gaa aag gat ggc act gtt acc aca gaa acc agc tcc gta gtc ctg act				1025
Glu Lys Asp Gly Thr Val Thr Thr Glu Thr Ser Ser Val Val Leu Thr				
214	219	224	229	
gct gct gta ccc aga ttc tgc tcc tgg ctg gtg gaa gat aat gaa gta				1073
Ala Ala Val Pro Arg Phe Cys Ser Trp Leu Val Glu Asp Asn Glu Val				
230	235	240	245	
aaa ttg tct gag aaa acc cag caa gca gtg agg ggg gat gag tct ttc				1121
Lys Leu Ser Glu Lys Thr Gln Gln Ala Val Arg Gly Asp Glu Ser Phe				
246	251	256	261	
ctg ggc act tat cta aca gga gga gaa gga gca tat ctt tat tcc agc				1169
Leu Gly Thr Tyr Leu Thr Gly Gly Glu Gly Ala Tyr Leu Tyr Ser Ser				
262	267	272	277	
aat cta cag tcc tgg cct gag gaa ggg aat gtt cat ttc ttc tct agt				1217
Asn Leu Gln Ser Trp Pro Glu Glu Gly Asn Val His Phe Phe Ser Ser				
278	283	288	293	
ggc ctt ctg ttt tct cac tgt cgt cat gga agt atc atc att tcc aag				1265
Gly Leu Leu Phe Ser His Cys Arg His Gly Ser Ile Ile Ile Ser Lys				
294	299	304	309	
gat cac atg aat tcc att tcc ttc tat gat ggg gat tcc acc agt act				1313
Asp His Met Asn Ser Ile Ser Phe Tyr Asp Gly Asp Ser Thr Ser Thr				
310	315	320	325	
gtt gct gct ctt ctc ata gac ttc aaa agc tca ttg ctt cct cac ctc				1361
Val Ala Ala Leu Leu Ile Asp Phe Lys Ser Ser Leu Leu Pro His Leu				
326	331	336	341	
cca gtt cat ttc cat gga tca agc aat ttt ctg atg att gcc ctt ttc				1409
Pro Val His Phe His Gly Ser Ser Asn Phe Leu Met Ile Ala Leu Phe				
342	347	352	357	
ccc aaa tcg aag ata tac caa gca ttt tac tca gag gtc ttc tcc ctc				1457
Pro Lys Ser Lys Ile Tyr Gln Ala Phe Tyr Ser Glu Val Phe Ser Leu				
358	363	368	373	
tgg aaa cag cag gat aac tca ggg atc tct tta aaa gtg atc cag gaa				1505
Trp Lys Gln Gln Asp Asn Ser Gly Ile Ser Leu Lys Val Ile Gln Glu				
374	379	384	389	
gat gga tta tct gtg gaa caa aag aga ttg cac tcc agt gca cag aag				1553
Asp Gly Leu Ser Val Glu Gln Lys Arg Leu His Ser Ser Ala Gln Lys				
390	395	400	405	
ctc ttc agt gcc ctg agc cag cct gct ggg gag aaa cgg agt tcc cta				1601
Leu Phe Ser Ala Leu Ser Gln Pro Ala Gly Glu Lys Arg Ser Ser Leu				
406	411	416	421	
aag tta ctc tca gcc aaa ctc cca gag ctg gac tgg ttt ctc cag cat				1649
Lys Leu Leu Ser Ala Lys Leu Pro Glu Leu Asp Trp Phe Leu Gln His				
422	427	432	437	

ttc gcc atc agc agc att agc cag gag cct gtg atg cgg acc cat ctt	1697
Phe Ala Ile Ser Ser Ile Ser Gln Glu Pro Val Met Arg Thr His Leu	
438 443 448 453	
cct gtg ctg ctg cag caa gct gaa atc aac act act cac aga ata gaa	1745
Pro Val Leu Leu Gln Gln Ala Glu Ile Asn Thr Thr His Arg Ile Glu	
454 459 464 469	
agt gac aag gta att atc agc att gta acc ggc ctc cca ggc tgt cac	1793
Ser Asp Lys Val Ile Ile Ser Ile Val Thr Gly Leu Pro Gly Cys His	
470 475 480 485	
gct agc gag ctc tgt gct ttt ctg gtc act ctg cat aag gaa tgt ggc	1841
Ala Ser Glu Leu Cys Ala Phe Leu Val Thr Leu His Lys Glu Cys Gly	
486 491 496 501	
aga tgg atg gtg tat cgc caa atc atg gac agc tct gaa tgt ttt cat	1889
Arg Trp Met Val Tyr Arg Gln Ile Met Asp Ser Ser Glu Cys Phe His	
502 507 512 517	
gct gca cac ttc cag aga tac ctt tcc agt gcc cta gag gcc cag cag	1937
Ala Ala His Phe Gln Arg Tyr Leu Ser Ser Ala Leu Glu Ala Gln Gln	
518 523 528 533	
aac cgc tct gcg cgc cag tca gcc tac atc cgc aag aag acc aga ctg	1985
Asn Arg Ser Ala Arg Gln Ser Ala Tyr Ile Arg Lys Lys Thr Arg Leu	
534 539 544 549	
ctg gtg gtg tta caa ggc tac aca gat gtt att gat gtt gtc cag gcc	2033
Leu Val Val Leu Gln Gly Tyr Thr Asp Val Ile Asp Val Val Gln Ala	
550 555 560 565	
ctg cag acc cac cca gac tca aat gtc aag gcc tcc ttc acc att ggt	2081
Leu Gln Thr His Pro Asp Ser Asn Val Lys Ala Ser Phe Thr Ile Gly	
566 571 576 581	
gcc atc aca gca tgt gtg gag ccc atg agc tgc tac atg gag cac aga	2129
Ala Ile Thr Ala Cys Val Glu Pro Met Ser Cys Tyr Met Glu His Arg	
582 587 592 597	
ttt ctc ttt cct aaa tgt ctt gac cag tgt tca caa ggc ctg gtg agt	2177
Phe Leu Phe Pro Lys Cys Leu Asp Gln Cys Ser Gln Gly Leu Val Ser	
598 603 608 613	
aac gtg gta ttc acc agt cac acc acg gag cag cgg cac cct ctc ctt	2225
Asn Val Val Phe Thr Ser His Thr Thr Glu Gln Arg His Pro Leu Leu	
614 619 624 629	
gtt cag ctg cag agc ctc atc agg gct gcc aat cct gct gca gcc ttc	2273
Val Gln Leu Gln Ser Leu Ile Arg Ala Ala Asn Pro Ala Ala Ala Phe	
630 635 640 645	
att ctt gca gaa aat ggg att gtc acc agg aat gaa gac att gag ctg	2321
Ile Leu Ala Glu Asn Gly Ile Val Thr Arg Asn Glu Asp Ile Glu Leu	
646 651 656 661	

att ctc tca gaa aac agt ttt tca agt cct gag atg cta cga tct cga	2369
Ile Leu Ser Glu Asn Ser Phe Ser Ser Pro Glu Met Leu Arg Ser Arg	
662 667 672 677	
tat tta atg tat cct ggc tgg tat gaa ggt aaa ttg aat gct gga tca	2417
Tyr Leu Met Tyr Pro Gly Trp Tyr Glu Gly Lys Leu Asn Ala Gly Ser	
678 683 688 693	
gtc tat ccc cta atg gtt cag atc tgc gta tgg ttt ggc cgt ccc ttg	2465
Val Tyr Pro Leu Met Val Gln Ile Cys Val Trp Phe Gly Arg Pro Leu	
694 699 704 709	
gag aag act cgc ttt gtg gcc aaa tgt aaa gca att cag tcc tcc atc	2513
Glu Lys Thr Arg Phe Val Ala Lys Cys Lys Ala Ile Gln Ser Ser Ile	
710 715 720 725	
aag cca agt ccc ttc tcc gga aac atc tac cac atc ctg ggc aaa gtg	2561
Lys Pro Ser Pro Phe Ser Gly Asn Ile Tyr His Ile Leu Gly Lys Val	
726 731 736 741	
aag ttt tca gac tct gag agg acc atg gag gtc tgc tac aac aca ctg	2609
Lys Phe Ser Asp Ser Glu Arg Thr Met Glu Val Cys Tyr Asn Thr Leu	
742 747 752 757	
gcc aac tcc ttg agc atc atg cca gtt ttg gaa gga ccc aca cca cca	2657
Ala Asn Ser Leu Ser Ile Met Pro Val Leu Glu Gly Pro Thr Pro Pro	
758 763 768 773	
cca gac tcc aaa agc gta tct caa gac agc agc ggg cag cag gag tgc	2705
Pro Asp Ser Lys Ser Val Ser Gln Asp Ser Ser Gly Gln Gln Glu Cys	
774 779 784 789	
tac ctt gtg ttc atc ggc tgc tcc ctg aag gaa gac agc atc aag gac	2753
Tyr Leu Val Phe Ile Gly Cys Ser Leu Lys Glu Asp Ser Ile Lys Asp	
790 795 800 805	
tgg ctg cgg cag tca gct aag cag aag cct cag agg aaa gcc ctg aag	2801
Trp Leu Arg Gln Ser Ala Lys Gln Lys Pro Gln Arg Lys Ala Leu Lys	
806 811 816 821	
acc agg ggg atg ctg acg caa cag gag atc agg agc atc cac gta aaa	2849
Thr Arg Gly Met Leu Thr Gln Gln Glu Ile Arg Ser Ile His Val Lys	
822 827 832 837	
cgc cac ttg gaa ccc cta cct gca ggc tac ttt tat aat ggc acc caa	2897
Arg His Leu Glu Pro Leu Pro Ala Gly Tyr Phe Tyr Asn Gly Thr Gln	
838 843 848 853	
ttt gtt aac ttc ttt ggt gac aaa act gat ttt cac cca ctc atg gac	2945
Phe Val Asn Phe Phe Gly Asp Lys Thr Asp Phe His Pro Leu Met Asp	
854 859 864 869	
cag ttc atg aat gac tac gtg gaa gaa gcc aac cgg gaa att gag aag	2993
Gln Phe Met Asn Asp Tyr Val Glu Glu Ala Asn Arg Glu Ile Glu Lys	
870 875 880 885	
tat aac cag gag ctg gaa cag cag gag tat cat gac ctc ttt gag ctg	3041

Tyr Asn Gln Glu Leu Glu Gln Gln Glu Tyr His Asp Leu Phe Glu Leu
 886 891 896 901

aag ccc tag aggaagg ctgggcccgt acgtcctgca gaatgtccac cttggagatg 3097
 Lys Pro *
 902

gacgaacggg tgtcttaacc tcagctctgc tggaggcctc tcccttaagg ggctgtcttt 3157
 gttctccttg gcctgtgtgg gctggcttga gtgcatgttg tctttattcc ctgtatagcg 3217
 ctgaagagca tcacctgcac cattgatattt gggggctcggg ggaataactca aggatgagca 3277
 gatggggcct gcccgctctac gtgtgcaact ggcagtccag gagctctcggg tttctgataa 3337
 caggatctcc tttgggctct tgaggttggg gagaagcatt aggattacac agaggagcta 3397
 ctgggactta gaaggaaccc tggtcgctg aactgtggcc gtgtctggga ggcgaggcca 3457
 cgacaggcct caagcctcag atgctgctcc acgagagcca tcttccccag tggagtgcct 3517
 gcctccoctg ctaggcccgt tccctgaag gagctggccg tactggccgt gggcccagtc 3577
 ctgggaggag cagcacagcc ttgccaggc ccagtccaca gagccagcag cttgggttga 3637
 gatgaatgat gtgttcacaa atgaggggat tcccttctg gactaaactg aaggagaggc 3697
 ttgttgcttt ccagagggtg gtggctctta agttgacatc agcttttccc cttgtgggtg 3757
 gttcttttagc tctcctgtca caccattcgg gtgtcctaata gtagggacaa gagcaagcct 3817
 gctgctcagg cccctggcg aggttcacc tcaactgtga agggggcgtc ctgcagctgg 3877
 ttagtcttag gcctgggtggc tgatcacttg tggggtcagt ctccagcacc cagcgtccc 3937
 acaagccttg ccaaggaagg cctgcttttc agccacaaac ttcaggaaac tcatcccccc 3997
 gctccccaaa gtgttgttgc tggccctggg cttgtgtggc tctgaggat tgggaatttc 4057
 aaataattgc aatacctgag ttagaattcc ttctaattgg atcgttttta gctggaccat 4117
 aaagcagagg ggaattacaa gtgtgtccca tgcctgacct tcataattgg tgtgggggac 4177
 aggggagtca cagccaactga tatttaggtg atgtctctta ggacttcagt gcctcagcta 4237
 cctgaactgt aaatgttttc tgaatttcac atattttttt ttgcatgcct taggaagaag 4297
 cacataggta aaaccagcag tttccagtaa tatagggggg ttttgagcaa ggcccctgga 4357
 gcagcgggaga gacaagatgg agcacatgta gtctgtgtgc ctggtcacac agaggcctgc 4417
 atgcaagtag caaagcagct ctcaagggtg tgtcagtaaa atatattaga aaaaaaaaaa 4477
 a 4478

<210> 561
 <211> 1537
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (82)..(1392)

<220>
 <221> misc_feature
 <222> (1)..(1537)
 <223> n = a,t,c or g

<400> 561

agcgggtnnn cctganacct tgcagcaccg gtccggaatt cccgggtcga cccacgcgtc 60

cgcccacgcg tccgagaaga t atg gat cac aaa tct cca ggc aac aaa gga 111
 Met Asp His Lys Ser Pro Gly Asn Lys Gly
 1 5

tca ttg gtt tat gca gga att aaa tca att gta aag tca tcg ttg gga 159
 Ser Leu Val Tyr Ala Gly Ile Lys Ser Ile Val Lys Ser Ser Leu Gly
 11 16 21 26

atg gtg gaa agc agc aga cat aat tgg agt ggg ttg gat aag caa agt 207
 Met Val Glu Ser Ser Arg His Asn Trp Ser Gly Leu Asp Lys Gln Ser
 27 32 37 42

gat att caa aat tta aat gaa gag aga atc tta gct tta cag ctt tgt 255
 Asp Ile Gln Asn Leu Asn Glu Glu Arg Ile Leu Ala Leu Gln Leu Cys
 43 48 53 58

ggg tgg ata aag aaa gga acg gat gta gac gtg ggg cca ttt ttg aac 303
 Gly Trp Ile Lys Lys Gly Thr Asp Val Asp Val Gly Pro Phe Leu Asn
 59 64 69 74

tcc ctt gta caa gaa ggg gaa tgg gaa aga gct gct gct gtg gca ttg 351
 Ser Leu Val Gln Glu Gly Glu Trp Glu Arg Ala Ala Ala Val Ala Leu
 75 80 85 90

ttc aac ttg gat att cgc cga gca atc caa atc ctg aat gaa ggg gca 399
 Phe Asn Leu Asp Ile Arg Arg Ala Ile Gln Ile Leu Asn Glu Gly Ala
 91 96 101 106

tct tct gaa aaa gga gat ctg aat ctc aat gtg gta gca atg gct tta 447
 Ser Ser Glu Lys Gly Asp Leu Asn Leu Asn Val Val Ala Met Ala Leu
 107 112 117 122

tcg ggt tat acg gat gag aag aac tcc ctt tgg aga gaa atg tgt agc 495
 Ser Gly Tyr Thr Asp Glu Lys Asn Ser Leu Trp Arg Glu Met Cys Ser
 123 128 133 138

aca ctg cga tta cag cta aat aac ccg tat ttg/tgt gtc atg ttt gca 543
 Thr Leu Arg Leu Gln Leu Asn Pro Tyr Leu Cys Val Met Phe Ala
 139 144 149 154

ttt ctg aca agt gaa aca gga tct tac gat gga gtt ttg tat gaa aac	591
Phe Leu Thr Ser Glu Thr Gly Ser Tyr Asp Gly Val Leu Tyr Glu Asn	
155 160 165 170	
aaa gtt gca gta cgt gac aga gtg gca ttt gct tgt aaa ttc ctt agt	639
Lys Val Ala Val Arg Asp Arg Val Ala Phe Ala Cys Lys Phe Leu Ser	
171 176 181 186	
gat act cag tta aat aga tac atc gaa aag ttg acc aat gaa atg aaa	687
Asp Thr Gln Leu Asn Arg Tyr Ile Glu Lys Leu Thr Asn Glu Met Lys	
187 192 197 202	
gag gct gga aat ttg gaa gga att ttg ctt aca ggc ctt act aaa gat	735
Glu Ala Gly Asn Leu Glu Gly Ile Leu Leu Thr Gly Leu Thr Lys Asp	
203 208 213 218	
gga gtg gac tta atg gag agt tat gtt gat aga act gga gat gtt caa	783
Gly Val Asp Leu Met Glu Ser Tyr Val Asp Arg Thr Gly Asp Val Gln	
219 224 229 234	
aca gca agt tac tgt atg tta cag ggt tca cct tta gat gtt ctt aaa	831
Thr Ala Ser Tyr Cys Met Leu Gln Gly Ser Pro Leu Asp Val Leu Lys	
235 240 245 250	
gat gaa agg gtt cag tac tgg att gag aat tat aga aat tta tta gat	879
Asp Glu Arg Val Gln Tyr Trp Ile Glu Asn Tyr Arg Asn Leu Leu Asp	
251 256 261 266	
gcc tgg agg ttt tgg cat aaa cga gct gaa ttt gat att cac agg agt	927
Ala Trp Arg Phe Trp His Lys Arg Ala Glu Phe Asp Ile His Arg Ser	
267 272 277 282	
aag ttg gat ccc agt tcc aag cct tta gca caa gtt ttt gtg agt tgc	975
Lys Leu Asp Pro Ser Ser Lys Pro Leu Ala Gln Val Phe Val Ser Cys	
283 288 293 298	
aat ttc tgt ggc aag tca atc tcc tac agc tgt tca gct gtg cct cat	1023
Asn Phe Cys Gly Lys Ser Ile Ser Tyr Ser Cys Ser Ala Val Pro His	
299 304 309 314	
cag ggc aga ggt ttt agt cag tat ggt gtg agt ggc tca cca acg aaa	1071
Gln Gly Arg Gly Phe Ser Gln Tyr Gly Val Ser Gly Ser Pro Thr Lys	
315 320 325 330	
tct aaa gtc aca agt tgt cct ggc tgt cga aaa cca ctt cct cga tgt	1119
Ser Lys Val Thr Ser Cys Pro Gly Cys Arg Lys Pro Leu Pro Arg Cys	
331 336 341 346	
gcg ctt tgt ctc att aat atg gga aca cca gtt tct agc tgt cct gga	1167
Ala Leu Cys Leu Ile Asn Met Gly Thr Pro Val Ser Ser Cys Pro Gly	
347 352 357 362	
gga acc aaa tca gat gaa aaa gtg gac ttg agc aag gac aaa aaa tta	1215
Gly Thr Lys Ser Asp Glu Lys Val Asp Leu Ser Lys Asp Lys Lys Leu	
363 368 373 378	

gcc caa ttt aac aac tgg ttt aca tgg tgt cat aat tgc agg cac ggt 1263
Ala Gln Phe Asn Asn Trp Phe Thr Trp Cys His Asn Cys Arg His Gly
379 384 389 394

gga cat gct gga cat atg ctt agt tgg ttc agg gac cat gca gag tgc 1311
Gly His Ala Gly His Met Leu Ser Trp Phe Arg Asp His Ala Glu Cys
395 400 405 410

cct gtg tct gca tgc acg tgt aaa tgt atg cag ttg gat aca acg ggg 1359
Pro Val Ser Ala Cys Thr Cys Lys Cys Met Gln Leu Asp Thr Thr Gly
411 416 421 426

aat ctg gta cct gca gag act gtc cag cca taa aatgttac caccttaaga 1410
Asn Leu Val Pro Ala Glu Thr Val Gln Pro *
427 432 437

gaacccttca agtgtggagc tttctagtag gtgtccttca tagctcagaa acatacctca 1470

gaacaagcca ttcattgactt acctgtaatg ggaaaataaa tcattctatc agatcaaaaa 1530

aaaaaaaa 1537

<210> 562
<211> 1168
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (148)..(615)

<400> 562

tcggtaccgg ccggaattc ccgggtcgac ccacgcgtcc gggaaaaaag agaccataga 60

cttccatcct ggcctagagc ggcccttaaa gtgccaggga gaggagggcg ggtggggacc 120

actccagaat tggccgctgg cggtatc atg gcg acc cgg aac ccc cct ccc 171
Met Ala Thr Arg Asn Pro Pro Pro
1 5

caa gac tat gaa agt gat gac gac tct tat gaa gtg ttg gat tta act 219
Gln Asp Tyr Glu Ser Asp Asp Asp Ser Tyr Glu Val Leu Asp Leu Thr
9 14 19 24

gag tat gca aga aga cac cag tgg tgg aat cga gtg ttt ggc cac agt 267
Glu Tyr Ala Arg Arg His Gln Trp Trp Asn Arg Val Phe Gly His Ser
25 30 35 40

tog gga cct atg gta gaa aaa tac tca gta gct acc cag att gta atg 315
Ser Gly Pro Met Val Glu Lys Tyr Ser Val Ala Thr Gln Ile Val Met
41 46 51 56

ggg ggc gtt act ggc tgg tgt gca gga ttt ctg ttc cag aaa gtt gga 363
Gly Gly Val Thr Gly Trp Cys Ala Gly Phe Leu Phe Gln Lys Val Gly

57	62	67	72	
aaa ctt gca gca act gca gta ggt ggt ggc ttt ctt ctt ctt cag att				411
Lys Leu Ala Ala Thr Ala Val Gly Gly Gly Phe Leu Leu Leu Gln Ile				
73	78	83	88	
gct agt cat agt ggc tat gtg cag att gac tgg aag aga gtt gaa aaa				459
Ala Ser His Ser Gly Tyr Val Gln Ile Asp Trp Lys Arg Val Glu Lys				
89	94	99	104	
gat gta aat aaa gca aaa aga cag att aag aaa cga gcg aac aaa gca				507
Asp Val Asn Lys Ala Lys Arg Gln Ile Lys Lys Arg Ala Asn Lys Ala				
105	110	115	120	
gca cct gaa atc aac aat tta att gaa gaa gca aca gaa ttt atc aag				555
Ala Pro Glu Ile Asn Asn Leu Ile Glu Glu Ala Thr Glu Phe Ile Lys				
121	126	131	136	
cag aac att gtg ata tcc agt gga ttt gtg gga ggc ttt ttg ctc gga				603
Gln Asn Ile Val Ile Ser Ser Gly Phe Val Gly Gly Phe Leu Leu Gly				
137	142	147	152	
ctt gca tct taa gga catgaatatt ctcccataac ggattcaact atgagaagag				658
Leu Ala Ser *				
153				
aagtggcagc aataaggcag tctctcaaaa gtcatactgc cagagtctct agggcaagga				718
gaaacaacta gctggacaat actcaattca caacttagca ttttgccatc tgaagcttgg				778
caaactagta tctgctgtaa aacaacctat atggtatgtg aaccgtagta ttccctgagca				838
aaacgtggct ttcatcgctt tgtaaaaatt tgcattctgtt tagaaactag cctataaaat				898
atcaccattg gatgtagata tggagagaaa agaaatatgt tggggtttatt gcttagcgaa				958
atattctctt tttattttaa taaaatgttc ttcattgtgt tttatggtat gtgtccataa				1018
tttaaaattc atgttatagt ttcagtatta aggctgactt ttttttttta agatatgttt				1078
gcaataagtt aaaaaactgt aatacccttt tgtggaaagc tttagaaatg atataattat				1138
taaagatatt aaacagacaa aaaaaaaaaa				1168

<210> 563
 <211> 3027
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (14) .. (787)

<400> 563

gcccccccaa ttg	atg gcg acc cat ggt ggc tcg cgt tta aac tta agc	49
	Met Ala Thr His Gly Gly Ser Arg Leu Asn Leu Ser	
	1 5 10	
ttg gta ccg agc tcg gat cca cta gtc cag tgt ggt gga att qac aaa	97	
Leu Val Pro Ser Ser Asp Pro Leu Val Gln Cys Gly Gly Ile His Lys		
13 18 23 28		
gga gcg gcg gcc ggg agc gga ctt acc tta cct tct ctg cct tcg gcg	145	
Gly Ala Ala Ala Gly Ser Gly Leu Thr Leu Pro Ser Leu Pro Ser Ala		
29 34 39 44		
cgc ttc tca gcc ggg ccg ccg acc caa agg agc cgt ccg act atg tct	193	
Arg Phe Ser Ala Gly Pro Pro Thr Gln Arg Ser Arg Pro Thr Met Ser		
45 50 55 60		
aac atg gag aaa cac ctg ttc aac ctg aag ttc gcg gcc aaa gaa ctg	241	
Asn Met Glu Lys His Leu Phe Asn Leu Lys Phe Ala Ala Lys Glu Leu		
61 66 71 76		
agt agg agt gcc aaa aaa tgc gat aag gag gaa aag gcc gaa aag gcc	289	
Ser Arg Ser Ala Lys Lys Cys Asp Lys Glu Glu Lys Ala Glu Lys Ala		
77 82 87 92		
aaa att aaa aag gcc att cag aag ggc aac atg gaa gtt gcg agg ata	337	
Lys Ile Lys Lys Ala Ile Gln Lys Gly Asn Met Glu Val Ala Arg Ile		
93 98 103 108		
cac gcc gaa aat gcc atc cgc cag aag aac cag gcg gtg aat ttc ttg	385	
His Ala Glu Asn Ala Ile Arg Gln Lys Asn Gln Ala Val Asn Phe Leu		
109 114 119 124		
aga atg agt gcg cga gtc gat gca gtg gct gcc agg gtc cag acg gcg	433	
Arg Met Ser Ala Arg Val Asp Ala Val Ala Arg Val Gln Thr Ala		
125 130 135 140		
gtg acg atg ggc aag gtg acc aag tcg atg gct ggt gtg gtt aag tcg	481	
Val Thr Met Gly Lys Val Thr Lys Ser Met Ala Gly Val Val Lys Ser		
141 146 151 156		
atg gat gcg aca ttg aag acc atg aat ctg gag aag att tct gct ttg	529	
Met Asp Ala Thr Leu Lys Thr Met Asn Leu Glu Lys Ile Ser Ala Leu		
157 162 167 172		
atg gac aaa ttc gag cac cag ttt gag act ctg gac gtc cag acg cag	577	
Met Asp Lys Phe Glu His Gln Phe Glu Thr Leu Asp Val Gln Thr Gln		
173 178 183 188		
caa atg gaa gac acg atg agc agc acg acg acg ctc acc act ccc cag	625	
Gln Met Glu Asp Thr Met Ser Ser Thr Thr Thr Leu Thr Thr Pro Gln		
189 194 199 204		
aac caa gtg gat atg ctg ctc cag gaa atg gca gat gag gcg ggc ctc	673	
Asn Gln Val Asp Met Leu Leu Gln Glu Met Ala Asp Glu Ala Gly Leu		
205 210 215 220		
gac ctc aac atg gag ctg ccg cag ggc cag acc ggc tcc gtg ggc acg	721	

agaaaataat tataggggcc cttccaagtt ctttgaaaga ttcataacca actattcact 2263
 attataacat gtttcccagt gtaaagtagt aaggaaaaaa aaagtgtaac aggtgcgtgc 2323
 agatgaggag tgaccctcat atttaagtta ttttatattt gactggacat tgttcagaag 2383
 tgtgctttaa gggacacttg ttggttgtct gccagcatc tctcaagaat atccctcctg 2443
 tcctccacat ggttgtgcag ggccatgtgt gaagacagca tgagtcttaa cccctctttt 2503
 atttatattt tgagacagag tctcgctctg ttgccaggc tggagtgtg tggcgogac 2563
 tctgctcact gcaacctcca cctccgggt tcaagtgatt ctctgcctc agcctgccga 2623
 gtagctggaa ttacaggtgt gcaccacat gccagctag ttttttgta ttttagtag 2683
 agacagggtt tcaactatgtt ggccaggctg gtcttgaact cctgacctca ggtgatccgc 2743
 ccacctcagc ctcccaaagt gctgggatta caggcatgag ccaactgcacc tggccttaac 2803
 cctcttttag attggaaaaa ataattacaa ctttaaaaat agcttagtgt tgaacccttt 2863
 ggtaaaactaa agaccctttt ataatgcaca tattccaac aaaattaata tattttgtga 2923
 gattaaacaa tgcttgata tgcttgaact ttcttaaaat atgtccatgt catactatta 2983
 tgaatgtaca ttttatgag tcataaatat tattttcaaa agca 3027

<210> 564
 <211> 1200
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (559)..(957)

<400> 564
 actgaattga atttaggtga cactatagaa gagctatgac gtcgcatgca cgcgtacgta 60
 agcttggatc ctctagagcg gccgcctact actactaaat tcgcgggccgc gtcgactttt 120
 tttttttttt tttttgaatg tgagccaaag atttatttct tcatttcttg catttgaaat 180
 actotccaat gacatccttg gctgagact ccttgccata gtccttaact actacacaac 240
 tgcaaccaac cactttacgg ggtttccct ctctgtcaat ttacaaagg cctaccatt 300
 ctctagttt cttgttgtca tcaaccttaa ttaggtgat ttggtgttca gcacaaagg 360
 cctccaccaa cttgacatac ataggctcat cacagttgga tgcaagcaca caaagatggg 420
 cttggcgctt gtctaaggct ttggcagctt cgcaattcc acgtgctagg ccatcgtgga 480

tgagggcagt cttcagaacc tcttgtaaag cagtattaac gtccattaca cctccagcag	540
caatgccttc ctcggccca tgg cgg tgg gtt acg ggt gaa gct gaa tct tga	591
Met Ala Glu Glu Gly Ile Ala Ala Gly Gly Val	
1 5	
acg cac cca agc ctc cgc ctc cgc gcg act cgg cgg cat tac tag tga	639
Met Asp Val Asn Thr Ala Leu Gln Glu Val Leu Lys Thr Ala Leu Ile	
12 17 22 27	
tta cta gtg aat tca cta gta ata tta cta gtg aat cac tag taa tat	687
His Asp Gly Leu Ala Arg Gly Ile Arg Glu Ala Ala Lys Ala Leu Asp	
28 33 38 43	
tac tag tga att cac tag taa tgt cgc gcg gag gcg gag gct tgg gtg	735
Lys Arg Gln Ala His Leu Cys Val Leu Ala Ser Asn Cys Asp Glu Pro	
44 49 54 59	
cgt tca aga ttc agc ttc acc cgt aac cca ccg cca tgg ccg agg aag	783
Met Tyr Val Lys Leu Val Glu Ala Leu Cys Ala Glu His Gln Ile Asn	
60 65 70 75	
gca ttg ctg ctg gag gtg taa tgg acg tta ata ctg ctt tac aag agg	831
Leu Ile Lys Val Asp Asp Asn Lys Lys Leu Gly Glu Trp Val Gly Leu	
76 81 86 91	
ttc tga aga ctg ccc tca tcc acg atg gcc tag cac gtg gaa ttc gcg	879
Cys Lys Ile Asp Arg Glu Gly Lys Pro Arg Lys Val Val Gly Cys Ser	
92 97 102 107	
aag ctg cca aag cct tag aca agc gcc aag ccc atc ttt gtg tgc ttg	927
Cys Val Val Val Lys Asp Tyr Gly Lys Glu Ser Gln Ala Lys Asp Val	
108 113 118 123	
cat cca act gtg atg agc cta tgt atg tca a gttggtggag gccctttgtg	978
Ile Glu Glu Tyr Phe Lys Cys Lys Lys *	
124 129	
ctgaacacca aatcaacctt attaggttg atgacaacaa gaaactagga gaatgggtag	1038
gcctttgtaa aattgacaga gaggggaaac cccgtaaagt ggttggttgc agttgtgtag	1098
tagttaagga ctatggcaag gagtctcagg ccaaggatgt cattgaagag tatttcaa	1158
gcaagaaatg aagaaataaa tctttggctc acaaaaaaaaa aa	1200

<210> 565
 <211> 5078
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (83)..(4666)

<400> 565

ggaagaagta cctacacagg aatcagtgaa gtgggaaatt aatgttatta ttaaaaaatcc	60
tgaaattgtg tttgtagctg ac atg aca aaa aat gat gct cct gct tta gtc	112
Met Thr Lys Asn Asp Ala Pro Ala Leu Val	
1 5	
att aca aca caa tgt gaa att tgc tat aaa ggt aac ctt gaa aat agt	160
Ile Thr Thr Gln Cys Glu Ile Cys Tyr Lys Gly Asn Leu Glu Asn Ser	
11 16 21 26	
aca atg act gct gcc att aaa gat ctc caa gtg aga gcc tgc ccg ttt	208
Thr Met Thr Ala Ala Ile Lys Asp Leu Gln Val Arg Ala Cys Pro Phe	
27 32 37 42	
ctt cca gtc aag aga aaa ggc aaa atc act act gtt ttg cag ccc tgt	256
Leu Pro Val Lys Arg Lys Gly Lys Ile Thr Thr Val Leu Gln Pro Cys	
43 48 53 58	
gac ttg ttt tat caa act act cag aaa ggt aca gat cca caa gtg atc	304
Asp Leu Phe Tyr Gln Thr Thr Gln Lys Gly Thr Asp Pro Gln Val Ile	
59 64 69 74	
gat atg tca gta aaa tcc ctg aca cta aag gtt tca cca gtt att ata	352
Asp Met Ser Val Lys Ser Leu Thr Leu Lys Val Ser Pro Val Ile Ile	
75 80 85 90	
aat act atg att acc ata act tca gca ctg tat aca act aag gaa acc	400
Asn Thr Met Ile Thr Ile Thr Ser Ala Leu Tyr Thr Thr Lys Glu Thr	
91 96 101 106	
atc cca gaa gaa acg gct tct tct act gca cat tta tgg gaa aag aag	448
Ile Pro Glu Glu Thr Ala Ser Ser Thr Ala His Leu Trp Glu Lys Lys	
107 112 117 122	
gat aca aag act tta aaa atg tgg ttt ctt gaa gaa tca aat gaa act	496
Asp Thr Lys Thr Leu Lys Met Trp Phe Leu Glu Glu Ser Asn Glu Thr	
123 128 133 138	
gaa aaa ata gct ccc aca act gaa ttg gta ccc aaa ggc gag atg ata	544
Glu Lys Ile Ala Pro Thr Thr Glu Leu Val Pro Lys Gly Glu Met Ile	
139 144 149 154	
aaa atg aac att gat tct att ttt ata gtt ctt gag gct gga att ggt	592
Lys Met Asn Ile Asp Ser Ile Phe Ile Val Leu Glu Ala Gly Ile Gly	
155 160 165 170	
cat aga aca gta cct atg ctt ctg gca aag tca cgt ttt tca ggg gaa	640
His Arg Thr Val Pro Met Leu Leu Ala Lys Ser Arg Phe Ser Gly Glu	
171 176 181 186	
ggc aaa aac tgg agt tcc cta ata aat ctg cac tgt cag ctt gag cta	688
Gly Lys Asn Trp Ser Ser Leu Ile Asn Leu His Cys Gln Leu Glu Leu	
187 192 197 202	
gaa gtg cat tat tat aat gaa atg ttt ggt gta tgg gag cct ttg ctt	736

Glu Val His Tyr Tyr Asn Glu Met Phe Gly Val Trp Glu Pro Leu Leu	
203 208 213 218	
gaa ccc tta gaa att gat cag act gag gat ttt aga cca tgg aat ctt	784
Glu Pro Leu Glu Ile Asp Gln Thr Glu Asp Phe Arg Pro Trp Asn Leu	
219 224 229 234	
ggt atc aag atg aaa aag aaa gca aaa atg gcc att gtt gag tca gat	832
Gly Ile Lys Met Lys Lys Lys Ala Lys Met Ala Ile Val Glu Ser Asp	
235 240 245 250	
cct gaa gaa gaa aac tac aaa gtg cca gaa tat aaa act gtc atc agt	880
Pro Glu Glu Glu Asn Tyr Lys Val Pro Glu Tyr Lys Thr Val Ile Ser	
251 256 261 266	
ttc cat tca aaa gac caa tta aac att aca tta tcc aaa tgt ggt ctt	928
Phe His Ser Lys Asp Gln Leu Asn Ile Thr Leu Ser Lys Cys Gly Leu	
267 272 277 282	
gta atg tta aac aat tta gtc aag gca ttt aca gaa gct gcc act gga	976
Val Met Leu Asn Asn Leu Val Lys Ala Phe Thr Glu Ala Ala Thr Gly	
283 288 293 298	
tct tca gct gac ttc gta aag gat cta gca cca ttt atg att tta aat	1024
Ser Ser Ala Asp Phe Val Lys Asp Leu Ala Pro Phe Met Ile Leu Asn	
299 304 309 314	
tcc ctt gga ctt act att tct gtt tcg cca agt gat tct ttt agt gta	1072
Ser Leu Gly Leu Thr Ile Ser Val Ser Pro Ser Asp Ser Phe Ser Val	
315 320 325 330	
ctc aac att cct atg gca aaa tca tat gta ttg aaa aat gga gaa agt	1120
Leu Asn Ile Pro Met Ala Lys Ser Tyr Val Leu Lys Asn Gly Glu Ser	
331 336 341 346	
tta agt atg gat tat atc cga acc aag gac aat gat cat ttc aat gca	1168
Leu Ser Met Asp Tyr Ile Arg Thr Lys Asp Asn Asp His Phe Asn Ala	
347 352 357 362	
atg acc agc cta agc agc aaa ctc ttc ttc att ctt ctt aca cct gtt	1216
Met Thr Ser Leu Ser Ser Lys Leu Phe Phe Ile Leu Leu Thr Pro Val	
363 368 373 378	
aac cat tct act gct gat aag att cct tta aca aaa gtg gga cga cgt	1264
Asn His Ser Thr Ala Asp Lys Ile Pro Leu Thr Lys Val Gly Arg Arg	
379 384 389 394	
ctg tac act gta aga cac aga gag tct ggc gtt gaa aga tct att gtt	1312
Leu Tyr Thr Val Arg His Arg Glu Ser Gly Val Glu Arg Ser Ile Val	
395 400 405 410	
tgt caa att gat aca gta gaa gga agt aag aag gtc aca att cgc tcc	1360
Cys Gln Ile Asp Thr Val Glu Gly Ser Lys Lys Val Thr Ile Arg Ser	
411 416 421 426	
cca gtg cag ata aga aat cat ttt tca gtc cca ctg tct gtt tac gaa	1408
Pro Val Gln Ile Arg Asn His Phe Ser Val Pro Leu Ser Val Tyr Glu	

427	432	437	442	
ggg gat acc tta ttg gga act gcc tca cct gaa aat gaa ttc aac ata				1456
Gly Asp Thr Leu Leu Gly Thr Ala Ser Pro Glu Asn Glu Phe Asn Ile				
443	448	453	458	
cca tta gga tct tac cga tca ttc att ttt ctg aag cca gaa gat gag				1504
Pro Leu Gly Ser Tyr Arg Ser Phe Ile Phe Leu Lys Pro Glu Asp Glu				
459	464	469	474	
aac tat caa atg tgt gaa gga att gac ttt gaa gag att ata aaa aat				1552
Asn Tyr Gln Met Cys Glu Gly Ile Asp Phe Glu Glu Ile Ile Lys Asn				
475	480	485	490	
gat ggt gct ctt cta aag aag aaa tgt aga tct aaa aac cct tct aag				1600
Asp Gly Ala Leu Leu Lys Lys Lys Cys Arg Ser Lys Asn Pro Ser Lys				
491	496	501	506	
gaa tca ttt ctc att aat att gtt cca gaa aaa gat aat tta aca tct				1648
Glu Ser Phe Leu Ile Asn Ile Val Pro Glu Lys Asp Asn Leu Thr Ser				
507	512	517	522	
cta tca gtg tat tca gaa gat ggt tgg gat tta cca tac ata atg cat				1696
Leu Ser Val Tyr Ser Glu Asp Gly Trp Asp Leu Pro Tyr Ile Met His				
523	528	533	538	
ttg tgg cca cct atc ctg ctc cga aat ctt ctt cct tac aaa att gct				1744
Leu Trp Pro Pro Ile Leu Leu Arg Asn Leu Leu Pro Tyr Lys Ile Ala				
539	544	549	554	
tat tat ata gag gga att gaa aat tcg gtt ttt act cta agt gaa gga				1792
Tyr Tyr Ile Glu Gly Ile Glu Asn Ser Val Phe Thr Leu Ser Glu Gly				
555	560	565	570	
cat tca gcc cag att tgt act gca cag ttg ggt aaa gcc agg cta cat				1840
His Ser Ala Gln Ile Cys Thr Ala Gln Leu Gly Lys Ala Arg Leu His				
571	576	581	586	
tta aaa tta ctt gac tat ctc aat cac gat tgg aaa agt gaa tat cac				1888
Leu Lys Leu Leu Asp Tyr Leu Asn His Asp Trp Lys Ser Glu Tyr His				
587	592	597	602	
ata aag cct aat cag caa gac att agt ttt gtc agt ttt act tgt gtt				1936
Ile Lys Pro Asn Gln Gln Asp Ile Ser Phe Val Ser Phe Thr Cys Val				
603	608	613	618	
aca gaa atg gaa aag act gat tta gat att gct gtc cat atg act tac				1984
Thr Glu Met Glu Lys Thr Asp Leu Asp Ile Ala Val His Met Thr Tyr				
619	624	629	634	
aat act ggt cag aca gtt gtg gca ttt cat agt cct tat tgg atg gtc				2032
Asn Thr Gly Gln Thr Val Val Ala Phe His Ser Pro Tyr Trp Met Val				
635	640	645	650	
aat aaa act ggc cgc atg tta cag tac aaa gca gac gga att cat cga				2080
Asn Lys Thr Gly Arg Met Leu Gln Tyr Lys Ala Asp Gly Ile His Arg				
651	656	661	666	

aag cat cca cct aat tat aaa aag cca gtt ctc ttt tct ttt cag cca	2128
Lys His Pro Pro Asn Tyr Lys Lys Pro Val Leu Phe Ser Phe Gln Pro	
667 672 677 682	
aat cac ttt ttt aat aac aat aag gtt caa ctt atg gta act gat agt	2176
Asn His Phe Phe Asn Asn Asn Lys Val Gln Leu Met Val Thr Asp Ser	
683 688 693 698	
gag ttg tcc aat cag ttt tca att gat act gtt ggt agt cat gga gct	2224
Glu Leu Ser Asn Gln Phe Ser Ile Asp Thr Val Gly Ser His Gly Ala	
699 704 709 714	
gtt aaa tgt aaa ggc ctg aaa atg gac tat caa gtt ggt gtc act ata	2272
Val Lys Cys Lys Gly Leu Lys Met Asp Tyr Gln Val Gly Val Thr Ile	
715 720 725 730	
gac ctg agc agt ttt aac att act aga att gtg aca ttt acc cct ttt	2320
Asp Leu Ser Ser Phe Asn Ile Thr Arg Ile Val Thr Phe Thr Pro Phe	
731 736 741 746	
tat atg att aaa aac aaa agc aaa tac cat ata tca gtg gct gaa gaa	2368
Tyr Met Ile Lys Asn Lys Ser Lys Tyr His Ile Ser Val Ala Glu Glu	
747 752 757 762	
gga aat gat aaa tgg ctc tct ctt gat ttg gag cag tgt atc ccc ttt	2416
Gly Asn Asp Lys Trp Leu Ser Leu Asp Leu Glu Gln Cys Ile Pro Phe	
763 768 773 778	
tgg cct gag tat gct tct agt aaa ctt ctt att caa gtc gaa agg agt	2464
Trp Pro Glu Tyr Ala Ser Ser Lys Leu Leu Ile Gln Val Glu Arg Ser	
779 784 789 794	
gaa gat cct ccc aaa agg ata tat ttt aac aag cag gaa aat tgt att	2512
Glu Asp Pro Pro Lys Arg Ile Tyr Phe Asn Lys Gln Glu Asn Cys Ile	
795 800 805 810	
cta ttg cgt cta gat aac gag ctt gga ggt att ata gca gaa gtg aat	2560
Leu Leu Arg Leu Asp Asn Glu Leu Gly Gly Ile Ile Ala Glu Val Asn	
811 816 821 826	
ttg gcc gag cat tct aca gtt att aca ttt tta gat tat cat gat gga	2608
Leu Ala Glu His Ser Thr Val Ile Thr Phe Leu Asp Tyr His Asp Gly	
827 832 837 842	
gca gct aca ttc ctc tta ata aat cac aca aag aat gaa ctt gtt caa	2656
Ala Ala Thr Phe Leu Leu Ile Asn His Thr Lys Asn Glu Leu Val Gln	
843 848 853 858	
tac aat caa agt tct ctc agt gaa ata gaa gat tcc ctc cct cct ggt	2704
Tyr Asn Gln Ser Ser Leu Ser Glu Ile Glu Asp Ser Leu Pro Pro Gly	
859 864 869 874	
aaa gcc gtg ttt tat aca tgg gct gat ccg gtg ggc tct aga agg ctg	2752
Lys Ala Val Phe Tyr Thr Trp Ala Asp Pro Val Gly Ser Arg Arg Leu	
875 880 885 890	

aag tgg aga tgt aga aaa agc cat ggt gaa gta aca cag aag gat gat	2800
Lys Trp Arg Cys Arg Lys Ser His Gly Glu Val Thr Gln Lys Asp Asp	
891 896 901 906	
atg atg atg cct ata gat ttg ggg gaa aag aca ata tat tta gtt tca	2848
Met Met Met Pro Ile Asp Leu Gly Glu Lys Thr Ile Tyr Leu Val Ser	
907 912 917 922	
ttc ttt gaa ggt tta caa cgc att att tta ttc act gaa gat cca agg	2896
Phe Phe Glu Gly Leu Gln Arg Ile Ile Leu Phe Thr Glu Asp Pro Arg	
923 928 933 938	
gta ttt aaa gta aca tat gaa agt gag aaa gca gag tta gca gag caa	2944
Val Phe Lys Val Thr Tyr Glu Ser Glu Lys Ala Glu Leu Ala Glu Gln	
939 944 949 954	
gaa att gca gtg gca tta caa gat gtt gga att tct ctt gtc aac aat	2992
Glu Ile Ala Val Ala Leu Gln Asp Val Gly Ile Ser Leu Val Asn Asn	
955 960 965 970	
tac acg aag caa gaa gta gcc tat ata ggc att aca agt tct gat gtg	3040
Tyr Thr Lys Gln Glu Val Ala Tyr Ile Gly Ile Thr Ser Ser Asp Val	
971 976 981 986	
gtt tgg gaa aca aag ccc aag aag aag gca aga tgg aag cca atg agt	3088
Val Trp Glu Thr Lys Pro Lys Lys Lys Ala Arg Trp Lys Pro Met Ser	
987 992 997 1002	
gta aag cac act gag aag tta gag aga gaa ttt aag gaa tat act gaa	3136
Val Lys His Thr Glu Lys Leu Glu Arg Glu Phe Lys Glu Tyr Thr Glu	
1003 1008 1013 1018	
tct tct cct tca gaa gat aag gtt att cag ttg gac act aat gtt ccg	3184
Ser Ser Pro Ser Glu Asp Lys Val Ile Gln Leu Asp Thr Asn Val Pro	
1019 1024 1029 1034	
gtt cgc cta acc cct act ggt cat aac atg aaa att ctg cag ccg cat	3232
Val Arg Leu Thr Pro Thr Gly His Asn Met Lys Ile Leu Gln Pro His	
1035 1040 1045 1050	
gta ata gct cta cga aga aat tat ctt cca gca tta aaa gtg gaa tat	3280
Val Ile Ala Leu Arg Asn Tyr Leu Pro Ala Leu Lys Val Glu Tyr	
1051 1056 1061 1066	
aac aca tct gca cat caa tca tca ttt aga att cag att tac aga ata	3328
Asn Thr Ser Ala His Gln Ser Ser Phe Arg Ile Gln Ile Tyr Arg Ile	
1067 1072 1077 1082	
cag atc caa aat cag ata cat ggt gct gta ttt ccc ttt gtg ttt tat	3376
Gln Ile Gln Asn Gln Ile His Gly Ala Val Phe Pro Phe Val Phe Tyr	
1083 1088 1093 1098	
cct gtt aaa cct cca aag tcg gtc acc atg gat tca gca cca aag ccc	3424
Pro Val Lys Pro Pro Lys Ser Val Thr Met Asp Ser Ala Pro Lys Pro	
1099 1104 1109 1114	
ttt aca gat gtc agt att gtc atg aga tct gca gga cat tcc cag ata	3472

1339	1344	1349	1354	
aaa atc acc ggt gct atg gct aag ggg gta gca gct atg acc atg gat				4192
Lys Ile Thr Gly Ala Met Ala Lys Gly Val Ala Ala Met Thr Met Asp				
1355	1360	1365	1370	
gaa gac tac caa cag aag aga aga gaa gcc atg aat aag caa cca gct				4240
Glu Asp Tyr Gln Gln Lys Arg Arg Glu Ala Met Asn Lys Gln Pro Ala				
1371	1376	1381	1386	
ggg ttt aga gaa ggc atc act cgt gga gga aaa ggc tta gtt tct gga				4288
Gly Phe Arg Glu Gly Ile Thr Arg Gly Gly Lys Gly Leu Val Ser Gly				
1387	1392	1397	1402	
ttt gtt agt ggc ata aca gga att gtt aca aaa cca atc aaa gga gct				4336
Phe Val Ser Gly Ile Thr Gly Ile Val Thr Lys Pro Ile Lys Gly Ala				
1403	1408	1413	1418	
caa aaa gga gga gca gct ggt ttc ttt aaa ggt gtt ggg aaa ggt tta				4384
Gln Lys Gly Gly Ala Ala Gly Phe Phe Lys Gly Val Gly Lys Gly Leu				
1419	1424	1429	1434	
gta gga gcg gta gca agg cca act gga ggc atc ata gac atg gct agc				4432
Val Gly Ala Val Ala Arg Pro Thr Gly Gly Ile Ile Asp Met Ala Ser				
1435	1440	1445	1450	
agt aca ttt cag ggg ata aaa aga gct aca gag act tct gaa gtg gag				4480
Ser Thr Phe Gln Gly Ile Lys Arg Ala Thr Glu Thr Ser Glu Val Glu				
1451	1456	1461	1466	
agt ctg cga cct cct cgg ttc ttc aat gaa gat gga gtt atc aga ccg				4528
Ser Leu Arg Pro Pro Arg Phe Phe Asn Glu Asp Gly Val Ile Arg Pro				
1467	1472	1477	1482	
tac agg ttg agg gat ggg act gga aat caa atg tta cag aaa att caa				4576
Tyr Arg Leu Arg Asp Gly Thr Gly Asn Gln Met Leu Gln Lys Ile Gln				
1483	1488	1493	1498	
ttc tac agg gag tgg att atg act cac agt agc agt agt gat gat gat				4624
Phe Tyr Arg Glu Trp Ile Met Thr His Ser Ser Ser Ser Asp Asp Asp				
1499	1504	1509	1514	
gat gat gat gat gat gat gat gag tca gat cta aac cat taa aattcat				4673
Asp Asp Asp Asp Asp Asp Asp Glu Ser Asp Leu Asn His *				
1515	1520	1525		
atgttcttta ttttacttgg aatgtttcat taacatgttt tgtatgactt ataccataat				4733
gccccatatgt ccattttatag ggaggtaaaaa cacattttct tttaaaatgt tttcctacac				4793
attttcataa agcaaaataa ttgtattatt taagcacaga aaaaaatgta ttttacatcc				4853
aaagtaggga gggcatccaa catattatag jatttgctttt atatatttta tagctttgta				4913
ttgcatagtt tgtctttaag agttcaagtt agacttaaata ataattttga tgttcaactgg				4973
ttttatttta aattgccttc ttatttggtta gcaaaatgcc tttttttaat ggtctctgta				5033

aattttctgg gctttaatgt aatgccactg tgtaaaaaaa aaaaa

5078

<210> 566
 <211> 2416
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (286)..(1752)
 <220>
 <221> misc_feature
 <222> (1)...(2416)
 <223> n = a,t,c or g

<400> 566
 gctgtaccgg tncggaattc ccgggtcgac gatttcgtct cagggcacag aggggtctctg 60
 cggccgtagc ggccgggggt gcggtagcca cttagattt gggcaaggac ttagattcg 120
 ggctctgttc tgtttcgcc gtcctgtctc ctgcgagggc tggcccaggc agccgcgctt 180
 cgaaggacgc cgccggggagc tgcggagcat gcgtggagtg gcagtgctaa cggctggtgt 240
 ctgcactgt tggcctgtga aggtacgtga agctgaaagc ctgga atg gct gga 294
 Met Ala Gly
 1
 aag ggg tca tca ggc agg cgg ccc ctg ctg ctg ggg ctg ctg gtg gcc 342
 Lys Gly Ser Ser Gly Arg Arg Pro Leu Leu Leu Gly Leu Leu Val Ala
 4 9 14 19
 gta gcc act gtc cac ctg gtc atc tgt ccc tac acc aaa gtg gag gag 390
 Val Ala Thr Val His Leu Val Ile Cys Pro Tyr Thr Lys Val Glu Glu
 20 25 30 35
 agc ttc aac ctg cag gcc aca cat gac ctg ctc tac cac tgg caa gac 438
 Ser Phe Asn Leu Gln Ala Thr His Asp Leu Leu Tyr His Trp Gln Asp
 36 41 46 51
 ctg gag cag tac gac cat ctt gag ttc ccc gga gtc gtc ccc agg acg 486
 Leu Glu Gln Tyr Asp His Leu Glu Phe Pro Gly Val Val Pro Arg Thr
 52 57 62 67
 ttc ctc ggg cca gtg gtg atc gca gtg ttc tcc agc ccc gcg gtt tac 534
 Phe Leu Gly Pro Val Val Ile Ala Val Phe Ser Ser Pro Ala Val Tyr
 68 73 78 83
 gtg ctt tcg ctg tta gaa atg tcc aag ttt tac tct cag cta ata gtt 582
 Val Leu Ser Leu Leu Glu Met Ser Lys Phe Tyr Ser Gln Leu Ile Val
 84 89 94 99

aga gga gtg ctt gga ctc ggc gtg att ttt gga ctc tgg acg tta caa	630
Arg Gly Val Leu Gly Leu Gly Val Ile Phe Gly Leu Trp Thr Leu Gln	
100 105 110 115	
aag gaa gtg aga cgg cac ttc ggg gcc atg gtg gcc acc atg ttc tgc	678
Lys Glu Val Arg Arg His Phe Gly Ala Met Val Ala Thr Met Phe Cys	
116 121 126 131	
tgg gtg acg gcc atg cag ttc cac ctg atg ttc tac tgc acg cgg aca	726
Trp Val Thr Ala Met Gln Phe His Leu Met Phe Tyr Cys Thr Arg Thr	
132 137 142 147	
ctg ccc aat gtg ctg gcc ctg cct gta gtc ctg ctg gcc ctc gcg gcc	774
Leu Pro Asn Val Leu Ala Leu Pro Val Val Leu Leu Ala Leu Ala Ala	
148 153 158 163	
tgg ctg cgg cac gag tgg gcc cgc ttc atc tgg ctg tca gcc ttc gcc	822
Trp Leu Arg His Glu Trp Ala Arg Phe Ile Trp Leu Ser Ala Phe Ala	
164 169 174 179	
atc atc gtg ttc agg gtg gag ctg tgc ctg ttc ctg ggc ctc ctg ctg	870
Ile Ile Val Phe Arg Val Glu Leu Cys Leu Phe Leu Gly Leu Leu Leu	
180 185 190 195	
ctg ctg gcc ttg ggc aac cga aag gtt tct gta gtc aga gcc ctt cgc	918
Leu Leu Ala Leu Gly Asn Arg Lys Val Ser Val Val Arg Ala Leu Arg	
196 201 206 211	
cac gcc gtc ccg gca ggg atc ctc tgt tta gga ctg acg gtt gct gtg	966
His Ala Val Pro Ala Gly Ile Leu Cys Leu Gly Leu Thr Val Ala Val	
212 217 222 227	
gac tct tat ttt tgg cgg cag ctc act tgg ccg gaa gga aag gtg ctt	1014
Asp Ser Tyr Phe Trp Arg Gln Leu Thr Trp Pro Glu Gly Lys Val Leu	
228 233 238 243	
tgg tac aac act gtc ctg aac aaa agc tcc aac tgg ggg acc tcc ccg	1062
Trp Tyr Asn Thr Val Leu Asn Lys Ser Ser Asn Trp Gly Thr Ser Pro	
244 249 254 259	
ctg ctg tgg tac ttc tac tca gcc ctg ccc cgc ggc ctg ggc tgc agc	1110
Leu Leu Trp Tyr Phe Tyr Ser Ala Leu Pro Arg Gly Leu Gly Cys Ser	
260 265 270 275	
ctg ctc ttc atc ccc ctg ggc ttg gta gac aga agg acg cac gcg ccg	1158
Leu Leu Phe Ile Pro Leu Gly Leu Val Asp Arg Arg Thr His Ala Pro	
276 281 286 291	
acg gtg ctg gca ctg ggc ttc atg gca ctc tac tcc ctc ctg cca cac	1206
Thr Val Leu Ala Leu Gly Phe Met Ala Leu Tyr Ser Leu Leu Pro His	
292 297 302 307	
aag gag cta cgc ttc atc atc tat gcc ttc ccc atg ctc aac atc acg	1254
Lys Glu Leu Arg Phe Ile Ile Tyr Ala Phe Pro Met Leu Asn Ile Thr	
308 313 318 323	
gct gcc aga ggc tgc tcc tac ctg ctg aat aac tat aaa aag tct tgg	1302

Ala Ala Arg Gly Cys Ser Tyr Leu Leu Asn Asn Tyr Lys Lys Ser Trp	
324 329 334 339	
ctg tac aaa gcg ggg tct ctg ctt gtg atc gga cac ctc gtg gtg aat	1350
Leu Tyr Lys Ala Gly Ser Leu Leu Val Ile Gly His Leu Val Val Asn	
340 345 350 355	
gcc gcc tac tca gcc acg gcc ctg tat gtg tcc cat ttc aac tac cca	1398
Ala Ala Tyr Ser Ala Thr Ala Leu Tyr Val Ser His Phe Asn Tyr Pro	
356 361 366 371	
ggg ggc gtc gca atg cag agg ctg cac cag ctg gtg ccc ccc cag aca	1446
Gly Gly Val Ala Met Gln Arg Leu His Gln Leu Val Pro Pro Gln Thr	
372 377 382 387	
gac gtc ctt ctg cac att gac gtg gca gcc gcc cag aca ggt gtg tct	1494
Asp Val Leu Leu His Ile Asp Val Ala Ala Ala Gln Thr Gly Val Ser	
388 393 398 403	
cgg ttt ctc caa gtc aac agc gcc tgg agg tac gac aag agg gag gat	1542
Arg Phe Leu Gln Val Asn Ser Ala Trp Arg Tyr Asp Lys Arg Glu Asp	
404 409 414 419	
gtg cag ccg ggg aca ggc atg ctg gca tac aca cac atc ctc atg gag	1590
Val Gln Pro Gly Thr Gly Met Leu Ala Tyr Thr His Ile Leu Met Glu	
420 425 430 435	
ggg gcc cct ggg ctc ctg gcc ctc tac agg gac aca cac cgg gtc ctg	1638
Ala Ala Pro Gly Leu Leu Ala Leu Tyr Arg Asp Thr His Arg Val Leu	
436 441 446 451	
gcc agc gtc gtg ggg acc aca ggt gtg agt ctg aac ctg acc caa ctg	1686
Ala Ser Val Val Gly Thr Thr Gly Val Ser Leu Asn Leu Thr Gln Leu	
452 457 462 467	
ccc ccc ttc aac gtc cac ctg cag aca aag ctg gtg ctt ctg gag agg	1734
Pro Pro Phe Asn Val His Leu Gln Thr Lys Leu Val Leu Leu Glu Arg	
468 473 478 483	
ctc ccc cgg ccg tcc tga ggggga ccaggcagcc ctcagcagcc acaggccttc	1788
Leu Pro Arg Pro Ser *	
484 489	
caggagctgt tatcactacc agtttctgga acaattccag cacaattatg acaattcaga	1848
gaagcaagtc aaaggactgg gcacctgcct ctgacagaca ccagaccagg tccagggcct	1908
cctccacagc ctcagctggg gctctcagca ccaaagaacg aggggcccag gtcttggttg	1968
caccccgga gccactgccc aggggtgatgg tggccagctc agggcttcct gcgggtgact	2028
gtcgcccaga ccagggtgcca ttcattgacta atcaggagca gcgggctcac ccaggcacct	2088
gtctgccagg aggccacgtg tgtctgccc acccaggggg agctgtattt tggcagcacc	2148
ccacgcttgc tgcccagggg cctcttgggg cacctaagac agcaccacct ctcaggggag	2208

accatggtgg ccccgccgc accccccac cctggtgcc ccaactgcaac tttgtattc 2268
acaggcatcc catctccatc acagataaaa tcttaggaga taaacacatt caaaaaggaa 2328
tgagataaaa agaataaggc aataaatgtt gattggaacc tctcaagatt acagaaaata 2388
atgagaatga aatttttaaaa aaaaaaaa 2416

<210> 567
<211> 2549
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1386)

<400> 567

atg ccg tat tca cta aac ctg gcc ata agg gac acc ttt gtg aat gcc 48
Met Pro Tyr Ser Leu Asn Leu Ala Ile Arg Asp Thr Phe Val Asn Ala
1 5 10

tct cgg acc ctg tac agc agc agc ccc aga gtc cta agc aac aac agt 96
Ser Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser
17 22 27 32

gac gcc aac ttg gag ctc atc aac acc tgg gtg gcc aag aac acc aac 144
Asp Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn
33 38 43 48

aac aag atc agc cgg ctg cta gac agt ctg ccc tcc gat acc cgc ctt 192
Asn Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu
49 54 59 64

gtc ctc ctc aat gct atc tac ctg agt gcc aag tgg aag aca aca ttt 240
Val Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe
65 70 75 80

gat ccc aag aaa acc aga atg gaa ccc ttt cac ttc aaa aac tca gtt 288
Asp Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val
81 86 91 96

ata aaa gtg ccc atg atg aat agc aag aag tac cct gtg gcc cat ttc 336
Ile Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe
97 102 107 112

att gac caa act ttg aaa gcc aag ttg agt cgt ggg gac agc ttg aag 384
Ile Asp Gln Thr Leu Lys Ala Lys Leu Ser Arg Gly Asp Ser Leu Lys
113 118 123 128

gag cca acc tca att gca gag agc agc cgt cac ccc agc tac cgc tca 432
Glu Pro Thr Ser Ile Ala Glu Ser Ser Arg His Pro Ser Tyr Arg Ser
129 134 139 144

gag ccc agc ttg gaa cca gag agc ttc cgt tct cct acc ttt ggc aaa	480
Glu Pro Ser Leu Glu Pro Glu Ser Phe Arg Ser Pro Thr Phe Gly Lys	
145 150 155 160	
agt ttt cac ttc gat cca cta tcc agt ggc tca cgc tcc tcc agc ctc	528
Ser Phe His Phe Asp Pro Leu Ser Ser Gly Ser Arg Ser Ser Ser Leu	
161 166 171 176	
aag tca gcc cag ggc aca ggc ttt gag ctg ggc cag ttg caa tcc att	576
Lys Ser Ala Gln Gly Thr Gly Phe Glu Leu Gly Gln Leu Gln Ser Ile	
177 182 187 192	
cgt tca gag ggc acc acc tcc acc tcc tat aag agc ctg gcc aac cag	624
Arg Ser Glu Gly Thr Thr Ser Thr Ser Tyr Lys Ser Leu Ala Asn Gln	
193 198 203 208	
aca cgc aat gga agc cta tct tat gac agc ttg ctc aca cct tca gac	672
Thr Arg Asn Gly Ser Leu Ser Tyr Asp Ser Leu Leu Thr Pro Ser Asp	
209 214 219 224	
agc cct gat ttt gag tca gtg cag gca ggg cct gag cca gac cca cct	720
Ser Pro Asp Phe Glu Ser Val Gln Ala Gly Pro Glu Pro Asp Pro Pro	
225 230 235 240	
tta ggc tat acc tct ccc ttc ctg tca gcc agg ctg gcc cag caa cgg	768
Leu Gly Tyr Thr Ser Pro Phe Leu Ser Ala Arg Leu Ala Gln Gln Arg	
241 246 251 256	
gaa gct gag agg cac cca cgt ttg gtg cca act ggc cca aca cac cga	816
Glu Ala Glu Arg His Pro Arg Leu Val Pro Thr Gly Pro Thr His Arg	
257 262 267 272	
gag ccc tca cca gtc cgt tac gac aat ctg tgc cgc cac att gtg gcc	864
Glu Pro Ser Pro Val Arg Tyr Asp Asn Leu Ser Arg His Ile Val Ala	
273 278 283 288	
tct ctc cag gaa cga gag aag ttg ctg cgc cag tca ccc cca ctc ccg	912
Ser Leu Gln Glu Arg Glu Lys Leu Leu Arg Gln Ser Pro Pro Leu Pro	
289 294 299 304	
ggc cgt gag gaa gaa cca ggc ttg ggg gac tca ggc att cag tca aca	960
Gly Arg Glu Glu Glu Pro Gly Leu Gly Asp Ser Gly Ile Gln Ser Thr	
305 310 315 320	
cca ggc tgc ggc cat gcc cct cgt act agt tcc tcc tca gat gat tca	1008
Pro Gly Ser Gly His Ala Pro Arg Thr Ser Ser Ser Ser Asp Asp Ser	
321 326 331 336	
aag aga tca cct ttg ggc aag act cca ctg gga cgc cca gct gtc ccc	1056
Lys Arg Ser Pro Leu Gly Lys Thr Pro Leu Gly Arg Pro Ala Val Pro	
337 342 347 352	
cgt ttt ggc aag cca gat ggg cta agg ggc cgg gga gta ggg tcc cct	1104
Arg Phe Gly Lys Pro Asp Gly Leu Arg Gly Arg Gly Val Gly Ser Pro	
353 358 363 368	
gaa cca ggc cca aca gcc cca tac ctg ggc cga tgc atg tct tac agc	1152

Glu Pro Gly Pro Thr Ala Pro Tyr Leu Gly Arg Ser Met Ser Tyr Ser	
369 374 379 384	
agc caa aaa gcc caa cct ggt gtc tct gag aca gaa gaa gtg gcc ttg	1200
Ser Gln Lys Ala Gln Pro Gly Val Ser Glu Thr Glu Glu Val Ala Leu	
385 390 395 400	
cag cca tta ctg aca ccc aaa gat gaa gta cag ctg aag acc acc tac	1248
Gln Pro Leu Leu Thr Pro Lys Asp Glu Val Gln Leu Lys Thr Thr Tyr	
401 406 411 416	
agc aaa tcc aac ggg cag ccc aag agc tta ggc tca gcc tcc cct ggc	1296
Ser Lys Ser Asn Gly Gln Pro Lys Ser Leu Gly Ser Ala Ser Pro Gly	
417 422 427 432	
cca ggc cag cca cct ctc agt agc ccc acg agg gga gga gtc aag aag	1344
Pro Gly Gln Pro Pro Leu Ser Ser Pro Thr Arg Gly Gly Val Lys Lys	
433 438 443 448	
gtg tca ggg gtt ggt ggt acc acc tat gag att tcg gtg tga gccttcg	1393
Val Ser Gly Val Gly Gly Thr Thr Tyr Glu Ile Ser Val *	
449 454 459	
gcacctcccc tccccaacgc ctctgcgcct acaccaaagg gccccaggtg gccaccttcc	1453
ttccctcaag gggctccctt cccgtgcatg gacatttttt aaaccaccga ttccaagagg	1513
atgaggagtgt ttttctaaaa tgcagtaggc ttggggagtc ggagagttgg ggccctgaga	1573
ctggggtagc aacccccctt tttatctttt aagaccttcc cttccttgat ccoctggacca	1633
gactcagtgg acatttgtgc aattgctcgc cctggaggga accagatcat ttttaaacca	1693
gaaataattt tttttattat tgttacggat tctatttttt tctcttctg cgttaccagg	1753
tgtgtgtgta catataatat atatatatat atatattata aatatcaaag aaattatata	1813
tctatcctgg gatgggaaaa tgagggaggg atacatatat ggagggggat cttactcttc	1873
ccattcctca gaccagcagg aaaagagggg agacgtcagt ctttttctctg tggttccctc	1933
tcatttgtcc cagttactaa ctacggaaat agcatcctct gctggtgcta agtgtgatta	1993
ggaagaagcc tggggagagg cgagtctgga attttgggtca caagagggaa ggacttggag	2053
aggagaatta gttttctagg ctcataggca tttagtttcc ctaggaaagg ggtcaaaact	2113
tcaagacact ggtggtggtg ggagatcagg aaaataactt ggcttagctc aaacaatatt	2173
ggataatccc ctcttggggg gagagggatt agagtgtgct cctactggcc ctttggagcc	2233
tcccctagct tacacagtta acttgattttt aaaatccaag gccaggagag aagaatccaa	2293
aaagcaatat ttttcatcac atgccaaaaa cgggggatag agagaaggag tggcaggcct	2353
aggccccctcc gattgtccct tgggggttac ccctcagccc acctcactat ggtgctgggt	2413

agaggggata cctgggttct aacctctaaa taggggagat cccagcctcc acaaagaggc 2473
 cctttttattt tttattctga ttagccattt taaaccaacg aggaataaaa agaaatcctg 2533
 atctaaaaaa aaaaaa 2549

<210> 568
 <211> 2321
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (304) .. (1992)

<400> 568
 cgacccacgc gtccgcgttt agtcaattt aagccaagtt cccaaatttt aagaaaagta 60
 tcggatagtg gctggttaaa acagaaaaac atcaaacaag ccatcaaatc tctgaaaaaa 120
 tatagtgaca aatcagcaga aaagagtcct tttccagaag agaaaagtca cattatagac 180
 aaagaagaag atataggtaa acgcagtcct tttcattaca caagttctat aaccacaaaa 240
 tttggagact cattctactt tttatcaaat catattaatt catatttcaa acgtaaggaa 300
 aaa atg tct caa caa aag gaa aat gaa cat ttc cgg gac aaa tca gaa 348
 Met Ser Gln Gln Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu
 1 5 10
 ctt gaa gat aaa aag gta gaa gag ggg aaa tta aga tct cca gat cct 396
 Leu Glu Asp Lys Lys Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro
 16 21 26 31
 ggc atc ctg gct tat aag cca ggc tca gaa tct gta cat acg gtg gac 444
 Gly Ile Leu Ala Tyr Lys Pro Gly Ser Glu Ser Val His Thr Val Asp
 32 37 42 47
 aag cct aca agt cct tct gcg ata cct gat gtt ctt caa gtt tca act 492
 Lys Pro Thr Ser Pro Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr
 48 53 58 63
 aaa caa agt att gct aac ttt ctt tct cgt ccc acg gaa ggt gta caa 540
 Lys Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln
 64 69 74 79
 gct tta gta ggt ggt tat att ggt gga ctt gtc ccc aaa tta aag tat 588
 Ala Leu Val Gly Gly Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr
 80 85 90 95
 gat tca aag agt cag tca gaa gaa cag gaa gag cct gct aaa act gat 636
 Asp Ser Lys Ser Gln Ser Glu Glu Gln Glu Pro Ala Lys Thr Asp
 96 101 106 111

cag gct gtc agc aaa gac aga aat gca gag gag aaa aag cgt tta tct Gln Ala Val Ser Lys Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser 112 117 122 127	684
ctt cag cga gaa aag att atc gca agg gtg agt att gat aac agg acc Leu Gln Arg Glu Lys Ile Ile Ala Arg Val Ser Ile Asp Asn Arg Thr 128 133 138 143	732
cgg gca tta gtt cag gca tta aga aga aca act gac cca aag ctc tgc Arg Ala Leu Val Gln Ala Leu Arg Arg Thr Thr Asp Pro Lys Leu Cys 144 149 154 159	780
att act agg gtt gaa gaa ctg act ttt cat ctt cta gaa ttt cct gaa Ile Thr Arg Val Glu Glu Leu Thr Phe His Leu Leu Glu Phe Pro Glu 160 165 170 175	828
gga aaa gga gtg gct gtc aag gaa aga att att cca tat tta tta cga Gly Lys Gly Val Ala Val Lys Glu Arg Ile Ile Pro Tyr Leu Leu Arg 176 181 186 191	876
ctg aga caa att aag gat gaa act ctt cag gct gca gtt aga gaa att Leu Arg Gln Ile Lys Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile 192 197 202 207	924
ttg gcc cta att ggc tat gtg gat cca gtg aaa ggg aga gga atc cga Leu Ala Leu Ile Gly Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg 208 213 218 223	972
att ctc tca att gat ggt gga gga aca agg ggc gtg gtt gct ctc cag Ile Leu Ser Ile Asp Gly Gly Gly Thr Arg Gly Val Val Ala Leu Gln 224 229 234 239	1020
acc cta cga aaa tta gtt gaa ctt act cag aag cca gtt cat cag ctc Thr Leu Arg Lys Leu Val Glu Leu Thr Gln Lys Pro Val His Gln Leu 240 245 250 255	1068
ttt gat tac att tgt ggt gta agc aca ggt gcc ata tta gct ttc atg Phe Asp Tyr Ile Cys Gly Val Ser Thr Gly Ala Ile Leu Ala Phe Met 256 261 266 271	1116
ttg ggg ttg ttt cat atg ccc ttg gat gaa tgt gag gaa ctt tat cga Leu Gly Leu Phe His Met Pro Leu Asp Glu Cys Glu Glu Leu Tyr Arg 272 277 282 287	1164
aaa tta gga tca gat gta ttt tca caa aat gtc att gtt gga aca gta Lys Leu Gly Ser Asp Val Phe Ser Gln Asn Val Ile Val Gly Thr Val 288 293 298 303	1212
aaa atg agt tgg agc cat gca ttt tat gac agt caa aca tgg gaa aac Lys Met Ser Trp Ser His Ala Phe Tyr Asp Ser Gln Thr Trp Glu Asn 304 309 314 319	1260
att ctt aag gat agg atg gga tct gca ctg atg att gaa aca gca aga Ile Leu Lys Asp Arg Met Gly Ser Ala Leu Met Ile Glu Thr Ala Arg 320 325 330 335	1308
aac ccc aca tgt cct aag gta gct gct gta agt acc ata gta aat aga	1356

Asn Pro Thr Cys Pro Lys Val Ala Ala Val Ser Thr Ile Val Asn Arg	
336 341 346 351	
ggg ata aca ccc aaa gct ttt gtg ttc aga aac tat ggt cat ttt cct	1404
Gly Ile Thr Pro Lys Ala Phe Val Phe Arg Asn Tyr Gly His Phe Pro	
352 357 362 367	
gga atc aac tct cat tat ttg gga ggc tgt cag tat aaa atg tgg cag	1452
Gly Ile Asn Ser His Tyr Leu Gly Gly Cys Gln Tyr Lys Met Trp Gln	
368 373 378 383	
gcc att aga gcc tca tct gct gct cca ggc tac ttt gca gaa tat gca	1500
Ala Ile Arg Ala Ser Ser Ala Ala Pro Gly Tyr Phe Ala Glu Tyr Ala	
384 389 394 399	
ttg gga aat gat ctt cat caa gat gga ggt ttg ctt ctg aat aac cct	1548
Leu Gly Asn Asp Leu His Gln Asp Gly Gly Leu Leu Leu Asn Asn Pro	
400 405 410 415	
tcg gca tta gct atg cat gag tgt aaa tgt ctt tgg cca gat gtg ccg	1596
Ser Ala Leu Ala Met His Glu Cys Lys Cys Leu Trp Pro Asp Val Pro	
416 421 426 431	
tta gag tgc ata gta tcc ctg ggc act gga cgt tat gag agt gat gtg	1644
Leu Glu Cys Ile Val Ser Leu Gly Thr Gly Arg Tyr Glu Ser Asp Val	
432 437 442 447	
aga aac acg gta aca tac aca agc ttg aaa act aaa ctt tct aat gtt	1692
Arg Asn Thr Val Thr Tyr Thr Ser Leu Lys Thr Lys Leu Ser Asn Val	
448 453 458 463	
atc aac agt gct aca gat aca gaa gaa gtc cat ata atg ctt gat ggc	1740
Ile Asn Ser Ala Thr Asp Thr Glu Glu Val His Ile Met Leu Asp Gly	
464 469 474 479	
ctg tta cct cct gac acc tat ttt aga ttc aat cct gta atg tgt gaa	1788
Leu Leu Pro Pro Asp Thr Tyr Phe Arg Phe Asn Pro Val Met Cys Glu	
480 485 490 495	
aac ata cct cta gat gaa agt cga aat gaa aag ctg gat cag ctg cag	1836
Asn Ile Pro Leu Asp Glu Ser Arg Asn Glu Lys Leu Asp Gln Leu Gln	
496 501 506 511	
ttg gaa ggg ttg aaa tac ata gaa aga aat gaa caa aaa atg aaa aaa	1884
Leu Glu Gly Leu Lys Tyr Ile Glu Arg Asn Glu Gln Lys Met Lys Lys	
512 517 522 527	
gtt gca aaa ata tta agt caa gaa aaa aca act ctg cag aaa att aat	1932
Val Ala Lys Ile Leu Ser Gln Glu Lys Thr Thr Leu Gln Lys Ile Asn	
528 533 538 543	
gat tgg ata aaa tta aaa act gat atg tat gaa gga ctt cca ttc ttt	1980
Asp Trp Ile Lys Leu Lys Thr Asp Met Tyr Glu Gly Leu Pro Phe Phe	
544 549 554 559	
tca aaa ttg tga tga gtatatgctt atgttctcat aaatgaaggt ctgtttagaa	2035
Ser Lys Leu *	

560

gatcaaccac attcaataag gaattgtggg gttcgacatg agttaacttt gaaatacgtg 2095
 tgaattctgg agaatcctga aaaagacggg gtttcaacca gcttgcatag cacagagaat 2155
 attcttgggtt acagaattca tatgggaact aggcttttaa gatgttaata attagctaag 2215
 ctttagtaac ccttactgtg ctagtagatt ttagtagata ttggtgttat attgtttgat 2275
 gtttgaaaat atattaatat atgtgccgaa caagaaaaaa aaaaaa 2321

<210> 569
 <211> 1279
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (103)..(1092)

<400> 569
 ccggtccgga attcccgggt cgacgatttc gtgcgcgctc gctttcccg cccgagtcctc 60
 gccgccttcc cgcgccccgc agcgccccgc agagcagtcg ag atg ggt gag tca 114
 Met Gly Glu Ser
 1
 agt gaa gac ata gac caa atg ttc agc act ttg ctg gga gag atg gat 162
 Ser Glu Asp Ile Asp Gln Met Phe Ser Thr Leu Leu Gly Glu Met Asp
 5 10 15 20
 ctt ctg act cag agt tta gga gtt gac act ctc cct cct cct gac cct 210
 Leu Leu Thr Gln Ser Leu Gly Val Asp Thr Leu Pro Pro Pro Asp Pro
 21 26 31 36
 aat cca ccc aga gct gaa ttt aac tac agt gtg ggg ttt aaa gat tta 258
 Asn Pro Pro Arg Ala Glu Phe Asn Tyr Ser Val Gly Phe Lys Asp Leu
 37 42 47 52
 aat gag tcc tta aat gca ctg gaa gac caa gat tta gat gct ctc atg 306
 Asn Glu Ser Leu Asn Ala Leu Glu Asp Gln Asp Leu Asp Ala Leu Met
 53 58 63 68
 gca gat ctg gta gca gac ata agt gag gct gag cag agg aca atc cag 354
 Ala Asp Leu Val Ala Asp Ile Ser Glu Ala Glu Gln Arg Thr Ile Gln
 69 74 79 84
 gca cag aaa gag tcc ttg cag aat caa cat cat tca gca tct cta caa 402
 Ala Gln Lys Glu Ser Leu Gln Asn Gln His His Ser Ala Ser Leu Gln
 85 90 95 100
 gca tca att ttc agt ggt gca gcc tct ctt ggt tat gga aca aat gtt 450
 Ala Ser Ile Phe Ser Gly Ala Ala Ser Leu Gly Tyr Gly Thr Asn Val

101	106	111	116	
gct gcc act ggt atc agc caa tat gag gat gac tta cca cct cca cca				498
Ala Ala Thr Gly Ile Ser Gln Tyr Glu Asp Asp Leu Pro Pro Pro Pro				
117	122	127	132	
gcc gat cct gtg tta gac ctt cca ctg cca cca cca cct cct gaa cct				546
Ala Asp Pro Val Leu Asp Leu Pro Leu Pro Pro Pro Pro Pro Glu Pro				
133	138	143	148	
ctc tct cag gaa gag gaa gaa gcc caa gcc aag gct gat aaa att aag				594
Leu Ser Gln Glu Glu Glu Glu Ala Gln Ala Lys Ala Asp Lys Ile Lys				
149	154	159	164	
ctg gcg ctg gaa aaa ctg aag gag gcc aag gtt aag aag ctc gtc gtc				642
Leu Ala Leu Glu Lys Leu Lys Glu Ala Lys Val Lys Lys Leu Val Val				
165	170	175	180	
aag gtg cac atg aat gat aac agc aca aag tca ctg atg gtg gat gag				690
Lys Val His Met Asn Asp Asn Ser Thr Lys Ser Leu Met Val Asp Glu				
181	186	191	196	
cgg cag ctg gcc cga gat gtt ctg gac aac ctt ttc gag aaa act cat				738
Arg Gln Leu Ala Arg Asp Val Leu Asp Asn Leu Phe Glu Lys Thr His				
197	202	207	212	
tgt gac tgc aat gta gac tgg tgt ctt tat gaa atc tac ccg gaa cta				786
Cys Asp Cys Asn Val Asp Trp Cys Leu Tyr Glu Ile Tyr Pro Glu Leu				
213	218	223	228	
caa att gag agg ttt ttt gaa gac cat gaa aat gtt gtt gaa gtc tta				834
Gln Ile Glu Arg Phe Phe Glu Asp His Glu Asn Val Val Glu Val Leu				
229	234	239	244	
tca gac tgg aca aga gac aca gaa aat aaa ata cta ttt ttg gag aaa				882
Ser Asp Trp Thr Arg Asp Thr Glu Asn Lys Ile Leu Phe Leu Glu Lys				
245	250	255	260	
gag gag aaa tat gct gta ttt aaa aac ccc cag aat ttc tac ttg gat				930
Glu Glu Lys Tyr Ala Val Phe Lys Asn Pro Gln Asn Phe Tyr Leu Asp				
261	266	271	276	
aac aga gga aaa aaa gaa agc aag gaa act aat gag aaa atg aat gct				978
Asn Arg Gly Lys Lys Glu Ser Lys Glu Thr Asn Glu Lys Met Asn Ala				
277	282	287	292	
aag aac aag gaa tcc tta ctt gag gta agg tta att ttg cag agt gga				1026
Lys Asn Lys Glu Ser Leu Leu Glu Val Arg Leu Ile Leu Gln Ser Gly				
293	298	303	308	
aga aaa gag aag gac gtt tgc tct att ttt aag tca ttt gct tcc gag				1074
Arg Lys Glu Lys Asp Val Cys Ser Ile Phe Lys Ser Phe Ala Ser Glu				
309	314	319	324	
aac aat gga aaa atc taa agacat acactgaaat tttaagttgg ggtgttaaaa				1128
Asn Asn Gly Lys Ile *				
325	330			

tcaaattatt tctaaattat agctatttag ataattcaac tgtttttctt ttttgagtca 1188
 tttgttacaa catgtggctt tagataaatg aagctggatt tgtaattctt gacttttaaa 1248
 aaactctagc attccaagtt tccattactt a 1279

<210> 570
 <211> 1546
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (251)..(940)

<400> 570
 tccctgtgcc gcttgtaccg gcacgtgtcg cagcacttcc tagagatccg cttcaagatt 60
 cagcggctgc tggagccgcg acagtacatg ctgctgctgc ccgagcacgt gctgggtcaag 120
 atcttcagct tctgtccac gcgcgcgctg gccgccctca agtgcacctg ccaccacttc 180
 aagggcatca tgcaggcggtt tggcgtgcgg gccacagact cgcgctggag ccgagacccg 240
 ctctaccgcg atg atc cgt gca aac agt gcc gca aga gat acg aga agg 289
 Met Ile Arg Ala Asn Ser Ala Ala Arg Asp Thr Arg Arg
 1 5 10
 gcg acg tgt cgc tct gcc gct ggc acc cca agc cct acc acc atg acc 337
 Ala Thr Cys Arg Ser Ala Ala Gly Thr Pro Ser Pro Thr Thr Met Thr
 14 19 24 29
 tgc ctt acg gac gtt cct act gga tgt gct gcc gtc gag ccg acc gcg 385
 Cys Leu Thr Asp Val Pro Thr Gly Cys Ala Ala Val Glu Pro Thr Ala
 30 35 40 45
 aga ctc ccg gct gcc gcc tgg gcc tcc acg ata aca act ggg tgc tgc 433
 Arg Leu Pro Ala Ala Ala Trp Ala Ser Thr Ile Thr Thr Gly Cys Cys
 46 51 56 61
 cct gca atg ggc cag gcg ggg gcc ggg ccg gcc ggg agg aag gga agt 481
 Pro Ala Met Gly Gln Ala Gly Ala Gly Pro Ala Gly Arg Lys Gly Ser
 62 67 72 77
 gaa gcc ggg gga ggg ccg ggg aga gcc cac cac gcc cac ccc tcc cct 529
 Glu Ala Gly Gly Gly Pro Gly Arg Ala His His Ala His Pro Ser Pro
 78 83 88 93
 ctc ccc cgg gag ccg agg gtc cgg act ggg ccg cct gcc cat tcc cct 577
 Leu Pro Arg Glu Pro Arg Val Arg Thr Gly Pro Pro Ala His Ser Pro
 94 99 104 109
 act cca ggc agc att gat ccc tca ccg gaa ctg agc tgg ggt tca gca 625

Thr	Pro	Gly	Ser	Ile	Asp	Pro	Ser	Pro	Glu	Leu	Ser	Trp	Gly	Ser	Ala		
110					115					120					125		
ggg	gtg	acc	cag	gaa	agc	cct	ctg	ctt	gat	cct	gtt	gat	ttt	cta	ctc	673	
Gly	Val	Thr	Gln	Glu	Ser	Pro	Leu	Leu	Asp	Pro	Val	Asp	Phe	Leu	Leu		
126					131					136					141		
ttc	aga	acc	agg	gcc	gtg	gac	cct	ctg	aga	agg	gtg	ttt	ttt	ttt	ttt	721	
Phe	Arg	Thr	Arg	Ala	Val	Asp	Pro	Leu	Arg	Arg	Val	Phe	Phe	Phe	Phe		
142					147					152					157		
tat	cag	cat	ctc	act	ttc	ttc	tcc	att	cag	ccc	caa	ccc	cct	ccc	tgc	769	
Tyr	Gln	His	Leu	Thr	Phe	Phe	Ser	Ile	Gln	Pro	Gln	Pro	Pro	Pro	Cys		
158					163					168					173		
cat	gct	ttc	cac	ccc	aag	gac	cca	cca	gca	ggg	agc	aga	cgg	cag	cta	817	
His	Ala	Phe	His	Pro	Lys	Asp	Pro	Pro	Ala	Gly	Ser	Arg	Arg	Gln	Leu		
174					179					184					189		
att	ttg	gta	cca	ctt	aag	ggt	ccc	ccc	att	ctg	gcc	ccc	atc	ctc	tcc	865	
Ile	Leu	Val	Pro	Leu	Lys	Gly	Pro	Pro	Ile	Leu	Ala	Pro	Ile	Leu	Ser		
190					195					200					205		
ctc	acc	cca	att	ctt	tct	cgc	tgg	agc	tgt	tat	ttc	cca	aga	agc	cgc	913	
Leu	Thr	Pro	Ile	Leu	Ser	Arg	Trp	Ser	Cys	Tyr	Phe	Pro	Arg	Ser	Arg		
206					211					216					221		
atc	gcc	caa	ggt	tgg	cac	ctc	tcc	taa	cctgc	cacacgacag	ctctcacctc					965	
Ile	Ala	Gln	Gly	Trp	His	Leu	Ser	*									
222					227												
tctaggaatt	gggggctgtc	aggtcacagg	tgggatctgg	catttttttta	tgacagtcca											1025	
tttctagatg	gtttgcctat	taaagaagtg	gggggggaaat	actgttttct	ccttaacctc											1085	
aagctaccag	tctctcctct	tccgcgtaga	ggaagagggg	ggcagacaaa	aaaaaagctg											1145	
aagtataaaa	accctcctcc	tcccgttatt	atttaagcta	ctgccatcaa	ccccaccccc											1205	
ataaagctgt	gaagcccttt	gcctcgcttt	tgacagcgtg	ggggggcccc	gtgggcaggg											1265	
acttcggatt	tgcatctctg	ggttggtttt	ccttcactc	tggggtctcg	ttcaggcatt											1325	
ggggtctcct	caccccagcc	acatgtttct	ttaagaatcc	tttgggtcaac	caggaccttg											1385	
atctttcagg	catttttggtc	tggggtatct	ttgtttgttc	tctctgtttt	ttgttttctt											1445	
ttttttcttt	ccatcgctgg	tctggaagct	tctagcgtgt	ggcatctgac	caattttgaa											1505	
ttggtccttt	ctataaaatc	aatattttata	aaaaaaaaaa	a												1546	

<210> 571
 <211> 3470
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1650)

<400> 571

atg gag ttt gcg gag ctg att aag acc ccg cgg gtg gac aat gtg gtg	48
Met Glu Phe Ala Glu Leu Ile Lys Thr Pro Arg Val Asp Asn Val Val	
1 5 10	
ctg cac cgg cct ttc tac ccg gct gtc gag ggc acc ctg tgc ctg acg	96
Leu His Arg Pro Phe Tyr Pro Ala Val Glu Gly Thr Leu Cys Leu Thr	
17 22 27 32	
ggc cac cac ttg atc ctg tcc tcc cgg cag gac aat acg gag gag ctg	144
Gly His His Leu Ile Leu Ser Ser Arg Gln Asp Asn Thr Glu Glu Leu	
33 38 43 48	
tgg ctc ctc cat tca aac atc gac gcc atc gac aag cga ttt gta gga	192
Trp Leu Leu His Ser Asn Ile Asp Ala Ile Asp Lys Arg Phe Val Gly	
49 54 59 64	
tca ctg ggt acc atc atc ata aaa tgt aaa gat ttt cga att att cag	240
Ser Leu Gly Thr Ile Ile Ile Lys Cys Lys Asp Phe Arg Ile Ile Gln	
65 70 75 80	
ttg gat att cct gga atg gag gaa tgc ttg aat ata gcc agt tcc att	288
Leu Asp Ile Pro Gly Met Glu Glu Cys Leu Asn Ile Ala Ser Ser Ile	
81 86 91 96	
gag gca ttg tct act ctg gac tcc atc act ctg atg tac cct ttc ttt	336
Glu Ala Leu Ser Thr Leu Asp Ser Ile Thr Leu Met Tyr Pro Phe Phe	
97 102 107 112	
tac cgt cct atg ttt gaa gtg ata gaa gat ggc tgg cat tcc ttc ctt	384
Tyr Arg Pro Met Phe Glu Val Ile Glu Asp Gly Trp His Ser Phe Leu	
113 118 123 128	
cct gag caa gaa ttt gaa ctc tat tct tca gct acc agt gaa tgg agg	432
Pro Glu Gln Glu Phe Glu Leu Tyr Ser Ser Ala Thr Ser Glu Trp Arg	
129 134 139 144	
cta agc tat gtc aat aag gaa ttt gct gtc tgt ccc tct tac cca cca	480
Leu Ser Tyr Val Asn Lys Glu Phe Ala Val Cys Pro Ser Tyr Pro Pro	
145 150 155 160	
att gtc aca gtg ccc aaa tcc atc gat gat gaa gct ctt cgg aag gta	528
Ile Val Thr Val Pro Lys Ser Ile Asp Asp Glu Ala Leu Arg Lys Val	
161 166 171 176	
gct aca ttt cga cat gga ggg cgc ttc cca gta cta agc tat tac cac	576
Ala Thr Phe Arg His Gly Gly Arg Phe Pro Val Leu Ser Tyr Tyr His	
177 182 187 192	
aaa aga aat ggg atg gta att atg cga agt ggt cag cca ctc act ggt	624
Lys Arg Asn Gly Met Val Ile Met Arg Ser Gly Gln Pro Leu Thr Gly	

193	198	203	208	
aca aac ggg agg agg tgc aag gag gac gag aag ctg ata aat gct acc				672
Thr Asn Gly Arg Arg Cys Lys Glu Asp Glu Lys Leu Ile Asn Ala Thr				
209	214	219	224	
ctc agg gct gga aag cgt ggc tac atc att gac acc cga tcc ctg aac				720
Leu Arg Ala Gly Lys Arg Gly Tyr Ile Ile Asp Thr Arg Ser Leu Asn				
225	230	235	240	
gtg gct cag caa act aga gcc aaa gga ggt ggc ttt gaa caa gaa gct				768
Val Ala Gln Gln Thr Arg Ala Lys Gly Gly Gly Phe Glu Gln Glu Ala				
241	246	251	256	
cat tat cct cag tgg agg cga att cat aag tcc att gag agg tat cac				816
His Tyr Pro Gln Trp Arg Arg Ile His Lys Ser Ile Glu Arg Tyr His				
257	262	267	272	
att ctt cag gag agc tta atc aaa ctt gtg gaa gct tgt aat gac caa				864
Ile Leu Gln Glu Ser Leu Ile Lys Leu Val Glu Ala Cys Asn Asp Gln				
273	278	283	288	
aca cat aac atg gac cga tgg ctc agt aaa ttg gag gcc tct aac tgg				912
Thr His Asn Met Asp Arg Trp Leu Ser Lys Leu Glu Ala Ser Asn Trp				
289	294	299	304	
ctg act cac atc aaa gag att ctg aca acc gcc tgc cta gcg gct cag				960
Leu Thr His Ile Lys Glu Ile Leu Thr Thr Ala Cys Leu Ala Ala Gln				
305	310	315	320	
tgc atc gac agg gaa gga gca tca ata ttg att cac gga aca gaa gga				1008
Cys Ile Asp Arg Glu Gly Ala Ser Ile Leu Ile His Gly Thr Glu Gly				
321	326	331	336	
act gat tcc aca ctc cag gtg acc tcc ttg gcc cag atc atc tta gag				1056
Thr Asp Ser Thr Leu Gln Val Thr Ser Leu Ala Gln Ile Ile Leu Glu				
337	342	347	352	
cca aga agc agg acc att cgt ggt ttt gag gcc ctg att gaa aga gag				1104
Pro Arg Ser Arg Thr Ile Arg Gly Phe Glu Ala Leu Ile Glu Arg Glu				
353	358	363	368	
tgg ctg cag gct ggt cac cca ttc cag cag cgc tgt gca cag tca gcc				1152
Trp Leu Gln Ala Gly His Pro Phe Gln Gln Arg Cys Ala Gln Ser Ala				
369	374	379	384	
tac tgt aac acc aag cag aag tgg gag gct cct gta ttt ctt ctc ttc				1200
Tyr Cys Asn Thr Lys Gln Lys Trp Glu Ala Pro Val Phe Leu Leu Phe				
385	390	395	400	
ttg gac tgc gtg tgg cag atc ctt cgt cag ttt ccc tgt tct ttt gag				1248
Leu Asp Cys Val Trp Gln Ile Leu Arg Gln Phe Pro Cys Ser Phe Glu				
401	406	411	416	
ttt aat gag att ttc ctc atc atg ctc ttt gag cat gct tat gcc tca				1296
Phe Asn Glu Ile Phe Leu Ile Met Leu Phe Glu His Ala Tyr Ala Ser				
417	422	427	432	

cag ttt gga aca ttt ctg ggc aac aat gaa agt gaa aga tgt aag ttg	1344
Gln Phe Gly Thr Phe Leu Gly Asn Asn Glu Ser Glu Arg Cys Lys Leu	
433 438 443 448	
aag cta cag cag aag acg atg tct ttg tgg tcc tgg gtt aat cag ccc	1392
Lys Leu Gln Gln Lys Thr Met Ser Leu Trp Ser Trp Val Asn Gln Pro	
449 454 459 464	
agt gag ctg agt aaa ttc acc aat ccc ctc ttt gaa gcc aac aac ctt	1440
Ser Glu Leu Ser Lys Phe Thr Asn Pro Leu Phe Glu Ala Asn Asn Leu	
465 470 475 480	
gtc atc tgg cct tca gtt gct ccg cag agt ctt cca ctg tgg gaa ggt	1488
Val Ile Trp Pro Ser Val Ala Pro Gln Ser Leu Pro Leu Trp Glu Gly	
481 486 491 496	
att ttc cta cgt tgg aat aga tcc tct aag tat ttg gat gaa gca tat	1536
Ile Phe Leu Arg Trp Asn Arg Ser Ser Lys Tyr Leu Asp Glu Ala Tyr	
497 502 507 512	
gaa gaa atg gtt aac atc att gaa tat aat aaa gaa tta caa gca aaa	1584
Glu Glu Met Val Asn Ile Ile Glu Tyr Asn Lys Glu Leu Gln Ala Lys	
513 518 523 528	
gtc aat atc ctt cga agg cag ttg gca gaa ctg gaa aca gag gac ggg	1632
Val Asn Ile Leu Arg Arg Gln Leu Ala Glu Leu Glu Thr Glu Asp Gly	
529 534 539 544	
atg cag gag agt ccc tga aaggtc tcctcgacc cttegcaagg accttcttgg	1686
Met Gln Glu Ser Pro *	
545 550	
gcctgtgtcc gccgttctct ccttgtgccc ttcagttcac ttttacacgg tagccttgaa	1746
gtgaaggcct tagatgtggg acccccctaa tgtaatggat ttctcaatac tgtatgaata	1806
atgaaactta ctatcataaa ccattgtttca tgtggcctgt tagggcctgt cactttggga	1866
gccggaagga ggtgctagtc attttatttt tacgtgaaat agatgacctt tttaatgcca	1926
tttgtgtttc atgccatttt atccaaagct ttttctctgt gtccactctc caaacagcat	1986
tctagagcag tcaaggagac agctaattct tctagggact atttggtggt ttaaaaaaag	2046
ggtcagactt ttaaacactc tgaccataga aatgtttttc aaaatggcaa caatggataa	2106
accaaggatt ttgtgtttta caatccattt ccagtgtctt cgccacataa aatagccatt	2166
ttcttttaaaa tagtttttga ctaacgaagc tgaaatctat tctcattctt gtttgtcaag	2226
aaaggaaaat ctgttattca aggtaaatta tttctacaag ggcaacaggt atggtcctcc	2286
gatatttaca ttaagaagag ttaaatttat ttttaacgtag aactataaag tatgtgcaat	2346
atacaattaa agtaggaatt tgttactgat tgagaattgt tactggtgaa ttggttttca	2406

ggttttgagc atacatatac aatgtgtttc aaatgctgct tgtaaaatta aaccatcatc 2466
 tagaatagag ttaattttatt ataatcaagc tacaaatagg ttttcttaaa ccagagatgc 2526
 actgcccttg tctaaagttc ttattgcact ggtttatatg tgtatgtgtg ttttattgtg 2586
 tgttttttta atttgtaagt attctaagag tttcctaata ctaagggttaa aattttcatg 2646
 ttgacctgag ccttttgcaa atttgctttg gctctattga tttgtccatt atgtgttagg 2706
 caaatataac ttaagtggag ggggaagttt atgaatataa tatagctctg tgttttaaac 2766
 ctgagaaaca gatttgagtg tttcagtatt atagaaacag tgatgactat tcatgctctg 2826
 ctagtctatg cctgcaactc caaatgtttg tggttcagta tttcccacct acattttctgt 2886
 ttggtgacat tgotcatttt aacaaatatg accgagtcta gtttttcttt aaaaggatag 2946
 tttatgagta atctttaaaa ccatttccat accatctgta tataaccatt tcggtagaga 3006
 acacactaca ctgaaccctg ctttagagct gtgtgttgag ctaaaaatat aattttttaa 3066
 aaattgacta gcaaaatcta tggccacact gagaagcctt tgaaaatggc aaatactttt 3126
 catcaccaat tgcccaattc atctttcttc tgcttcctca gccttgtagc aaaggctaca 3186
 cagcagccca cagtccacag tctttttggg aaaattggcc tgccaccttc ttttaagctca 3246
 gtttatTTTT gacttacttt ctttgcgtga gttatgaacc ttggggcatt aaaatcccat 3306
 ggcaaggagc ataagagatg ttctcgtagc tctgcgttgt gtgaaatgtc catcttagtt 3366
 ttgttaaaaa aaaaaaaaaag tcgagcggcc gcgaagcgag tagtagtagg cggccgctct 3426
 agaggatcca agcttacgta cgcggtgcacg cgacgtcata gctc 3470

<210> 572
 <211> 2728
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (202)..(1212)

<220>
 <221> misc_feature
 <222> (1)...(2728)
 <223> n = a,t,c or g

<400> 572
 tcgaccccag catcgaacgc ctgcaggtag cggtccggaa ttcccgggtc gacccacgcg 60
 tccgttttat gcttggttgg tcggtggaat atgttgggat ttatgtttgc ctctgaacaa 120

gtgtcttgct cacatcgtaa atgactttct ctccgaaacg ctaaattatc tttcccgcag	180
gagctcatat ccttattttc c atg aca gat ctt aac gac aat ata tgc aaa	231
Met Thr Asp Leu Asn Asp Asn Ile Cys Lys	
1 5	
aga tat ata aag atg ata act aat ata gtt ata ctg agc ctg atc att	279
Arg Tyr Ile Lys Met Ile Thr Asn Ile Val Ile Leu Ser Leu Ile Ile	
11 16 21 26	
tgc att tcg tta gct ttc tgg att ata tca atg act gca agc acc tat	327
Cys Ile Ser Leu Ala Phe Trp Ile Ile Ser Met Thr Ala Ser Thr Tyr	
27 32 37 42	
tat ggt aac tta cga cct att tct ccg tgg cgt tgg ctg ttt tct gtt	375
Tyr Gly Asn Leu Arg Pro Ile Ser Pro Trp Arg Trp Leu Phe Ser Val	
43 48 53 58	
gtt gtt cct gtt ctg atc gtc tct aat ggc ctt aaa aag aaa agt cta	423
Val Val Pro Val Leu Ile Val Ser Asn Gly Leu Lys Lys Lys Ser Leu	
59 64 69 74	
gat cac agt ggg gct cta gga ggg cta gtc gtt gga ttt atc cta acc	471
Asp His Ser Gly Ala Leu Gly Gly Leu Val Val Gly Phe Ile Leu Thr	
75 80 85 90	
att gca aat ttc agc ttt ttt acc tct ttg ctg atg ttt ttc ttg tct	519
Ile Ala Asn Phe Ser Phe Phe Thr Ser Leu Leu Met Phe Phe Leu Ser	
91 96 101 106	
tct tcg aaa ctc act aaa tgg aag gga gaa gtg aag aag cgt cta gat	567
Ser Ser Lys Leu Thr Lys Trp Lys Gly Glu Val Lys Lys Arg Leu Asp	
107 112 117 122	
tca gaa tat aag gaa ggt ggg caa agg aat tgg gtt cag gtg ttc tgt	615
Ser Glu Tyr Lys Glu Gly Gly Gln Arg Asn Trp Val Gln Val Phe Cys	
123 128 133 138	
aat gga gct gta ccc aca gaa ctg gcc ctg ctg tac atg ata gaa aat	663
Asn Gly Ala Val Pro Thr Glu Leu Ala Leu Leu Tyr Met Ile Glu Asn	
139 144 149 154	
ggc ccc ggg gaa atc cca gtc gat ttt tcc aag cag tac tcc gct tcc	711
Gly Pro Gly Glu Ile Pro Val Asp Phe Ser Lys Gln Tyr Ser Ala Ser	
155 160 165 170	
tgg atg tgt ttg tct ctc ttg gct gca ctg gcc tgc tct gct gga gac	759
Trp Met Cys Leu Ser Leu Leu Ala Ala Leu Ala Cys Ser Ala Gly Asp	
171 176 181 186	
aca tgg gct tca gaa gtt ggc cca gtt ctg agt aaa agt tct cca aga	807
Thr Trp Ala Ser Glu Val Gly Pro Val Leu Ser Lys Ser Ser Pro Arg	
187 192 197 202	
ctg ata aca acc tgg gag aaa gtt cca gtt ggt acc aat gga gga gtt	855
Leu Ile Thr Thr Trp Glu Lys Val Pro Val Gly Thr Asn Gly Gly Val	

203	208	213	218	
aca gtg gtg ggc ctt gtc tcc agt ctc ctt ggt ggt acc ttt gtg ggc				903
Thr Val Val Gly Leu Val Ser Ser Leu Leu Gly Gly Thr Phe Val Gly				
219	224	229	234	
att gca tac ttc ctc aca cag ctg att ttt gtg aat gat tta gac att				951
Ile Ala Tyr Phe Leu Thr Gln Leu Ile Phe Val Asn Asp Leu Asp Ile				
235	240	245	250	
tct gcc ccg cag tgg cca att att gca ttt ggt ggt tta gct gga tta				999
Ser Ala Pro Gln Trp Pro Ile Ile Ala Phe Gly Gly Leu Ala Gly Leu				
251	256	261	266	
cta gga tca att gtg gac tca tac tta ggg gct aca atg cag tat act				1047
Leu Gly Ser Ile Val Asp Ser Tyr Leu Gly Ala Thr Met Gln Tyr Thr				
267	272	277	282	
ggg ttg gat gaa agc act ggc atg gtg gtc aac agc cca aca aat aag				1095
Gly Leu Asp Glu Ser Thr Gly Met Val Val Asn Ser Pro Thr Asn Lys				
283	288	293	298	
gca agg cac ata gca ggg aaa ccc att ctt gat aac aac gca gtg aat				1143
Ala Arg His Ile Ala Gly Lys Pro Ile Leu Asp Asn Asn Ala Val Asn				
299	304	309	314	
ctg ttt tct tct gtt ctt att gcc ctc ttg ctc cca act gct gct tgg				1191
Leu Phe Ser Ser Val Leu Ile Ala Leu Leu Leu Pro Thr Ala Ala Trp				
315	320	325	330	
ggt ttt tgg ccc agg ggg tga ac tttatttcat ttccacaggt tgaaactggt				1244
Gly Phe Trp Pro Arg Gly *				
331	336			
gagtccagct aaatttgcaa ttccaacttt catcctaaga ataataactg taatggcaaa				1304
goggaaatgc cagttcctcc tgtattccat tgagatggga tttcacattt tcctctcatc				1364
aactccccctg taatagctag cgtctttcta gtgaaagaga agaattccta gaacttatgc				1424
atTTTTTTTcc tgcTgaatgg aagtcttgag caatgaagct atattgtccc tacatattac				1484
tatatattga actgaaagtt cttacataat caatgtcaag ttttgtctta ttttgttttg				1544
tttgttttaa ccagtgtagg aaataaaagt gatgatattt aaaatagttc tcagttgaag				1604
cagagaaatg ccaactgtgct agttgcccaa atgttgatc tattttaaat agtttaagct				1664
gatgtgtatg ggagcctaaa caagtgtagt atcctgaact tctcccatata attgctatc				1724
acaattggga aaagtgtgga gattgggtcc tagtgagttt tgtggcctac tccacatttg				1784
ttcttccttc ctcaggggta gtgatgaaaa aaagtaaata tctttttcat atgtccatta				1844
gaatgtatga aaaaaatcat ttttaactaaa agcaaaagaa ttttatctta tatctaaaaa				1904
atatataact tactatatgt ttcagttgct ctctgaacaa aaattatctt caatttaata				1964

tgtggaatgt gttttctagc tttctttgaa ttatgtatgg caacctgggt tagcactggc	2024
atcctgaaca gttaagagtc actgggaaat tattgtattt ctttataaat ttactgtcat	2084
atcaattgct ggaaaatgct atgatttttc tattattacc ttctaagttg tattctctct	2144
tacactgtag cctcaactaa ggcaattctg ctatgtttgt tottcactat gatttactgt	2204
gtgccaaagg agttttgaca gggtaacagag tattttaacta aaagtatttt taaatgtttc	2264
tcatgtgatt tctgtacctt cttcctcctg ccccttttgc ttttttaaag aaactgggga	2324
aggatttatg aatacaccac caccagagtg gataatgctt agaattcttt attgggtggc	2384
ctactatggt gatgatctag aactgactta cttcaggaca gaagaaaaaa caatcacacc	2444
cttaaccttt aagccagtta gatcaggggg ttgcaacaat tgggttaaac tttgggtata	2504
cattggaagc accagggcat gtttgctttt tttgtttatg tgtttgtttt ttgagacaga	2564
gtotcacact gtgttccag cactcgga ggctgaggca ggagaatcgc tggaacctgg	2624
gatgtggagg ttgcagtga ccaagattgc accactgtac tccagcctgg gcaacagagg	2684
gagactccat ctgactcca tctcananna naaaaaaaaa aaaa	2728

<210> 573
 <211> 1270
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (334) .. (906)

<400> 573	
gcacgagaga ttctctgagg cctgggaaag cagcattgaa aaaaaaggag gatggtgtta	60
ttaaagagtt aagcattgcc atgcagctcc taagaaactg tctttatcaa aatgaggaat	120
gtaaagaagc agctcttgaa gctcaccttg tcctgtctt gcactctctc tggccttgga	180
ttttgatgga tgattcattg atgcaaattt ctctgcagct cctttgtgtc tatactgcaa	240
attttccaaa tggttgcagt tctctttgtt ggtcaagttg tggacaacac cctgttcaag	300
ctacacatag aggagcctg agcaactctc tgg atg ctg tgt atc cta aag ttg	354
	Met Leu Cys Ile Leu Lys Leu
	1 5
gct tcc cag atg cca ctg gag aac acc acg gtt cag cag atg gtt ttt	402
Ala Ser Gln Met Pro Leu Glu Asn Thr Thr Val Gln Gln Met Val Phe	
8 13 18 23	

atg ctt ctt tca aac ctg gcc ttg tcg cat gac tgt aaa gga gta att	450
Met Leu Leu Ser Asn Leu Ala Leu Ser His Asp Cys Lys Gly Val Ile	
24 29 34 39	
cag aag agt aac ttc tta cag aac ttc ctc tct cta gca ttg cca aaa	498
Gln Lys Ser Asn Phe Leu Gln Asn Phe Leu Ser Leu Ala Leu Pro Lys	
40 45 50 55	
gga gga aat aaa cat cta agt aat ctg act att ctt tgg ttg aag tta	546
Gly Gly Asn Lys His Leu Ser Asn Leu Thr Ile Leu Trp Leu Lys Leu	
56 61 66 71	
ctc ctg aat ata tca tct gga gaa gat ggg caa caa atg att ctg agg	594
Leu Leu Asn Ile Ser Ser Gly Glu Asp Gly Gln Gln Met Ile Leu Arg	
72 77 82 87	
ctt gat ggc tgt cta gac tta cta aca gag atg agc aaa tac aag cac	642
Leu Asp Gly Cys Leu Asp Leu Leu Thr Glu Met Ser Lys Tyr Lys His	
88 93 98 103	
aag agc agc cct tta ttg cct ctt ctt atc ttt cat aat gtt tgc ttc	690
Lys Ser Ser Pro Leu Leu Pro Leu Leu Ile Phe His Asn Val Cys Phe	
104 109 114 119	
agt cct gca aat aaa ccc aag atc ctg gct aat gaa aaa gtc att act	738
Ser Pro Ala Asn Lys Pro Lys Ile Leu Ala Asn Glu Lys Val Ile Thr	
120 125 130 135	
gtg ctt gct gcc tgt ctg gaa agt gag aat caa aat gct cag agg att	786
Val Leu Ala Ala Cys Leu Glu Ser Glu Asn Gln Asn Ala Gln Arg Ile	
136 141 146 151	
gga gca gct gcc ctt tgg gct ctg att tac aat tat cag aag gca aaa	834
Gly Ala Ala Ala Leu Trp Ala Leu Ile Tyr Asn Tyr Gln Lys Ala Lys	
152 157 162 167	
aca gct ttg aaa agc cca tca gta aaa aga aga gtg gat gaa gca tac	882
Thr Ala Leu Lys Ser Pro Ser Val Lys Arg Arg Val Asp Glu Ala Tyr	
168 173 178 183	
tcc tta gca aag aaa act cct taa ttcttctga gtgccatggg atgctacacc	936
Ser Leu Ala Lys Lys Thr Pro *	
184 189	
ttgaagctga cagtcacaa caggggagct aaagttgaag ccagctgtgt gtagcagctg	996
ttacctgaag acgtgctacc tctctacaaa gtgttgatcc ccttctttcc catgagagag	1056
agaactggtg atactccaac accgtccagt tgtggcagct ctccagaagt aatagcagct	1116
gacaactttc tgtgcctttt cctttctgtt gaaaaggcat agaaagttct gggaacataa	1176
acatttttac ccttttctat gccatttatt ttgtaaaaat cctattttaac agttatttaa	1236
taaaacaata tttttagaaa ctaaaaaaaaaaaaa	1270

Tyr	Leu	Phe	Gly	Val	Ile	Val	Val	Pro	Ala	Val	Val	Gln	Leu	Leu	Ser		
101					106					111					116		
ctt	ccc	ttt	ctc	ccg	gac	agc	cca	cgc	tac	ctg	ctc	ttg	gag	aag	cac		740
Leu	Pro	Phe	Leu	Pro	Asp	Ser	Pro	Arg	Tyr	Leu	Leu	Leu	Glu	Lys	His		
117					122					127					132		
aac	gag	gca	aga	gct	gtg	aaa	gcc	ttc	caa	acg	ttc	ttg	ggg	aaa	gca		788
Asn	Glu	Ala	Arg	Ala	Val	Lys	Ala	Phe	Gln	Thr	Phe	Leu	Gly	Lys	Ala		
133					138					143					148		
cac	gtt	tcc	caa	gag	gta	gag	gag	gtc	ctg	gct	gag	agc	cgc	gtg	cag		836
His	Val	Ser	Gln	Glu	Val	Glu	Glu	Val	Leu	Ala	Glu	Ser	Arg	Val	Gln		
149					154					159					164		
agg	agc	atc	cgc	ctg	gtg	tcc	gtg	ctg	gag	ctg	ctg	aga	gct	ccc	tac		884
Arg	Ser	Ile	Arg	Leu	Val	Ser	Val	Leu	Glu	Leu	Leu	Arg	Ala	Pro	Tyr		
165					170					175					180		
gtc	cgc	tgg	cag	gtg	gtc	acc	gtg	att	gtc	acc	atg	gcc	tgc	tac	cag		932
Val	Arg	Trp	Gln	Val	Val	Thr	Val	Ile	Val	Thr	Met	Ala	Cys	Tyr	Gln		
181					186					191					196		
ctc	tgt	ggc	ctc	aat	gca	att	tgg	ttc	tat	acc	aac	agc	atc	ttt	gga		980
Leu	Cys	Gly	Leu	Asn	Ala	Ile	Trp	Phe	Tyr	Thr	Asn	Ser	Ile	Phe	Gly		
197					202					207					212		
aaa	gct	ggg	atc	cct	ccg	gca	aag	atc	cca	tac	gtc	acc	ttg	agt	aca		1028
Lys	Ala	Gly	Ile	Pro	Pro	Ala	Lys	Ile	Pro	Tyr	Val	Thr	Leu	Ser	Thr		
213					218					223					228		
ggg	ggc	atc	gag	act	ttg	gct	gcc	gtc	ttc	tct	ggg	ttg	gtc	att	gag		1076
Gly	Gly	Ile	Glu	Thr	Leu	Ala	Ala	Val	Phe	Ser	Gly	Leu	Val	Ile	Glu		
229					234					239					244		
cac	ctg	gga	cgg	aga	ccc	ctc	ctc	att	ggg	ggc	ttt	ggg	ctc	atg	ggc		1124
His	Leu	Gly	Arg	Arg	Pro	Leu	Leu	Ile	Gly	Gly	Phe	Gly	Leu	Met	Gly		
245					250					255					260		
ctc	ttc	ttt	ggg	acc	ctc	acc	atc	acg	ctg	acc	ctg	cag	gac	cac	gcc		1172
Leu	Phe	Phe	Gly	Thr	Leu	Thr	Ile	Thr	Leu	Thr	Leu	Gln	Asp	His	Ala		
261					266					271					276		
ccc	tgg	gtc	ccc	tac	ctg	agt	atc	gtg	ggc	att	ctg	gcc	atc	atc	gcc		1220
Pro	Trp	Val	Pro	Tyr	Leu	Ser	Ile	Val	Gly	Ile	Leu	Ala	Ile	Ile	Ala		
277					282					287					292		
tct	ttc	tgc	agt	ggg	cca	ggg	ggc	atc	ccg	ttc	atc	ttg	act	ggg	gag		1268
Ser	Phe	Cys	Ser	Gly	Pro	Gly	Gly	Ile	Pro	Phe	Ile	Leu	Thr	Gly	Glu		
293					298					303					308		
ttc	ttc	cag	caa	tct	cag	cgg	ccg	gct	gcc	ttc	atc	att	gca	ggc	acc		1316
Phe	Phe	Gln	Gln	Ser	Gln	Arg	Pro	Ala	Ala	Phe	Ile	Ile	Ala	Gly	Thr		
309					314					319					324		
gtc	aac	tgg	ctc	tcc	aac	ttt	gct	gtt	ggg	ctc	ctc	ttc	cca	ttc	att		1364
Val	Asn	Trp	Leu	Ser	Asn	Phe	Ala	Val	Gly	Leu	Leu	Phe	Pro	Phe	Ile		

325	330	335	340	
cag aaa agt ctg gac acc tac tgt ttc cta gtc ttt gct aca att tgt				1412
Gln Lys Ser Leu Asp Thr Tyr Cys Phe Leu Val Phe Ala Thr Ile Cys				
341	346	351	356	
atc aca ggt gct atc tac ctg tat ttt gtg ctg cct gag acc aaa aac				1460
Ile Thr Gly Ala Ile Tyr Leu Tyr Phe Val Leu Pro Glu Thr Lys Asn				
357	362	367	372	
aga acc tat gca gaa atc agc cag gca ttt tcc aaa agg aac aaa gca				1508
Arg Thr Tyr Ala Glu Ile Ser Gln Ala Phe Ser Lys Arg Asn Lys Ala				
373	378	383	388	
tac cca cca gaa gag aaa atc gac tca gct gtc act gat ggt aag ata				1556
Tyr Pro Pro Glu Glu Lys Ile Asp Ser Ala Val Thr Asp Gly Lys Ile				
389	394	399	404	
aat gga agg cct taa caagtttctt cctccacgtt ggacaattat gtcaaaaaca				1611
Asn Gly Arg Pro *				
405				
ggattgtcta catggatgat ctcaacttttc aggaaactta aaatttacc attattggga				1671
agcttaaagt aattgaagct atgcaagtct tttatattat taaatattta aaagtaaacc				1731
tgtactaatc taacattgca actgtggttag cattattcac aactgaatct cccaaaccct				1791
tctggaagct gcaaggaatc actctatggt tcagtagacc cagcgttctt ctatataggt				1851
agatgacctg ccttcttcat gactcaaccc atgatttcaa aatgaaattg gggaaatagt				1911
aggttaatgc tttatcaaag aaaaatcaat ttggtctgat aggggactca acggattaga				1971
gatcacagac tgagggtcta gtcccagctt taccacaagc agccttgacc tgccctcaac				2031
ctgggtccca gtgcctcaat gaccctaggc ttccatccct gatataggct ttcagaagtc				2091
agtggaaaga ttattcatag tgcctaagaa atgcctgttt ccaatatttg accttgtaga				2151
tctcaggctt tggagagcct aataccaaca caccagcctg cagattttgt ctttcccaaa				2211
ctgtgttcca ggaatgggct caaaaacttca gggctgacgc tgtcctcacc ccagactatt				2271
agagtctctgt gtgctcacag agaacatgaa gaagagcaat gtgtagaaga cttaactttc				2331
tcataactgc agcagggact gaaaattgac ctccatccaa atgaaaaata atgttgagga				2391
tgattctaaa gctaaacctt ggcttgggtg ggaaaaaana aaaaaatttg tggattaatt				2451
gggtggatcc tctggccac aagttgtggg ggctcagagt gtcagcacat gtacctcatg				2511
tttaccaagt ctagaagaga tttctctgaa aaggtaatga gctgtcttga aaaatgggga				2571
gttcaccatc actcaaagtg ctcaaggga gactgggtga ttactcatct tgactgttgc				2631
taagaaaatc tgtgtcaact ttggaggaag gtgtttggaa tagatatgtt gaggggctct				2691

tctaactctt acatgctaaa gttgtttgag taagatctac ttacagcctg ccatcgtaat 2751
 gtgtggcttg tggtttgggc gatttcctat acttgcttct aaaatgaaac aacgtgtcct 2811
 aaagtaaagt aaagtgcact tgaattagca a 2842

<210> 575
 <211> 3475
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (293)..(1996)

<220>
 <221> misc_feature
 <222> (1)...(3475)
 <223> n = a,t,c or g

<400> 575
 aaacgcagat tcctcatcgc attctcagag attctgttgg ttagtattgg gatggggcct 60
 tttttccccc atgattctac gcggccacgt gttggttaacc aatatacaga tgactgggtc 120
 cttcccagtc ccacgcgttt actcgatgaa ggcagcctcc caccgggctc ctggccccgc 180
 ccgagcccca cccctgctc ccttcgggcc cggactgggt cccatcgccc cacctccggt 240
 cgctggacgt gctctcgct agctccgcct ttogtaagtc ccccgctc gc atg 295
 Met
 1
 atg gct gcg gtg ccg ccg ggc ctg gag ccg tgg aac cgt gtg aga atc 343
 Met Ala Ala Val Pro Pro Gly Leu Glu Pro Trp Asn Arg Val Arg Ile
 2 7 12 17
 cct aag gcg ggg aac cgc agc gca gtg aca gtg cag aac ccc ggc gcg 391
 Pro Lys Ala Gly Asn Arg Ser Ala Val Thr Val Gln Asn Pro Gly Ala
 18 23 28 33
 gcc ctt gac ctt tgc att gca gct gta att aaa gaa tgc cat ctg gtc 439
 Ala Leu Asp Leu Cys Ile Ala Ala Val Ile Lys Glu Cys His Leu Val
 34 39 44 49
 ata ctg tcg ctg aag agc caa acc tta gat gca gaa aca gat gtg tta 487
 Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp Ala Glu Thr Asp Val Leu
 50 55 60 65
 tgt gca gtc ctt tac agc aat cac aac aga atg ggc cgc cac aaa ccc 535
 Cys Ala Val Leu Tyr Ser Asn His Asn Arg Met Gly Arg His Lys Pro
 66 71 76 81

cat ttg gcc ctc aaa cag gtt gag caa tgt tta aag cgt ttg aaa aac	583
His Leu Ala Leu Lys Gln Val Glu Gln Cys Leu Lys Arg Leu Lys Asn	
82 87 92 97	
atg aat ttg gag ggc tca att caa gac ctg ttt gag ttg ttt tct tcc	631
Met Asn Leu Glu Gly Ser Ile Gln Asp Leu Phe Glu Leu Phe Ser Ser	
98 103 108 113	
aat gaa aat cag ccc tta act acc aaa gta tgt gtt gtc ccc agt cag	679
Asn Glu Asn Gln Pro Leu Thr Thr Lys Val Cys Val Val Pro Ser Gln	
114 119 124 129	
cca gtg gtg gag ttg gtg ttg atg aag gtt ttg gga gcc tgc aag ttg	727
Pro Val Val Glu Leu Val Leu Met Lys Val Leu Gly Ala Cys Lys Leu	
130 135 140 145	
ttg ctc cgc ttg ttg gac tgc tgc tgc aaa act ttt ctt ttg act gtg	775
Leu Leu Arg Leu Leu Asp Cys Cys Cys Lys Thr Phe Leu Leu Thr Val	
146 151 156 161	
aaa cat cta ggt ttg caa gag ttc att att tta aac ctt gtg atg gtt	823
Lys His Leu Gly Leu Gln Glu Phe Ile Ile Leu Asn Leu Val Met Val	
162 167 172 177	
ggg ctg gtg agc agg tta tgg gtt ctc tat aaa ggt gtc tta aaa agg	871
Gly Leu Val Ser Arg Leu Trp Val Leu Tyr Lys Gly Val Leu Lys Arg	
178 183 188 193	
ttg att ttg tta tat gag cct ttg ttt gga ttg ctt caa gag gtc gct	919
Leu Ile Leu Leu Tyr Glu Pro Leu Phe Gly Leu Leu Gln Glu Val Ala	
194 199 204 209	
agg att caa cca atg cct tac ttc aaa gat ttt acc ttt cct tct gat	967
Arg Ile Gln Pro Met Pro Tyr Phe Lys Asp Phe Thr Phe Pro Ser Asp	
210 215 220 225	
atc act gaa ttt tta gga cag cca tat ttt gaa gcc ttt aag aaa aaa	1015
Ile Thr Glu Phe Leu Gly Gln Pro Tyr Phe Glu Ala Phe Lys Lys Lys	
226 231 236 241	
atg cct ata gct ttt gca gct aaa gga ata aat aaa ttg cta aat aaa	1063
Met Pro Ile Ala Phe Ala Ala Lys Gly Ile Asn Lys Leu Leu Asn Lys	
242 247 252 257	
ctg ttt tta ata aat gag cag tca cca aga gcc agt gaa gaa acc ttg	1111
Leu Phe Leu Ile Asn Glu Gln Ser Pro Arg Ala Ser Glu Glu Thr Leu	
258 263 268 273	
ctt gga att tca aaa aaa gct aaa caa atg aag atc aat gta cag aat	1159
Leu Gly Ile Ser Lys Lys Ala Lys Gln Met Lys Ile Asn Val Gln Asn	
274 279 284 289	
aat gtg gat ctt gga cag cca gta aag aat aag aga gtc ttc aaa gaa	1207
Asn Val Asp Leu Gly Gln Pro Val Lys Asn Lys Arg Val Phe Lys Glu	
290 295 300 305	
gag tca tca gaa ttt gat gtg agg gct ttc tgc aac cag ctg aaa cac	1255

Glu Ser Ser Glu Phe Asp Val Arg Ala Phe Cys Asn Gln Leu Lys His	
306 311 316 321	
aaa gct act cag gag acc agt ttt gat ttt aaa tgt tct caa tcc aga	1303
Lys Ala Thr Gln Glu Thr Ser Phe Asp Phe Lys Cys Ser Gln Ser Arg	
322 327 332 337	
cta aag aca acc aag tat tct tct cag aaa gtg ata gga act cct cat	1351
Leu Lys Thr Thr Lys Tyr Ser Ser Gln Lys Val Ile Gly Thr Pro His	
338 343 348 353	
gcc aaa agt ttt gtg caa aga ttc cga gag gct gag tcc ttc aca caa	1399
Ala Lys Ser Phe Val Gln Arg Phe Arg Glu Ala Glu Ser Phe Thr Gln	
354 359 364 369	
ctt tct gaa gaa atc cag atg gca gtt gta tgg tgc agg agc aaa aaa	1447
Leu Ser Glu Glu Ile Gln Met Ala Val Val Trp Cys Arg Ser Lys Lys	
370 375 380 385	
ctc aag gct cag gcc att ttt ctg ggt aac aaa ctt ctt aaa agc aac	1495
Leu Lys Ala Gln Ala Ile Phe Leu Gly Asn Lys Leu Leu Lys Ser Asn	
386 391 396 401	
cgg ctt aaa cat ctg gaa gct caa ggt act agt ttg cca aag aaa cta	1543
Arg Leu Lys His Leu Glu Ala Gln Gly Thr Ser Leu Pro Lys Lys Leu	
402 407 412 417	
gag tgc ata aaa acg tct att tgc aac cac ctt ctt cgt ggc tca ggt	1591
Glu Cys Ile Lys Thr Ser Ile Cys Asn His Leu Leu Arg Gly Ser Gly	
418 423 428 433	
atc aaa act tca aag cat cat ctg aga cag aga aga tca cag aat aaa	1639
Ile Lys Thr Ser Lys His His Leu Arg Gln Arg Arg Ser Gln Asn Lys	
434 439 444 449	
ttt tta cgg aga caa agg aaa cca cag aga aag ttg cag tcg act ctt	1687
Phe Leu Arg Arg Gln Arg Lys Pro Gln Arg Lys Leu Gln Ser Thr Leu	
450 455 460 465	
tta agg gaa att cag cag ttc tct caa ggg act cgg aag agt gct aca	1735
Leu Arg Glu Ile Gln Gln Phe Ser Gln Gly Thr Arg Lys Ser Ala Thr	
466 471 476 481	
gat acc agt gct aag tgg aga ctc tca cac tgt act gtg cat aga act	1783
Asp Thr Ser Ala Lys Trp Arg Leu Ser His Cys Thr Val His Arg Thr	
482 487 492 497	
gat ctc tac cct aac agt aag cag ctc ttg aat agt gga gtt tca atg	1831
Asp Leu Tyr Pro Asn Ser Lys Gln Leu Leu Asn Ser Gly Val Ser Met	
498 503 508 513	
cct gtc ata caa act aag gag aaa atg att cat gaa aat ctt aga ggc	1879
Pro Val Ile Gln Thr Lys Glu Lys Met Ile His Glu Asn Leu Arg Gly	
514 519 524 529	
atc cat gaa aat gaa act gat tcg tgg acg gtg atg caa ata aat aaa	1927
Ile His Glu Asn Glu Thr Asp Ser Trp Thr Val Met Gln Ile Asn Lys	

530	535	540	545	
aac agt aca tca gga acc att aag gag aca gat gac att gat gat att				1975
Asn Ser Thr Ser Gly Thr Ile Lys Glu Thr Asp Asp Ile Asp Asp Ile				
546	551	556	561	
ttt gct tta atg gga gtt tag at gttagtcat atgtgagact ttttaagtgat				2028
Phe Ala Leu Met Gly Val *				
562	567			
taacaaggct agttcagtgt tctaagtaga actgctaaga tctggaagta ccacctggac				2088
tcacagagga gctgcttttag tgcagcattg cacaggagtt catttcagtt cagtctacat				2148
ttaaagtagc attgtgtcat ttcatacaaca agtattttctt ttttggtctc aactacatgt				2208
caggtgttaa tatgaaaaat ctgccacagc ctacccttga gaagcagatg taattccttg				2268
agtgaggcta gtaagtctct gaaaaactga ataattttat gacttactag gcaatttaat				2328
aatcgtttgc aaaaaccatt gtgtcttgag gtaaataagg agcgggggtg ggagatagca				2388
aggaaacacc tgaaaggcca atttggtctt attggctcca ttatacatag gtccgcctct				2448
gaatactaaa gttttagct cctgacattt atgttttctt gtttatatgt tggaattgat				2508
caacaagggt tgccactgct tgtattacca gggactgggt acaaccatta tttctcttca				2568
tttgcttggc ttatctcata ttaaagttag tttggagtgc tccaaaacgt ttttaattta				2628
tttatttggg taccagtgat tgattccaaa taaacctttt tacaaaaagg caataagggtg				2688
gtttatgggt acatatgaaa tataatagga taacaggtag atgagaaagt aaaatgaaaa				2748
aatgagggtta ggagatacaa agtagacca ggaatgaggg tagaacattt ataatttgggt				2808
gttgatgctg tcatctgata ggggatgttg ctogtactgt tgctctgagg ggagtacatc				2868
ttgagtattt tcaaataatg atgtgaagtt tgaggtaggt atctttccaa tgttctaact				2928
ttactagaat taggttatta agcttctcta gtgcccttaa cttttgttac atagagattt				2988
aaagaaaaag aaagtagtac cttagtatgt accgcacctt tcttttctc agccacccta				3048
tcataacaga agttatttcc ctccattctt ttatttgggt ttgttcttcc cctgtctgcc				3108
ttctccattt tctcagttat ctctaccagt ggttctcaaa ctttagactt tttgagaatc				3168
acctggtggg ttgctaaaag atgcagatta gccctttccc agagactgat aaacaggggc				3228
cagaaacctg catttttaac atggagccca agtgattttg atccagggtg ccccaaatac				3288
cagttatata aacactactt tagcttctct pctgaagcct taagtaaact ggtttaattc				3348
ttaatctgta gtcagttttc atattcctga attccaccac actggactag tggatccgag				3408
ctcggtacca agcttaagtt taaacgctag ccagcttggg tctcgcaacc aaaannnggg				3468

gnttcaa

3475

<210> 576
<211> 3319
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (293)..(1840)

<220>
<221> misc_feature
<222> (1)...(3319)
<223> n = a,t,c or g

<400> 576

aaacgcagat	tctcatcgc	attctcagag	attctgttg	ttagtattgg	gatggggcct	60
tttttcccc	atgattctac	gcggccacgt	gttggttaacc	aatatacaga	tgactgggtc	120
cttcccagtc	ccacgcgttt	actcgatgaa	ggcagcctcc	caccgggctc	ctggccccgc	180
ccgagcccca	ccccctgctc	ccttcgggcc	eggactgggt	cccatcgccc	cacctccggt	240
cgctggacgt	gtctctcggt	agctccgcct	ttcgtaagtc	ccccgcctc	gc atg	295
					Met	
					1	
atg gct gcg gtg ccg ccg ggc ctg gag ccg tgg aac cgt gtg aga atc	343					
Met Ala Ala Val Pro Pro Gly Leu Glu Pro Trp Asn Arg Val Arg Ile						
2 7 12 17						
cct aag gcg ggg aac cgc agc gca gtg aca gtg cag aac ccc ggc gcg	391					
Pro Lys Ala Gly Asn Arg Ser Ala Val Thr Val Gln Asn Pro Gly Ala						
18 23 28 33						
gcc ttg gtt gag caa tgt tta aag cgt ttg aaa aac atg aat ttg gag	439					
Ala Leu Val Glu Gln Cys Leu Lys Arg Leu Lys Asn Met Asn Leu Glu						
34 39 44 49						
ggc tca att caa gac ctg ttt gag ttg ttt tct tcc aat gaa aat cag	487					
Gly Ser Ile Gln Asp Leu Phe Glu Leu Phe Ser Ser Asn Glu Asn Gln						
50 55 60 65						
ccc tta act acc aaa gta tgt gtt gtc ccc agt cag cca gtg gtg gag	535					
Pro Leu Thr Thr Lys Val Cys Val Val Pro Ser Gln Pro Val Val Glu						
66 71 76 81						
ttg gtg ttg atg aag gtt ttg gga gcc tgc aag ttg ttg ctc cgc ttg	583					
Leu Val Leu Met Lys Val Leu Gly Ala Cys Lys Leu Leu Leu Arg Leu						
82 87 92 97						

ttg gac tgc tgc tgc aaa act ttt ctt ttg act gtg aaa cat cta ggt	631
Leu Asp Cys Cys Cys Lys Thr Phe Leu Leu Thr Val Lys His Leu Gly	
98 103 108 113	
ttg caa gag ttc att att tta aac ctt gtg atg gtt ggg ctg gtg agc	679
Leu Gln Glu Phe Ile Ile Leu Asn Leu Val Met Val Gly Leu Val Ser	
114 119 124 129	
agg tta tgg gtt ctc tat aaa ggt gtc tta aaa agg ttg att ttg tta	727
Arg Leu Trp Val Leu Tyr Lys Gly Val Leu Lys Arg Leu Ile Leu Leu	
130 135 140 145	
tat gag cct ttg ttt gga ttg ctt caa gag gtc gct agg att caa cca	775
Tyr Glu Pro Leu Phe Gly Leu Leu Gln Glu Val Ala Arg Ile Gln Pro	
146 151 156 161	
atg cct tac ttc aaa gat ttt acc ttt cct tct gat atc act gaa ttt	823
Met Pro Tyr Phe Lys Asp Phe Thr Phe Pro Ser Asp Ile Thr Glu Phe	
162 167 172 177	
tta gga cag cca tat ttt gaa gcc ttt aag aaa aaa atg cct ata gct	871
Leu Gly Gln Pro Tyr Phe Glu Ala Phe Lys Lys Lys Met Pro Ile Ala	
178 183 188 193	
ttt gca gct aaa gga ata aat aaa ttg cta aat aaa ctg ttt tta ata	919
Phe Ala Ala Lys Gly Ile Asn Lys Leu Leu Asn Lys Leu Phe Leu Ile	
194 199 204 209	
aat gag cag tca cca aga gcc agt gaa gaa acc ttg ctt gga att tca	967
Asn Glu Gln Ser Pro Arg Ala Ser Glu Glu Thr Leu Leu Gly Ile Ser	
210 215 220 225	
aaa aaa gct aaa caa atg aag atc aat gta cag aat aat gtg gat ctt	1015
Lys Lys Ala Lys Gln Met Lys Ile Asn Val Gln Asn Asn Val Asp Leu	
226 231 236 241	
gga cag cca gta aag aat aag aga gtc ttc aaa gaa gag tca tca gaa	1063
Gly Gln Pro Val Lys Asn Lys Arg Val Phe Lys Glu Glu Ser Ser Glu	
242 247 252 257	
ttt gat gtg agg gct ttc tgc aac cag ctg aaa cac aaa gct act cag	1111
Phe Asp Val Arg Ala Phe Cys Asn Gln Leu Lys His Lys Ala Thr Gln	
258 263 268 273	
gag acc agt ttt gat ttt aaa tgt tct caa tcc aga cta aag aca acc	1159
Glu Thr Ser Phe Asp Phe Lys Cys Ser Gln Ser Arg Leu Lys Thr Thr	
274 279 284 289	
aag tat tct tct cag aaa gtg ata gga act cct cat gcc aaa agt ttt	1207
Lys Tyr Ser Ser Gln Lys Val Ile Gly Thr Pro His Ala Lys Ser Phe	
290 295 300 305	
gtg caa aga ttc cga gag gct gag tcc ttc aca caa ctt tct gaa gaa	1255
Val Gln Arg Phe Arg Glu Ala Glu Ser Phe Thr Gln Leu Ser Glu Glu	
306 311 316 321	
atc cag atg gca gtt gta tgg tgc agg agc aaa aaa ctc aag gct cag	1303

Ile Gln Met Ala Val Val Trp Cys Arg Ser Lys Lys Leu Lys Ala Gln
322 327 332 337

gcc att ttt ctg ggt aac aaa ctt ctt aaa agc aac cgg ctt aaa cat 1351
Ala Ile Phe Leu Gly Asn Lys Leu Leu Lys Ser Asn Arg Leu Lys His
338 343 348 353

ctg gaa gct caa ggt act agt ttg cca aag aaa cta gag tgc ata aaa 1399
Leu Glu Ala Gln Gly Thr Ser Leu Pro Lys Lys Leu Glu Cys Ile Lys
354 359 364 369

acg tct att tgc aac cac ctt ctt cgt ggc tca ggt atc aaa act tca 1447
Thr Ser Ile Cys Asn His Leu Leu Arg Gly Ser Gly Ile Lys Thr Ser
370 375 380 385

aag cat cat ctg aga cag aga aga tca cag aat aaa ttt tta cgg aga 1495
Lys His His Leu Arg Gln Arg Arg Ser Gln Asn Lys Phe Leu Arg Arg
386 391 396 401

caa agg aaa cca cag aga aag ttg cag tcg act ctt tta agg gaa att 1543
Gln Arg Lys Pro Gln Arg Lys Leu Gln Ser Thr Leu Leu Arg Glu Ile
402 407 412 417

cag cag ttc tct caa ggg act cgg aag agt gct aca gat acc agt gct 1591
Gln Gln Phe Ser Gln Gly Thr Arg Lys Ser Ala Thr Asp Thr Ser Ala
418 423 428 433

aag tgg aga ctc tca cac tgt act gtg cat aga act gat ctc tac cct 1639
Lys Trp Arg Leu Ser His Cys Thr Val His Arg Thr Asp Leu Tyr Pro
434 439 444 449

aac agt aag cag ctc ttg aat agt gga gtt tca atg cct gtc ata caa 1687
Asn Ser Lys Gln Leu Leu Asn Ser Gly Val Ser Met Pro Val Ile Gln
450 455 460 465

act aag gag aaa atg att cat gaa aat ctt aga ggc atc cat gaa aat 1735
Thr Lys Glu Lys Met Ile His Glu Asn Leu Arg Gly Ile His Glu Asn
466 471 476 481

gaa act gat tcg tgg acg gtg atg caa ata aat aaa aac agt aca tca 1783
Glu Thr Asp Ser Trp Thr Val Met Gln Ile Asn Lys Asn Ser Thr Ser
482 487 492 497

gga acc att aag gag aca gat gac att gat gat att ttt gct tta atg 1831
Gly Thr Ile Lys Glu Thr Asp Asp Ile Asp Asp Ile Phe Ala Leu Met
498 503 508 513

gga gtt tag atgttcg ttcataatgtg agacttttaa gtgattaaca aggctagtgc 1887
Gly Val *
514

agtgttctaa gtagaactgc taagatctgg aagtaaccacc tggactcaca gaggagctgc 1947

tttagtgcag cattgcacag gagttcattt cagttcagtc tacatttaaa gtagcattgt 2007

gtcattttcat caacaagtat ttcttttttg gcttcaacta catgtcaggt gttaatatga 2067

aaaatctgcc acagcctacc cttgagaagc agatgtaatt ccttgagtga ggctagtaag	2127
tctctgaaaa actgaataat tttatgactt actaggcaat ttaataatcg tttgcaaaaa	2187
ccattgtgtc ttgaggtaaa tgaggagcgg ggggtgggaga tagcaaggaa acacctgaaa	2247
ggccaatttg gtcttatttg ctccattata cataggtccg cctctgaata ctaaagtttg	2307
tagctcctga ctttatgtt ttcttgttta tatgttgga ttgatcaaca aggtttgcc	2367
ctgcttgat taccaggac tggttacaac cattatttct cttcatttgc ttggcttctc	2427
tcatattaaa gtgagtttg agttctcaa aacgttttaa ttttatttat ttgggtacca	2487
gtgattgatt ccaaataaac ctttttaca aaaggcaata aggtggttta tggttacata	2547
tgaaatataa taggataaca ggtagatgag aaagtaaat gaaaaaatga ggtaggaga	2607
tacaaagtag acccaggaat gaggctagaa cttttataat ttggtgttga tgctgtctc	2667
tgatagggga tgttgctcgt actgttgctc tgaggggagt acatcttgag tttttcaaa	2727
taatgatgtg aagtttgagg taggtatctt tccaatgttc taactttact agaattaggt	2787
tattaagctt ctctagtgc ctttaactttt gttacataga gatttaaaga aaaagaaagt	2847
agtaacctag tatgtaccgc atccttcttt tctcagcca ccctatcata acagaagtta	2907
tttcccttcc attctttatt tggctttgtt ctttccctgt ctgccttctc cttttctca	2967
gttatctcta ccagtgggtc tcaaacttta gactttttga gaatcacctg gtgggttgct	3027
aaaagatgca gattagccct tttccagaga ctgataaaca ggggccagaa acctgcattt	3087
ttaacatgga gcccaagtga ttttgatcca ggtggcccc aaatccagtt atataaacac	3147
tacttttagct tctctcctga agccttaagt aaactgggtt aattcttaat ctgtagtcag	3207
ttttcatatt cctgaattcc accacactgg actagtggat ccgagctcgg taccaagctt	3267
aagtttaaac gctagccagc ttgggtctcg caacccaaan nngggnttc aa	3319

<210> 577

<211> 2124

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (261)..(1319)

<400> 577

cggtaccggt ccggaattcc cgggtcgacg atttcgtgtg agggagctgc tggcgggtgg	60
---	----

gtt aat ttg aat aat ata aag aat atc cca att cca acc cta aaa gat	914
Val Asn Leu Asn Asn Ile Lys Asn Ile Pro Ile Pro Thr Leu Lys Asp	
203 208 213 218	
ttt gca aag gct ttg gaa acc aac aca cat gtg aaa tgt ttc agt ctt	962
Phe Ala Lys Ala Leu Glu Thr Asn Thr His Val Lys Cys Phe Ser Leu	
219 224 229 234	
gca gcc acc cgg agc aat gac cct gtt gct act gct ttt gca gaa atg	1010
Ala Ala Thr Arg Ser Asn Asp Pro Val Ala Thr Ala Phe Ala Glu Met	
235 240 245 250	
ctg aaa gtg aac aaa act ttg aag agc tta aat gtg gag tcc aac ttt	1058
Leu Lys Val Asn Lys Thr Leu Lys Ser Leu Asn Val Glu Ser Asn Phe	
251 256 261 266	
atc acg gga gtt ggg att ctg gca ctg att gat gcg tta aga gat aat	1106
Ile Thr Gly Val Gly Ile Leu Ala Leu Ile Asp Ala Leu Arg Asp Asn	
267 272 277 282	
gaa acc ctg gca gag ctc aag att gac aat cag agg cag cag ttg ggg	1154
Glu Thr Leu Ala Glu Leu Lys Ile Asp Asn Gln Arg Gln Gln Leu Gly	
283 288 293 298	
aca gct gta gaa ttg gaa atg gcc aag atg ctt gag gaa aat aca aat	1202
Thr Ala Val Glu Leu Glu Met Ala Lys Met Leu Glu Glu Asn Thr Asn	
299 304 309 314	
atc ctt aaa ttt gga tat cag ttt aca cag cag gga cca cga acc aga	1250
Ile Leu Lys Phe Gly Tyr Gln Phe Thr Gln Gln Gly Pro Arg Thr Arg	
315 320 325 330	
gca gct aat gct ata aca aaa aac aat gac tta gtg cgt aag aga cga	1298
Ala Ala Asn Ala Ile Thr Lys Asn Asn Asp Leu Val Arg Lys Arg Arg	
331 336 341 346	
gtt gaa gga gat cac cag taa gt ctgcaaaggt gtaatctttg gaagacttca	1351
Val Glu Gly Asp His Gln *	
347 352	
gaagatcacc aagggctcat gttggtgaca tcatgtaaaa ttttctggg tagaagggaa	1411
aagactggaa aaattttttt agtgacatgc attttttttt tagttgttat caaattgtaa	1471
aatcagtaat gtgatatttt atattctgaa acatttctac tttctgctaa aatcaatttt	1531
aatttagttt aattgaatga tttatgatga atcttgggca aaaaaataca actgtaaaaa	1591
atctcacagg tcatttgtgt agaataattt gaacattgtg aggaccaatc ttttttaa	1651
caaaagggat gttgctggtg tcagaattgt tattgcttca ttttagacata aaacacttaa	1711
gtgttttctt tcaactccgtg acctggagag ttttccattt tttgcaagtt tagtaactgcc	1771
caaattttact cattctacag tgttactgca ctttgaacgt attgacccat gtcacccaag	1831

agaagcaaac atatggatgc actagagaca actcgggttg ctgctctcag ttaagggcta 1891
 tgagttcttg gggctctaagt atctgtaaaa ttatcctctc catcagctct cactgatcat 1951
 taatgtttct ggatatttct taccctaaga tttgcttacc aacaaatcaa agaaacgctt 2011
 cactaattat ttttaaattg agaaaatagt attcagagggc aaagattttt atattctttt 2071
 ttgagaccaa gtctcactct agcctgggca atgagagtga aaatcttatc tca 2124

<210> 578
 <211> 1372
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (105)..(998)

<400> 578
 taagcttgcg gccgcgggggt ccggaactgc ttgttcgggc agtgggaagag acgcgccggc 60
 gttggccgct gctgctagca cgttgaaccc cagggtcggg accg atg tcg gct tgg 116
 Met Ser Ala Trp
 1
 gct gct gcc agc cta agc agg gcc gct gcc gaa tgc ttg ctg gca cga 164
 Ala Ala Ala Ser Leu Ser Arg Ala Ala Ala Glu Cys Leu Leu Ala Arg
 5 10 15 20
 ggc ccc ggg gtc agg gcg gct cct ccg cgc gac ccc cgg ccc tcc cac 212
 Gly Pro Gly Val Arg Ala Ala Pro Pro Arg Asp Pro Arg Pro Ser His
 21 26 31 36
 ccc gag ccc cgg ggc tgc ggt gcc gct ccg ggc agg acg ctg cac ttt 260
 Pro Glu Pro Arg Gly Cys Gly Ala Ala Pro Gly Arg Thr Leu His Phe
 37 42 47 52
 acc gcg gct gtc ccc gcc ggg cac aac aag tgg tcc aaa gtc agg cac 308
 Thr Ala Ala Val Pro Ala Gly His Asn Lys Trp Ser Lys Val Arg His
 53 58 63 68
 atc aag ggt ccg aag gac gtc gaa agg agt cgc atc ttc tcc aaa ctc 356
 Ile Lys Gly Pro Lys Asp Val Glu Arg Ser Arg Ile Phe Ser Lys Leu
 69 74 79 84
 tgt ttg aac atc cgc ctg gca gtg aaa gaa gga ggc ccc aac cct gag 404
 Cys Leu Asn Ile Arg Leu Ala Val Lys Glu Gly Gly Pro Asn Pro Glu
 85 90 95 100
 cac aac agc aac ctg gcc aat atc tta gag gtg tgt cgc agc aaa cat 452
 His Asn Ser Asn Leu Ala Asn Ile Leu Glu Val Cys Arg Ser Lys His
 101 106 111 116

atg ccc aag tca acg att gag aca gca ctg aaa atg gag aaa tcc aag	500
Met Pro Lys Ser Thr Ile Glu Thr Ala Leu Lys Met Glu Lys Ser Lys	
117 122 127 132	
gac act tat ttg ctg tat gag ggt cga ggc cct ggt ggc tct tct ctg	548
Asp Thr Tyr Leu Leu Tyr Glu Gly Arg Gly Pro Gly Gly Ser Ser Leu	
133 138 143 148	
ctc atc gag gca tta tct aac agt agc cac aag tgc caa gca gac att	596
Leu Ile Glu Ala Leu Ser Asn Ser Ser His Lys Cys Gln Ala Asp Ile	
149 154 159 164	
aga cat atc ctg aat aag aat gga gga gtg atg gct gta gga gct cgt	644
Arg His Ile Leu Asn Lys Asn Gly Gly Val Met Ala Val Gly Ala Arg	
165 170 175 180	
cac tct ttt gac aaa aag ggg gtg att gtg gtt gaa gtg gag gac aga	692
His Ser Phe Asp Lys Lys Gly Val Ile Val Val Glu Val Glu Asp Arg	
181 186 191 196	
gag aag aag gct gtg aac cta gag cgt gcc ctg gag atg gca atc gaa	740
Glu Lys Lys Ala Val Asn Leu Glu Arg Ala Leu Glu Met Ala Ile Glu	
197 202 207 212	
gca gga gct gag gat gtc aag gaa act gaa gat gaa gaa gaa agg aac	788
Ala Gly Ala Glu Asp Val Lys Glu Thr Glu Asp Glu Glu Glu Arg Asn	
213 218 223 228	
gtt ttt aaa ttt att tgt gat gcc tct tca ctg cac caa gtg agg aag	836
Val Phe Lys Phe Ile Cys Asp Ala Ser Ser Leu His Gln Val Arg Lys	
229 234 239 244	
aag ctg gac tcc ctg ggc ctg tgt tct gtg tcc tgt gca cta gag ttc	884
Lys Leu Asp Ser Leu Gly Leu Cys Ser Val Ser Cys Ala Leu Glu Phe	
245 250 255 260	
atc ccc aac tca aag gtg cag ctg gct gag ccc gac ctg gaa cag gcc	932
Ile Pro Asn Ser Lys Val Gln Leu Ala Glu Pro Asp Leu Glu Gln Ala	
261 266 271 276	
gca cat ctc att cag gct ctc agc aac cac gag gat gtg att cac gtc	980
Ala His Leu Ile Gln Ala Leu Ser Asn His Glu Asp Val Ile His Val	
277 282 287 292	
tat gat aac att gaa taa ccaggc tacatgtgcc cccgggttcc ttcctagaaa	1034
Tyr Asp Asn Ile Glu *	
293 298	
tgtggcagcc cattccagca cacaggcttc tgcagcaatc tctgagggtta aagccggtgg	1094
gaggctcagc aggccaggag gcccaaggac aggacttgcg accttgaagc caaaggaatc	1154
tcacttggtg ggctctcttg tcagctctgc tgctgtctca gagccatctg gatgagtgtc	1214
cogacacct ctcggatgca gggcaggacc acccagctgg tcagactctg atgttgggta	1274
gctggcctct gtggggattg taagtgcct gaggcgctct gtactagaaa ctgctcttaa	1334

taataacggt gattattggt tgctgcaaaa aaaaaaaa

1372

<210> 579
<211> 2224
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (121)..(1953)

<220>
<221> misc_feature
<222> (1)...(2224)
<223> n = a,t,c or g

<400> 579
agggacggna atttgacgcc gtngatcgat cgcgggtttcc cgggtcgcacc cacgcgtgcg 60
gccgactgtg tggcagctga ggaagagttt tgcacgtgga tcgccgttcg ggtgggagcgag 120
atg gag aca gcc ccc aag ccg ggc aag gat gtc ccg ccc aag aaa gac 168
Met Glu Thr Ala Pro Lys Pro Gly Lys Asp Val Pro Pro Lys Lys Asp
1 5 10 15
aaa ctt cag acc aag aga aag aaa ccg cgg cga tac tgg gag gaa gag 216
Lys Leu Gln Thr Lys Arg Lys Lys Pro Arg Arg Tyr Trp Glu Glu Glu
17 22 27 32
acc gtt ccg acc aca gcc gga gcc tct cca ggg cct cct cgt aac aag 264
Thr Val Pro Thr Thr Ala Gly Ala Ser Pro Gly Pro Pro Arg Asn Lys
33 38 43 48
aag aat cgg gag ctc cgt cct cag aga cca aaa aat gct tac atc tta 312
Lys Asn Arg Glu Leu Arg Pro Gln Arg Pro Lys Asn Ala Tyr Ile Leu
49 54 59 64
aag aag tct cgg atc tct aag aag cct cag gtc ccg aag aaa ccc cga 360
Lys Lys Ser Arg Ile Ser Lys Lys Pro Gln Val Pro Lys Lys Pro Arg
65 70 75 80
gaa tgg aag aac ccg gag tcc cag cgc ggc ttg tcc ggg gcc caa gat 408
Glu Trp Lys Asn Pro Glu Ser Gln Arg Gly Leu Ser Gly Ala Gln Asp
81 86 91 96
cca ttc cca ggc ccc gcc ccc gtc cct gtg gaa gtg gtc cag aag ttc 456
Pro Phe Pro Gly Pro Ala Pro Val Pro Val Glu Val Val Gln Lys Phe
97 102 107 112
tgt cgc att gac aaa tcc cga aag cta cca cat tct aaa gcc aaa act 504
Cys Arg Ile Asp Lys Ser Arg Lys Leu Pro His Ser Lys Ala Lys Thr
113 118 123 128

cga agc cga ctt gag gtg gct gaa gct gag gaa gag gaa aca agt atc	552
Arg Ser Arg Leu Glu Val Ala Glu Ala Glu Glu Glu Glu Thr Ser Ile	
129 134 139 144	
aaa gct gct cgt tct gag ctg ctg ctt gct gaa gaa cct ggg ttt ctg	600
Lys Ala Ala Arg Ser Glu Leu Leu Leu Ala Glu Glu Pro Gly Phe Leu	
145 150 155 160	
gaa ggg gag gat ggg gaa gac aca gca aag ata tgc cag gct gac att	648
Glu Gly Glu Asp Gly Glu Asp Thr Ala Lys Ile Cys Gln Ala Asp Ile	
161 166 171 176	
gtg gag gct gtg gac att gca agt gca gcc aag cac ttt gac ttg aat	696
Val Glu Ala Val Asp Ile Ala Ser Ala Ala Lys His Phe Asp Leu Asn	
177 182 187 192	
ctg cgg cag ttt gga ccc tac aga cta aac tac tct cga act gga aga	744
Leu Arg Gln Phe Gly Pro Tyr Arg Leu Asn Tyr Ser Arg Thr Gly Arg	
193 198 203 208	
cac ctg gct ttt gga ggg cgc cga ggt cat gtg gct gcc ctt gat tgg	792
His Leu Ala Phe Gly Gly Arg Arg Gly His Val Ala Ala Leu Asp Trp	
209 214 219 224	
gta aca aag aag ctt atg tgc gag atc aac gtc atg gag gcg gtg cgg	840
Val Thr Lys Lys Leu Met Cys Glu Ile Asn Val Met Glu Ala Val Arg	
225 230 235 240	
gac atc cgg ttt ctc cat tct gag gca ctg ctt gct gtt gct cag aac	888
Asp Ile Arg Phe Leu His Ser Glu Ala Leu Leu Ala Val Ala Gln Asn	
241 246 251 256	
cgc tgg ctc cac atc tat gac aat cag ggc att gag ctc cac tgt atc	936
Arg Trp Leu His Ile Tyr Asp Asn Gln Gly Ile Glu Leu His Cys Ile	
257 262 267 272	
cgc cgc tgt gac cga gta aca cgg ctt gag ttc ctg ccc ttc cac ttc	984
Arg Arg Cys Asp Arg Val Thr Arg Leu Glu Phe Leu Pro Phe His Phe	
273 278 283 288	
ctc ctg gct aca gct tca gaa aca ggg ttt cta acc tac ctg gat gtg	1032
Leu Leu Ala Thr Ala Ser Glu Thr Gly Phe Leu Thr Tyr Leu Asp Val	
289 294 299 304	
tca gtg ggg aag att gtg gca gct ctg aat gct cga gct ggg cgg ctc	1080
Ser Val Gly Lys Ile Val Ala Ala Leu Asn Ala Arg Ala Gly Arg Leu	
305 310 315 320	
gat gtt atg agt cag aac cct tac aat gcc gtc atc cat ctc gga cac	1128
Asp Val Met Ser Gln Asn Pro Tyr Asn Ala Val Ile His Leu Gly His	
321 326 331 336	
agc aat ggt act gtg tct tta tgg agt cca gct atg aag gag cca ctg	1176
Ser Asn Gly Thr Val Ser Leu Trp Ser Pro Ala Met Lys Glu Pro Leu	
337 342 347 352	
gca aag att ctc tgt cat cgt ggt ggg gtc cgg gct gtg gca gta gat	1224

Ala Lys Ile Leu Cys His Arg Gly Gly Val Arg Ala Val Ala Val Asp	
353 358 363 368	
tct aca ggc acg tac atg gcc acc tct ggc cta gac cac cag ctg aag	1272
Ser Thr Gly Thr Tyr Met Ala Thr Ser Gly Leu Asp His Gln Leu Lys	
369 374 379 384	
atc ttt gac ttg cga ggg acg tac cag cct ctg agc act cgg acc ctg	1320
Ile Phe Asp Leu Arg Gly Thr Tyr Gln Pro Leu Ser Thr Arg Thr Leu	
385 390 395 400	
ccc cat gga gca ggg cac ctg gcc ttc tcc cag agg gga ctg ctg gtg	1368
Pro His Gly Ala Gly His Leu Ala Phe Ser Gln Arg Gly Leu Leu Val	
401 406 411 416	
gcg gga atg ggt gac gtt gtc aac atc tgg gca ggg cag ggc aag gcc	1416
Ala Gly Met Gly Asp Val Val Asn Ile Trp Ala Gly Gln Gly Lys Ala	
417 422 427 432	
agc cca ccc tcc ctt gaa cag ccc tac ctc acc cac cgg ctc tca ggc	1464
Ser Pro Pro Ser Leu Glu Gln Pro Tyr Leu Thr His Arg Leu Ser Gly	
433 438 443 448	
cct gtg cat ggc ctt cag ttc tgc ccc ttt gaa gat gtg ctg ggg gtg	1512
Pro Val His Gly Leu Gln Phe Cys Pro Phe Glu Asp Val Leu Gly Val	
449 454 459 464	
ggg cac act ggg ggc atc acc agc atg ctg gtc cct ggg gcc ggt gag	1560
Gly His Thr Gly Gly Ile Thr Ser Met Leu Val Pro Gly Ala Gly Glu	
465 470 475 480	
ccc aac ttc gat ggc ctg gag agt aat cca tac aga agc cgg aag cag	1608
Pro Asn Phe Asp Gly Leu Glu Ser Asn Pro Tyr Arg Ser Arg Lys Gln	
481 486 491 496	
cgc cag gag tgg gag gtg aag gcc ctg cta gag aag gta cct gca gag	1656
Arg Gln Glu Trp Glu Val Lys Ala Leu Leu Glu Lys Val Pro Ala Glu	
497 502 507 512	
ctt att tgt ctg gac cca cga gcc ctg gcc gag gtg gat gtc atc tcc	1704
Leu Ile Cys Leu Asp Pro Arg Ala Leu Ala Glu Val Asp Val Ile Ser	
513 518 523 528	
ctg gag cag gga aag aag gag cag ata gag agg ctg ggc tat gac ccg	1752
Leu Glu Gln Gly Lys Lys Glu Gln Ile Glu Arg Leu Gly Tyr Asp Pro	
529 534 539 544	
cag gct aag gct ccc ttc cag cca aag cca aag cag aag ggc cgc agc	1800
Gln Ala Lys Ala Pro Phe Gln Pro Lys Pro Lys Gln Lys Gly Arg Ser	
545 550 555 560	
tcc acg gca agc ctg gtg aag agg aag agg aag gtc atg gat gag gaa	1848
Ser Thr Ala Ser Leu Val Lys Arg Lys Arg Lys Val Met Asp Glu Glu	
561 566 571 576	
cac agg gac aag gtc cgg cag agc ctt cag cag cag cat cat aag gag	1896
His Arg Asp Lys Val Arg Gln Ser Leu Gln Gln Gln His His Lys Glu	

577	582	587	592	
gcg aag gcc aag ccc acg ggg gcc cgg cca tct gcc ctg gac aga ttt				1944
Ala Lys Ala Lys Pro Thr Gly Ala Arg Pro Ser Ala Leu Asp Arg Phe				
593	598	603	608	
gtg cgc tga gccagac tccaggggtg cctgggaaca gtctctcccc aagatcacct				2000
Val Arg *				
609				
gtagggaaat gagtgttccc tggaacaagg aggtgggggc agtgtggccc cttccccaac				2060
tgggggtgga cagctgtctc ctgggggtggg ttggtattaa agaggaaagc gatttttttg				2120
aaaaaaaaaa aaaagggggg gccgttttaa aggatccttg ggggggcca agtttaccg				2180
ggcatgcaac gtaatagttc tttccctata gggagccgaa ttat				2224

<210> 580
 <211> 2083
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (121)..(1812)

<220>
 <221> misc_feature
 <222> (1)...(2083)
 <223> n = a,t,c or g

<400> 580	
agggacggna atttgacgcc gtngatcgat cgcggtttcc cgggtcgacc cacgcgtgag	60
gccgactgtg tggcagctga ggaagagttt tgcacgtgga tcgccgttcg ggtgggagag	120
atg gag aca gcc ccc aag ccg ggc aag gat gtc ccg ccc aag aaa gac	168
Met Glu Thr Ala Pro Lys Pro Gly Lys Asp Val Pro Pro Lys Lys Asp	
1 5 10 15	
aaa ctt cag acc aag aga aag aaa ccg cgg cga tac tgg gag gaa gag	216
Lys Leu Gln Thr Lys Arg Lys Lys Pro Arg Arg Tyr Trp Glu Glu Glu	
17 22 27 32	
acc gtt ccg acc aca gcc gga gcc tct cca ggg cct cct cgt aac aag	264
Thr Val Pro Thr Thr Ala Gly Ala Ser Pro Gly Pro Pro Arg Asn Lys	
33 38 43 48	
aag aat cgg gag ctc cgt cct cag aga cca aaa aat gct tac atc tta	312
Lys Asn Arg Glu Leu Arg Pro Gln Arg Pro Lys Asn Ala Tyr Ile Leu	
49 54 59 64	
aag aag tct cgg atc tct aag aag cct cag gtc ccg aag aaa ccc cga	360

Lys	Lys	Ser	Arg	Ile	Ser	Lys	Lys	Pro	Gln	Val	Pro	Lys	Lys	Pro	Arg		
65					70					75					80		
gaa	tgg	aag	aac	ccg	gag	tcc	cag	cgc	ggc	ttg	tcc	ggg	gcc	caa	gat	408	
Glu	Trp	Lys	Asn	Pro	Glu	Ser	Gln	Arg	Gly	Leu	Ser	Gly	Ala	Gln	Asp		
81					86					91					96		
cca	ttc	cca	ggc	ccc	gcc	ccc	gtc	cct	gtg	gaa	gtg	gtc	cag	aag	ttc	456	
Pro	Phe	Pro	Gly	Pro	Ala	Pro	Val	Pro	Val	Glu	Val	Val	Gln	Lys	Phe		
97					102					107					112		
tgt	cgc	att	gac	aaa	tcc	cga	aag	cta	cca	cat	tct	aaa	gcc	aaa	act	504	
Cys	Arg	Ile	Asp	Lys	Ser	Arg	Lys	Leu	Pro	His	Ser	Lys	Ala	Lys	Thr		
113					118					123					128		
cga	agc	cga	ctt	gag	gtg	gct	gaa	gct	gag	gaa	gag	gaa	aca	agt	atc	552	
Arg	Ser	Arg	Leu	Glu	Val	Ala	Glu	Ala	Glu	Glu	Glu	Glu	Thr	Ser	Ile		
129					134					139					144		
aaa	gct	gct	cgt	tct	gag	ctg	ctg	ctt	gct	gaa	gaa	cct	ggg	ttt	ctg	600	
Lys	Ala	Ala	Arg	Ser	Glu	Leu	Leu	Leu	Ala	Glu	Glu	Pro	Gly	Phe	Leu		
145					150					155					160		
gaa	ggg	gag	gat	ggg	gaa	gac	aca	gca	aag	ata	tgc	cag	gct	gac	att	648	
Glu	Gly	Glu	Asp	Gly	Glu	Asp	Thr	Ala	Lys	Ile	Cys	Gln	Ala	Asp	Ile		
161					166					171					176		
gtg	gag	gct	gtg	gac	att	gca	agt	gca	gcc	aag	cac	ttt	gac	ttg	aat	696	
Val	Glu	Ala	Val	Asp	Ile	Ala	Ser	Ala	Ala	Lys	His	Phe	Asp	Leu	Asn		
177					182					187					192		
ctg	cgg	cag	ttt	gga	ccc	tac	aga	cta	aac	tac	tct	cga	act	gga	aga	744	
Leu	Arg	Gln	Phe	Gly	Pro	Tyr	Arg	Leu	Asn	Tyr	Ser	Arg	Thr	Gly	Arg		
193					198					203					208		
cac	ctg	gct	ttt	gga	ggg	cgc	cga	ggt	cat	gtg	gct	gcc	ctt	gat	tgg	792	
His	Leu	Ala	Phe	Gly	Gly	Arg	Arg	Gly	His	Val	Ala	Ala	Leu	Asp	Trp		
209					214					219					224		
gta	aca	aag	aag	ctt	atg	tgc	gag	atc	aac	gtc	atg	gag	gcg	gtg	cgg	840	
Val	Thr	Lys	Lys	Leu	Met	Cys	Glu	Ile	Asn	Val	Met	Glu	Ala	Val	Arg		
225					230					235					240		
gac	atc	cgg	ttt	ctc	cat	tct	gag	gca	ctg	ctt	gct	gtt	gct	cag	aac	888	
Asp	Ile	Arg	Phe	Leu	His	Ser	Glu	Ala	Leu	Leu	Ala	Val	Ala	Gln	Asn		
241					246					251					256		
cgc	tgg	ctc	cac	atc	tat	gac	aat	cag	ggc	att	gag	ctc	cac	tgt	atc	936	
Arg	Trp	Leu	His	Ile	Tyr	Asp	Asn	Gln	Gly	Ile	Glu	Leu	His	Cys	Ile		
257					262					267					272		
cgc	cgc	tgt	gac	cga	gta	aca	cgg	ctt	gag	ttc	ctg	ccc	ttc	cac	ttc	984	
Arg	Arg	Cys	Asp	Arg	Val	Thr	Arg	Leu	Glu	Phe	Leu	Pro	Phe	His	Phe		
273					278					283					288		
ctc	ctg	gct	aca	gct	tca	gaa	aca	ggg	ttt	cta	acc	tac	ctg	gat	gtg	1032	
Leu	Leu	Ala	Thr	Ala	Ser	Glu	Thr	Gly	Phe	Leu	Thr	Tyr	Leu	Asp	Val		

289	294	299	304	
tca gtg ggg aag att	gtg gca gct ctg aat	gct cga gct ggg cgg ctc		1080
Ser Val Gly Lys Ile	Val Ala Ala Leu Asn	Ala Arg Ala Gly Arg Leu		
305	310	315	320	
gat gtt atg agt cag	aac cct tac aat gcc	gtc atc cat ctc gga cac		1128
Asp Val Met Ser Gln	Asn Pro Tyr Asn Ala	Val Ile His Leu Gly His		
321	326	331	336	
agc aat ggt act gtg	tct tta tgg agt cca	gct atg aag gag cca ctg		1176
Ser Asn Gly Thr Val	Ser Leu Trp Ser Pro	Ala Met Lys Glu Pro Leu		
337	342	347	352	
gca aag att ctc tgt	cat cgt ggt ggg gtc	cgg gct gtg gca gta gat		1224
Ala Lys Ile Leu Cys	His Arg Gly Gly Val	Arg Ala Val Ala Val Asp		
353	358	363	368	
tct aca ggc acg tac	atg gcc acc tct ggc	cta gac cac cag ctg aag		1272
Ser Thr Gly Thr Tyr	Met Ala Thr Ser Gly	Leu Asp His Gln Leu Lys		
369	374	379	384	
atc ttt gac ttg cga	ggg acg tac cag cct	ctg agc act cgg acc ctg		1320
Ile Phe Asp Leu Arg	Gly Thr Tyr Gln Pro	Leu Ser Thr Arg Thr Leu		
385	390	395	400	
ccc cat gga gca ggg	cac ctg gcc ttc tcc	cag agg gga ctg ctg gtg		1368
Pro His Gly Ala Gly	His Leu Ala Phe Ser	Gln Arg Gly Leu Leu Val		
401	406	411	416	
gcg gga atg ggt gac	gtt gtc aac atc tgg	gca ggg cag ggc aag gcc		1416
Ala Gly Met Gly Asp	Val Val Asn Ile Trp	Ala Gly Gln Gly Lys Ala		
417	422	427	432	
agc cca ccc tcc ctt	gaa cag ccc tac ctc	acc cac cgg ctc tca ggc		1464
Ser Pro Pro Ser Leu	Glu Gln Pro Tyr Leu	Thr His Arg Leu Ser Gly		
433	438	443	448	
cct gtg cat ggc ctt	cag ttc tgc ccc ttt	gaa gat gtg ctg ggg gtg		1512
Pro Val His Gly Leu	Gln Phe Cys Pro Phe	Glu Asp Val Leu Gly Val		
449	454	459	464	
ggg cac act ggg ggc	atc acc agc atg ctg	gtc cct ggg gcc ggt gag		1560
Gly His Thr Gly Gly	Ile Thr Ser Met Leu	Val Pro Gly Ala Gly Glu		
465	470	475	480	
ccc aac ttc gat ggc	ctg gag agt aat cca	tac aga agc cgg aag cag		1608
Pro Asn Phe Asp Gly	Leu Glu Ser Asn Pro	Tyr Arg Ser Arg Lys Gln		
481	486	491	496	
cgc cag gag tgg gag	gtg aag gcc ctg cta	gag aag gta cct gca gag		1656
Arg Gln Glu Trp Glu	Val Lys Ala Leu Leu	Glu Lys Val Pro Ala Glu		
497	502	507	512	
ctt att tgt ctg gac	cca cga gcc ctg gcc	gag gtg gat gtc atc tcc		1704
Leu Ile Cys Leu Asp	Pro Arg Ala Leu Ala	Glu Val Asp Val Ile Ser		
513	518	523	528	

ctg gag cag gga aag aag gag cag agc ctt cag cag cag cat cat aag 1752
 Leu Glu Gln Gly Lys Lys Glu Gln Ser Leu Gln Gln His His Lys
 529 534 539 544

gag gcg aag gcc aag ccc acg ggg gcc cgg cca tct gcc ctg gac aga 1800
 Glu Ala Lys Ala Lys Pro Thr Gly Ala Arg Pro Ser Ala Leu Asp Arg
 545 550 555 560

ttt gtg cgc tga gcc agactccagg gttgcctggg aacagtctct cccaagatc 1855
 Phe Val Arg *
 561

acctgtaggg aaatgagtgt tccctggaac aaggaggtgg gggcagtgtg gccccttccc 1915

caactggggg tggacagctg tctcctgggg tgggttggtta ttaaagagga aagcgatttt 1975

ttggaaaaaa aaaaaaagg gggggccgtt ttaaaggatc cttggggggg cccaagttta 2035

cccgggcatg caacgtaata gttctttccc tatagggagc cgaattat 2083

<210> 581
 <211> 1654
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (496) .. (1302)

<400> 581

gcacgagggtg acattagcat cgggcagacc cgccggacga aggggtcgcc aggttcccgt 60

ctgctttcgg aggcggatcg agcgggtgac ttttgtgcat tcgttttaaat ttttgaaat 120

ctctcttttt tctccctcg ctgctgcog ggcattgctt gatctggcgg ccgctcctac 180

caccctgggc agccgagcag agtgggtccc agcgggtctc cctccctgcc tccctgactt 240

tgcaacaccg cgttccggga ggaccggcct cggcgaggga ggaggcgggg gagctgcgaa 300

caccagacc caaacctga catgctctgg ggcggagagg aggaagccag gagctgagcg 360

cgccgcgggg gctgcttcgc cctccgctc cgagcgccgg gctccggggc cctgccctg 420

cgctgggca gcagccttgc tgggtcttggg ggcgcccccc gcttcccgcc ccgggggtcc 480

gcggccggca ggacc atg ctg ctg aaa gag tac cgg atc tgc atg ccg ctc 531

Met Leu Leu Lys Glu Tyr Arg Ile Cys Met Pro Leu
 1 5 10

acc gta gac gag tac aaa att gga cag ctg tac atg atc agc aaa cac 579

Thr Val Asp Glu Tyr Lys Ile Gly Gln Leu Tyr Met Ile Ser Lys His
 13 18 23 28

agc cat gaa cag agt gac cgg gga gaa ggg gtg gag gtc gtc cag aat	627
Ser His Glu Gln Ser Asp Arg Gly Glu Gly Val Glu Val Val Gln Asn	
29 34 39 44	
gag ccc ttt gag gac cct cac cat ggc aat ggg cag ttc acc gag aag	675
Glu Pro Phe Glu Asp Pro His His Gly Asn Gly Gln Phe Thr Glu Lys	
45 50 55 60	
cgg gtg tat ctc aac agc aaa ctg cct agt tgg gct aga gct gtt gtc	723
Arg Val Tyr Leu Asn Ser Lys Leu Pro Ser Trp Ala Arg Ala Val Val	
61 66 71 76	
ccc aaa ata ttt tat gtg aca gag aag gct tgg aac tat tat ccc tac	771
Pro Lys Ile Phe Tyr Val Thr Glu Lys Ala Trp Asn Tyr Tyr Pro Tyr	
77 82 87 92	
aca att aca gaa tac aca tgt tcc ttt ctg ccg aaa ttc tcc att cat	819
Thr Ile Thr Glu Tyr Thr Cys Ser Phe Leu Pro Lys Phe Ser Ile His	
93 98 103 108	
ata gaa acc aag tat gag gac aac aaa gga agc aat gac acc att ttc	867
Ile Glu Thr Lys Tyr Glu Asp Asn Lys Gly Ser Asn Asp Thr Ile Phe	
109 114 119 124	
gac aat gaa gcc aaa gac gtg gag aga gaa gtt tgc ttt att gat att	915
Asp Asn Glu Ala Lys Asp Val Glu Arg Glu Val Cys Phe Ile Asp Ile	
125 130 135 140	
gcc tgc gat gaa att cca gag cgc tac tac aaa gaa tct gag gat cct	963
Ala Cys Asp Glu Ile Pro Glu Arg Tyr Tyr Lys Glu Ser Glu Asp Pro	
141 146 151 156	
aag cac ttc aag tca gag aag aca gga cgg gga cag ttg agg gaa ggc	1011
Lys His Phe Lys Ser Glu Lys Thr Gly Arg Gly Gln Leu Arg Glu Gly	
157 162 167 172	
tgg aga gat agt cat cag cct atc atg tgc tcc tac aag ctg gtg act	1059
Trp Arg Asp Ser His Gln Pro Ile Met Cys Ser Tyr Lys Leu Val Thr	
173 178 183 188	
gtg aag ttt gag gtc tgg ggg ctt cag acc aga gtg gaa caa ttt gta	1107
Val Lys Phe Glu Val Trp Gly Leu Gln Thr Arg Val Glu Gln Phe Val	
189 194 199 204	
cac aag gtg gtc cga gac att ctg ctg att gga cat aga cag gct ttt	1155
His Lys Val Val Arg Asp Ile Leu Leu Ile Gly His Arg Gln Ala Phe	
205 210 215 220	
gca tgg gtt gat gag tgg tat gat atg aca atg gat gat gtt cgg gaa	1203
Ala Trp Val Asp Glu Trp Tyr Asp Met Thr Met Asp Asp Val Arg Glu	
221 226 231 236	
tac gag aaa aac atg cat gaa caa acc aac ata aaa gtt tgc aat cag	1251
Tyr Glu Lys Asn Met His Glu Gln Thr Asn Ile Lys Val Cys Asn Gln	
237 242 247 252	

77	82	87	92	
gaa agt aag gca gta att aag cag cag ctt gaa agt gtc tcc aat gga				459
Glu Ser Lys Ala Val Ile Lys Gln Gln Leu Glu Ser Val Ser Asn Gly				
93	98	103	108	
tgg act gta tac cgt att gcc aga cag gct tcc aga atg ggt aat cat				507
Trp Thr Val Tyr Arg Ile Ala Arg Gln Ala Ser Arg Met Gly Asn His				
109	114	119	124	
gac atg gcc aaa gag ctt tat cag agt ttg ctg act cag gtt gcc tca				555
Asp Met Ala Lys Glu Leu Tyr Gln Ser Leu Leu Thr Gln Val Ala Ser				
125	130	135	140	
gaa cat ttc tac ttc tgg cta aat agt ttg aag gag ttt tca cat gca				603
Glu His Phe Tyr Phe Trp Leu Asn Ser Leu Lys Glu Phe Ser His Ala				
141	146	151	156	
gaa cag tgt ctc act ggg ttg caa gag gaa aat tat agt tca gca ctt				651
Glu Gln Cys Leu Thr Gly Leu Gln Glu Glu Asn Tyr Ser Ser Ala Leu				
157	162	167	172	
tct tgc att gct gaa tct tta aaa ttc tat cac aaa ggg att gct tcc				699
Ser Cys Ile Ala Glu Ser Leu Lys Phe Tyr His Lys Gly Ile Ala Ser				
173	178	183	188	
tta aca gca gct agt aca cca ctg aat cct tta agc ttt cag tgt gaa				747
Leu Thr Ala Ala Ser Thr Pro Leu Asn Pro Leu Ser Phe Gln Cys Glu				
189	194	199	204	
ttt gta aaa ctc agg att gac ctt tta caa gcc ttc tct caa ctt atc				795
Phe Val Lys Leu Arg Ile Asp Leu Leu Gln Ala Phe Ser Gln Leu Ile				
205	210	215	220	
tgt act tgt aat agc ctg aag aca agc cca cca cct gca att gcc aca				843
Cys Thr Cys Asn Ser Leu Lys Thr Ser Pro Pro Pro Ala Ile Ala Thr				
221	226	231	236	
aca att gcc atg acc tta gga aat gac ctc cag agg tgt ggt cgc atc				891
Thr Ile Ala Met Thr Leu Gly Asn Asp Leu Gln Arg Cys Gly Arg Ile				
237	242	247	252	
tcc aat cag atg aaa cag tcc atg gaa gaa ttt cga agc ctt gct tct				939
Ser Asn Gln Met Lys Gln Ser Met Glu Glu Phe Arg Ser Leu Ala Ser				
253	258	263	268	
cga tat gga gat ctt tac cag gca tct ttt gat gct gac tca gca act				987
Arg Tyr Gly Asp Leu Tyr Gln Ala Ser Phe Asp Ala Asp Ser Ala Thr				
269	274	279	284	
ttg agg aat gtt gaa cta cag cag cag agc tgt tta ctg ata tct cat				1035
Leu Arg Asn Val Glu Leu Gln Gln Gln Ser Cys Leu Leu Ile Ser His				
285	290	295	300	
gca ata gaa gcc ctg att ttg gat cca gaa tca gca agt ttc cag gaa				1083
Ala Ile Glu Ala Leu Ile Leu Asp Pro Glu Ser Ala Ser Phe Gln Glu				
301	306	311	316	

tat gga tct act gga aca gcc cat gct gat agt gaa tat gaa aga aga	1131
Tyr Gly Ser Thr Gly Thr Ala His Ala Asp Ser Glu Tyr Glu Arg Arg	
317 322 327 332	
atg atg tct gta tat aat cat gtc ttg gag gag gta gaa tca ctc aat	1179
Met Met Ser Val Tyr Asn His Val Leu Glu Glu Val Glu Ser Leu Asn	
333 338 343 348	
cgg aaa tat acc cct gtt tct tat atg cac aca gca tgc ctc tgc aat	1227
Arg Lys Tyr Thr Pro Val Ser Tyr Met His Thr Ala Cys Leu Cys Asn	
349 354 359 364	
gcc atc att gct ttg ctg aaa gtt ccc ctt tct ttc cag aga tat ttt	1275
Ala Ile Ile Ala Leu Leu Lys Val Pro Leu Ser Phe Gln Arg Tyr Phe	
365 370 375 380	
ttc cag aaa cta cag tct acc agc atc aag ctt gct ctg tca cca tgc	1323
Phe Gln Lys Leu Gln Ser Thr Ser Ile Lys Leu Ala Leu Ser Pro Ser	
381 386 391 396	
ccc cgg aat cct gca gag ccc att gct gtc cag aat aac cag cag ctg	1371
Pro Arg Asn Pro Ala Glu Pro Ile Ala Val Gln Asn Asn Gln Gln Leu	
397 402 407 412	
gcg cta aag gta gag gga gtg gtt cag cac gga tct aaa cca gga ctc	1419
Ala Leu Lys Val Glu Gly Val Val Gln His Gly Ser Lys Pro Gly Leu	
413 418 423 428	
ttc cgc aaa att cag tct gtc tgt ctg aat gtt tct tcc aca ctg cag	1467
Phe Arg Lys Ile Gln Ser Val Cys Leu Asn Val Ser Ser Thr Leu Gln	
429 434 439 444	
agt aaa tct gga caa gac tac aag ata ccc att gac aac atg acc aat	1515
Ser Lys Ser Gly Gln Asp Tyr Lys Ile Pro Ile Asp Asn Met Thr Asn	
445 450 455 460	
gag atg gag caa agg gtt gaa cct cat aat gat tac ttc agt act caa	1563
Glu Met Glu Gln Arg Val Glu Pro His Asn Asp Tyr Phe Ser Thr Gln	
461 466 471 476	
ttt ctg ttg aac ttt gct atc ctt gga aca cac aac att aca gtg gaa	1611
Phe Leu Leu Asn Phe Ala Ile Leu Gly Thr His Asn Ile Thr Val Glu	
477 482 487 492	
tct tct gtg aaa gat gcc aat ggt ata gta tgg aag act ggt ccc aga	1659
Ser Ser Val Lys Asp Ala Asn Gly Ile Val Trp Lys Thr Gly Pro Arg	
493 498 503 508	
act acc ata ttt gta aaa tcc ctg gaa gac cct tat tcc cag caa att	1707
Thr Thr Ile Phe Val Lys Ser Leu Glu Asp Pro Tyr Ser Gln Gln Ile	
509 514 519 524	
cgc tta caa cag cag caa gcc cag cag cca tta cag cag cag cag caa	1755
Arg Leu Gln Gln Gln Gln Ala Gln Gln Pro Leu Gln Gln Gln Gln Gln	
525 530 535 540	

cgc aat gcc tac aca cgg ttt taa ccatggaatg aatgcactgc agactctcaa 1809
 Arg Asn Ala Tyr Thr Arg Phe *
 541 546
 gagatcaatc aaattgccag aaacagtttg gtttttcata tggaataagt attaaagtta 1869
 cagtgtagtt catttattca ttgatttttg taatgtaata ttctggaaaa aattttgttt 1929
 tottaaaaaat tttgtctgac agctgggcgt ggttgctcac gcctgtaatc ccagcacttt 1989
 gggaggctga ggtgggcggc tcacgaggag atcaagacca tcctggctaa cacagtgaaa 2049
 ccccgctctcc actaaaaaat acaaaaaaat tagccgagca tgggtggcagg cgctgtagt 2109
 cccagctact tgggaggctg aggcaggaga atggtgtgaa cctgggaggc ggagcttgca 2169
 gtgagccgag actgtgctcc agcctgggcg acagagcgag actccgtctc aaaaaaataa 2229
 ataaatacat tttgtctgaa aaataaaaaa aaaaaa 2265

<210> 583
 <211> 2091
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (167)..(1606)

<400> 583
 tgtcctctct ccattgaaga ttgaacgcct gcggtaccgg tccggaattc ccgggtcgac 60
 ccacgcgtcc gctggagcag agcctgccgc gaacccccgg agcccacgat ccctcgtgcc 120
 atccctcgaa tccaccagca cgagcgtccc acccgcgctt gggacc atg gcc act 175
 Met Ala Thr
 1

gac tca tgg gcc ctg gcg gtg gac gag cag gaa gct gcg gct gag tcg 223
 Asp Ser Trp Ala Leu Ala Val Asp Glu Gln Glu Ala Ala Ala Glu Ser
 4 9 14 19

ttg agc aac ttg cat ctt aag gaa gag aaa atc aaa cca gat acc aat 271
 Leu Ser Asn Leu His Leu Lys Glu Glu Lys Ile Lys Pro Asp Thr Asn
 20 25 30 35

ggt gct gtt gtc aag acc aat gcc aat gca gag aag aca gat gaa gaa 319
 Gly Ala Val Val Lys Thr Asn Ala Asn Ala Glu Lys Thr Asp Glu Glu
 36 41 46 51

gag aaa gag gac aga gct gcc cag tcc tta ctc aac aag ctg atc aga 367
 Glu Lys Glu Asp Arg Ala Ala Gln Ser Leu Leu Asn Lys Leu Ile Arg
 52 57 62 67

agc aac ctt gtt gat aac aca aac caa gtg gaa gtc ctg cag cgg gat	415
Ser Asn Leu Val Asp Asn Thr Asn Gln Val Glu Val Leu Gln Arg Asp	
68 73 78 83	
cca aac tcc cct ctg tac tcg gtg aag tct ttt gaa gag ctt cgg ctg	463
Pro Asn Ser Pro Leu Tyr Ser Val Lys Ser Phe Glu Glu Leu Arg Leu	
84 89 94 99	
aaa cca cag ctt ctc caa gga gtc tat gcc atg ggt ttc aat cgt cca	511
Lys Pro Gln Leu Leu Gln Gly Val Tyr Ala Met Gly Phe Asn Arg Pro	
100 105 110 115	
tcc aag ata caa gag aac gca ttg cca ctg atg ctt gct gag ccc cca	559
Ser Lys Ile Gln Glu Asn Ala Leu Pro Leu Met Leu Ala Glu Pro Pro	
116 121 126 131	
cag aac tta att gcc caa tct cag tct ggt act ggt aaa aca gct gcc	607
Gln Asn Leu Ile Ala Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Ala	
132 137 142 147	
ttc gtg ctg gcc atg ctt agc caa gta gaa cct gca aac aaa tac ccc	655
Phe Val Leu Ala Met Leu Ser Gln Val Glu Pro Ala Asn Lys Tyr Pro	
148 153 158 163	
cag tgt cta tgt ctc tcc cca acg tat gag ctc gcc ctc caa aca gga	703
Gln Cys Leu Cys Leu Ser Pro Thr Tyr Glu Leu Ala Leu Gln Thr Gly	
164 169 174 179	
aaa gtg att gaa caa atg ggc aaa ttt tac cct gaa ctg aag cta gct	751
Lys Val Ile Glu Gln Met Gly Lys Phe Tyr Pro Glu Leu Lys Leu Ala	
180 185 190 195	
tat gct gtt cga ggc aat aaa ttg gaa aga ggc cag aag atc agt gag	799
Tyr Ala Val Arg Gly Asn Lys Leu Glu Arg Gly Gln Lys Ile Ser Glu	
196 201 206 211	
cag att gtc att ggc acc cct ggg act gtg ctg gac tgg tgc tcc aag	847
Gln Ile Val Ile Gly Thr Pro Gly Thr Val Leu Asp Trp Cys Ser Lys	
212 217 222 227	
ctc aag ttc att gat ccc aag aaa atc aag gtg ttt gtt ctg gat gag	895
Leu Lys Phe Ile Asp Pro Lys Lys Ile Lys Val Phe Val Leu Asp Glu	
228 233 238 243	
gct gat gtc atg ata gcc act cag ggc cac caa gat cag agc atc cgc	943
Ala Asp Val Met Ile Ala Thr Gln Gly His Gln Asp Gln Ser Ile Arg	
244 249 254 259	
atc cag agg atg ctg ccc agg aac tgc cag atg ctg ctt ttc tcc gcc	991
Ile Gln Arg Met Leu Pro Arg Asn Cys Gln Met Leu Leu Phe Ser Ala	
260 265 270 275	
acc ttt gaa gac tct gtg tgg aag ttt gcc cag aaa gtg gtc cca gac	1039
Thr Phe Glu Asp Ser Val Trp Lys Phe Ala Gln Lys Val Val Pro Asp	
276 281 286 291	
cca aac gtt atc aaa ctg aag cgt gag gaa gag acc ctg gac acc atc	1087

Pro Asn Val Ile Lys Leu Lys Arg Glu Glu Glu Thr Leu Asp Thr Ile	
292 297 302 307	
aag cag tac tat gtc ctg tgc agc agc aga gac gag aag ttc cag gcc	1135
Lys Gln Tyr Tyr Val Leu Cys Ser Ser Arg Asp Glu Lys Phe Gln Ala	
308 313 318 323	
ttg tgt aac ctc tac ggg gcc atc acc att gct caa gcc atg atc ttc	1183
Leu Cys Asn Leu Tyr Gly Ala Ile Thr Ile Ala Gln Ala Met Ile Phe	
324 329 334 339	
tgc cat act cgc aaa aca gct agt tgg ctg gca gca gag ctc tca aaa	1231
Cys His Thr Arg Lys Thr Ala Ser Trp Leu Ala Ala Glu Leu Ser Lys	
340 345 350 355	
gaa ggc cac cag gtg gct ctg ctg agt ggg gag atg atg gtg gaa cag	1279
Glu Gly His Gln Val Ala Leu Leu Ser Gly Glu Met Met Val Glu Gln	
356 361 366 371	
agg gct gca gtg att gag cgc ttc cga gag ggc aaa gag aag gtt ttg	1327
Arg Ala Ala Val Ile Glu Arg Phe Arg Glu Gly Lys Glu Lys Val Leu	
372 377 382 387	
gtg acc acc aac gtg tgt gcc cgc ggc att gat gtt gaa caa gtg tct	1375
Val Thr Thr Asn Val Cys Ala Arg Gly Ile Asp Val Glu Gln Val Ser	
388 393 398 403	
gtc gtc atc aac ttt gat ctt ccc gtg gac aag gac ggg aat cct gac	1423
Val Val Ile Asn Phe Asp Leu Pro Val Asp Lys Asp Gly Asn Pro Asp	
404 409 414 419	
aat gag acc tac ctg cac cgg atc ggg cgc acg ggc cgc ttt ggc aag	1471
Asn Glu Thr Tyr Leu His Arg Ile Gly Arg Thr Gly Arg Phe Gly Lys	
420 425 430 435	
agg ggc ctg gca gtg aac atg gtg gac agc aag cac agc atg aac atc	1519
Arg Gly Leu Ala Val Asn Met Val Asp Ser Lys His Ser Met Asn Ile	
436 441 446 451	
ctg aac aga atc cag gag cat ttt aat aag aag ata gaa aga ttg gac	1567
Leu Asn Arg Ile Gln Glu His Phe Asn Lys Lys Ile Glu Arg Leu Asp	
452 457 462 467	
aca gat gat ttg gac gag att gag aaa ata gcc aac tga gaagctccac	1616
Thr Asp Asp Leu Asp Glu Ile Glu Lys Ile Ala Asn *	
468 473 478	
cagccactga tgccagccct ggcaactgccc ctgcacagga gacaagtgcg ttcagggcac	1676
aggccccgac atcaccccaa ggacaacggc acaagtagag agaaactacc tacctcactt	1736
caaattatgt ttggacttga caaaaatgta tgcaaatgat gggggatggt agaaaaaaat	1796
tatttacaca accttgaag attagcatg aatacacaga gatttacctt ttggaagttt	1856
catcttttaa tttggccagt gtttccttca tgctaatacta gatgctgtgg ctgattactt	1916

cgg gcc cag gca gca aag gca ggg gct cct ggc aag gcc tga ccccatg 621
 Arg Ala Gln Ala Ala Lys Ala Gly Ala Pro Gly Lys Ala *
 117 122 127

gtgggggggag gggagggggag gggaggggaat gaggcagctc taggatctat actgtagcta 681
 ataaaaatgta aaaacacctg aaaaaaaaaa aagtcgaccg gccgcgaatt tagtagtagt 741
 aggcggccgc tctagaggat ccaagcttac gtacgcgtgc atgcgacgtc atagctcttc 801
 tatagtgtca cctaaattca attca 826

<210> 585
 <211> 907
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (225) .. (695)

<400> 585
 tggaggaacg ggtcgagcca cgcgtccggc gtttcgccca ccattctctg gggacagggg 60
 ggagtccata tccgggacgg gggggaggtg gcggtgcccc tcagggctac ctctcaagag 120
 tgctatcatt tccgcaggcc agatcagaaa agggagctca ggtaccttcc agagagtgag 180
 acccagcgcc ottgtctcgc acccagtagg ctttcatccc cgcc atg gcg gag ctg 236
 Met Ala Glu Leu
 1

atc cag aag aag cta cag gga gaa gtg gag aaa tat caa cag cta cag 284
 Ile Gln Lys Lys Leu Gln Gly Glu Val Glu Lys Tyr Gln Gln Leu Gln
 5 10 15 20

aag gac tta agt aaa tcc atg tcg ggg agg cag aaa ctt gaa gca caa 332
 Lys Asp Leu Ser Lys Ser Met Ser Gly Arg Gln Lys Leu Glu Ala Gln
 21 26 31 36

cta aca gaa aat aat atc gtg aaa gag gtg agg gac tgg gat ttg tgg 380
 Leu Thr Glu Asn Asn Ile Val Lys Glu Val Arg Asp Trp Asp Leu Trp
 37 42 47 52

ggc gag gag gga cct gta cta gcc atg gtt ctg atc aca tat gtc cca 428
 Gly Glu Glu Gly Pro Val Leu Ala Met Val Leu Ile Thr Tyr Val Pro
 53 58 63 68

tcc ctc cat cag gaa ctg gcc ctg ctg gat ggg tcc aac gtg gtc ttt 476
 Ser Leu His Gln Glu Leu Ala Leu Leu Asp Gly Ser Asn Val Val Phe
 69 74 79 84

aaa ctt ctg ggt ccg gtg cta gtc aaa cag gag ctg ggg gag gct cgg 524
 Lys Leu Leu Gly Pro Val Leu Val Lys Gln Glu Leu Gly Glu Ala Arg

85	90	95	100	
gcc aca gta ggg aag agg ctg gac tat atc aca gct gaa att aag cga				572
Ala Thr Val Gly Lys Arg Leu Asp Tyr Ile Thr Ala Glu Ile Lys Arg				
101	106	111	116	
tac gaa tcc cag ctt cgg gat ctt gag cgg cag tca gag caa cag agg				620
Tyr Glu Ser Gln Leu Arg Asp Leu Glu Arg Gln Ser Glu Gln Gln Arg				
117	122	127	132	
gag acc ctt gct cag ctg cag cag gag ttc cag cgg gcc cag gca gca				668
Glu Thr Leu Ala Gln Leu Gln Gln Glu Phe Gln Arg Ala Gln Ala Ala				
133	138	143	148	
aag gca ggg gct cct ggc aag gcc tga cccca tgggtgggggg aggggagggg				720
Lys Ala Gly Ala Pro Gly Lys Ala *				
149	154			
aggggagggga atgaggcagc tctaggatct atactgtagc taataaaatg taaaaacacc				780
tgaaaaaaaaaaa aaagtcgac cggccgcgaa tttagtagta gtaggcggcc gctctagagg				840
atccaagctt acgtacgcgt gcatgcgacg tcatagctct tctatagtgt cacctaaatt				900
caattca				907
<210> 586				
<211> 4272				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> (309)..(1616)				
<400> 586				
acaatcttgt. ctgtagggg tattgcatta ctaaaccaga agtgatcttt aagatcgagc				60
aaggagaaga gccctggata ttagaaaaag gattcccaag ccagtggccac ccagaaagga				120
aatggaaagt tgatgacgtg ttagagagca gccaggaaaa tgaagatgac catttttggg				180
agctttctatt ccacaacaac aaaacagtaa gtgtagaaaa tggagataga ggaagcaaaa				240
ctttcaattt gggcacagac cctgtttctt taagaaatta tccctataaa atatgtgact				300
catgtgaa atg aat ttg aaa aat att tcg ggc tta att att agt aaa aag				350
Met Asn Leu Lys Asn Ile Ser Gly Leu Ile Ile Ser Lys Lys				
1	5	10		
aac tgt tcc aga aag aag cct gat gag ttt aat gta tgt gag aaa ttg				398
Asn Cys Ser Arg Lys Lys Pro Asp Glu Phe Asn Val Cys Glu Lys Leu				
15	20	25	30	

ctc ctt gat att agg cat gag aaa atc cct att gga gag aag tct tat	446
Leu Leu Asp Ile Arg His Glu Lys Ile Pro Ile Gly Glu Lys Ser Tyr	
31 36 41 46	
aaa tat gat caa aaa agg aat gcc att aat tat cac cag gat ctc agt	494
Lys Tyr Asp Gln Lys Arg Asn Ala Ile Asn Tyr His Gln Asp Leu Ser	
47 52 57 62	
cag cca agt ttt ggc caa tct ttt gag tat agt aaa aat gga caa ggc	542
Gln Pro Ser Phe Gly Gln Ser Phe Glu Tyr Ser Lys Asn Gly Gln Gly	
63 68 73 78	
ttc cat gat gag gca gca ttt ttt aca aat aag aga tct cag ata gga	590
Phe His Asp Glu Ala Ala Phe Phe Thr Asn Lys Arg Ser Gln Ile Gly	
79 84 89 94	
gag aca gtc tgt aaa tat aac gaa tgt gga aga acc ttc att gaa agt	638
Glu Thr Val Cys Lys Tyr Asn Glu Cys Gly Arg Thr Phe Ile Glu Ser	
95 100 105 110	
tta aag ctg aat ata tct caa aga cct cat ttg gaa atg gag ccg tat	686
Leu Lys Leu Asn Ile Ser Gln Arg Pro His Leu Glu Met Glu Pro Tyr	
111 116 121 126	
gga tgc agt att tgc ggg aag tcc ttc tgc atg aat tta agg ttt gga	734
Gly Cys Ser Ile Cys Gly Lys Ser Phe Cys Met Asn Leu Arg Phe Gly	
127 132 137 142	
cat cag aga gct ctt aca aag gac aat cct tat gaa tat aat gaa tat	782
His Gln Arg Ala Leu Thr Lys Asp Asn Pro Tyr Glu Tyr Asn Glu Tyr	
143 148 153 158	
ggg gaa atc ttc tgt gac aat tca gct ttc att atc cat cag gga gct	830
Gly Glu Ile Phe Cys Asp Asn Ser Ala Phe Ile Ile His Gln Gly Ala	
159 164 169 174	
tac aca aga aag att ctc cgt gaa tat aaa gtg agt gac aaa acc tgg	878
Tyr Thr Arg Lys Ile Leu Arg Glu Tyr Lys Val Ser Asp Lys Thr Trp	
175 180 185 190	
gaa aag tca gct ctc tta aaa cat caa ata gta cac atg ggg gga aag	926
Glu Lys Ser Ala Leu Leu Lys His Gln Ile Val His Met Gly Gly Lys	
191 196 201 206	
tct tat gat tac aat gaa aat ggg agt aat ttc agc aag aag tca cat	974
Ser Tyr Asp Tyr Asn Glu Asn Gly Ser Asn Phe Ser Lys Lys Ser His	
207 212 217 222	
ctt acc cag ctt cgg aga gct cac aca gga gaa aaa acc ttt gaa tgt	1022
Leu Thr Gln Leu Arg Arg Ala His Thr Gly Glu Lys Thr Phe Glu Cys	
223 228 233 238	
ggg gaa tgt ggg aaa acc ttc tgg gag aag tca aac ctc act caa cat	1070
Gly Glu Cys Gly Lys Thr Phe Trp Glu Lys Ser Asn Leu Thr Gln His	
239 244 249 254	
cag aga aca cac aca gga gag aag ccc tat gaa tgt act gaa tgt ggg	1118

Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Thr Glu Cys Gly	
255 260 265 270	
aaa gcc ttt tgc cag aaa cca cac ctg acc aac cat cag cga aca cat	1166
Lys Ala Phe Cys Gln Lys Pro His Leu Thr Asn His Gln Arg Thr His	
271 276 281 286	
aca gga gaa aaa ccc tat gaa tgt aag caa tgt gga aaa aca ttc tgc	1214
Thr Gly Glu Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Thr Phe Cys	
287 292 297 302	
gtg aag tca aac ctc act gaa cat cag aga aca cac aca ggg gag aag	1262
Val Lys Ser Asn Leu Thr Glu His Gln Arg Thr His Thr Gly Glu Lys	
303 308 313 318	
ccc tat gaa tgt aat gca tgt ggg aaa tcc ttc tgc cac aga tca gcc	1310
Pro Tyr Glu Cys Asn Ala Cys Gly Lys Ser Phe Cys His Arg Ser Ala	
319 324 329 334	
ctc act gtg cat cag aga aca cac aca ggg gag aaa ccg ttt ata tgt	1358
Leu Thr Val His Gln Arg Thr His Thr Gly Glu Lys Pro Phe Ile Cys	
335 340 345 350	
aat gaa tgt gga aaa tcc ttc tgt gtg aag tca aac ctc att gta cat	1406
Asn Glu Cys Gly Lys Ser Phe Cys Val Lys Ser Asn Leu Ile Val His	
351 356 361 366	
caa aga act cac act ggg gag aaa cca tat aag tgt aat gaa tgt ggg	1454
Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Asn Glu Cys Gly	
367 372 377 382	
aaa acc ttc tgt gaa aaa tca gct ctc act aaa cat cag agg act cac	1502
Lys Thr Phe Cys Glu Lys Ser Ala Leu Thr Lys His Gln Arg Thr His	
383 388 393 398	
aca ggg gag aag ccg tat gag tgt aat gca tgt ggg aag acc ttt agt	1550
Thr Gly Glu Lys Pro Tyr Glu Cys Asn Ala Cys Gly Lys Thr Phe Ser	
399 404 409 414	
cag agg tca gtg ctc acc aaa cat cag aga att cac aca agg gtg aaa	1598
Gln Arg Ser Val Leu Thr Lys His Gln Arg Ile His Thr Arg Val Lys	
415 420 425 430	
gct ctt tca aca tcc tga atgtta gaagccttca tacacttggtg aaattgggtta	1652
Ala Leu Ser Thr Ser *	
431 436	
tacagtttca aaaaaggaga tcagagaaaag ccaaagaatg tcagaaattt gtagaaaatg	1712
acttcttggtt tgaatatgta aaagctttca agaaaaatta aaacttttca ttagaaaatt	1772
tgtactgagg ggaattctat tcacttaagt aatatggtga aaatatttat ctggaattta	1832
tggtggttag tggtatatcc cagacgtgat accaaaattt tggtgcaaat ataatggaca	1892
atattttattt ataccatat tcacagtgga atctgaagct tataaaagtt gaatgacagc	1952

agcattaaac	atatatgtga	agagtccccg	atgtttgtag	accttatgtg	agtatgcaaa	2012
tatataaatt	tgagtatgct	tgatttgtat	attggaactc	aacatgatca	taaggagaag	2072
atacgtaccc	ttaattgagt	aactactatg	gtatttgtta	atattttcta	cactaaatac	2132
cattggtgtc	tttatagggt	gacataatta	tatatgtgta	tgtacatatg	tttgtgtgta	2192
tatgtaaata	tatttctaca	cacatactta	aatatagtga	tgtgctagta	taacctcata	2252
ctgacttaaa	agttctgatt	gttaaatttt	aaggaatttt	gtgagccagt	tattaaagc	2312
agtcattatt	taaaatatgt	aaacttacag	ttaaaaacaa	aggtaataaa	tactcagcac	2372
tcatcacttc	ctaattattt	tgctacattt	cactattacc	tttgctgttt	tacttattta	2432
atctgtatga	tgaaaatact	gtataatagt	gtgcactgca	catctgtctc	ttcccagctc	2492
cacattcagt	gctgtcttgg	tagcttgga	ttagtgggag	tgtttacacc	atggaaattg	2552
acaaactata	aatcaggggt	ttaattttct	cagagaacct	gctgtcaa	atttacagca	2612
catcactgtg	tatatatgaa	aacgtatttg	gcaatacaaa	ccacataccc	cttctatttc	2672
ctgacataaa	taaatggcta	tgggcattta	cagctgaacc	acgtcttcaa	gaaagaagcc	2732
aaaaatattt	ccgtgaggtt	tttaactacc	tctgaatctg	tctactcta	aatactaccg	2792
gagtcctctt	gtaggttggc	cagtatatgt	ttttagtga	atattatttc	acaaagaact	2852
atatcacgta	cctttcctct	gactgtttcc	tggcatatat	gcatgaatat	ggccattatt	2912
gaactatcac	ttcagtaaag	aagttaaaca	gtacttttct	gaggtttttc	agctacctct	2972
gggtcattct	gtaatgtaaa	tgttgttaat	aagaatgggt	tttacataaa	ttatgcaaag	3032
gttaacaagc	agtaacactg	cactcctcaa	aaagtggcgg	tatgtaatga	aaggcccttt	3092
tgatatcctt	gatttttcat	tgtgtatctg	tttgggcaag	gtctatgtaa	cactagtctt	3152
gcgtattagt	attttagagt	atctctgcct	cccttgctct	gttgtttctt	ttgccccctt	3212
ggaacacatt	ggtcagcagt	tctaagagac	actgcccaca	tgatggccat	tccctacttc	3272
atccttgctg	agctaaattt	tatatttttg	tgcaccttc	tcccagatga	cttaggtggt	3332
aagtcagat	tagtcaaagc	taatcatgga	agttccattt	taatgattct	gttgggggtga	3392
acttgggagc	aatgagatgt	ttgggaagta	ttgtgtagta	cttctgggaa	agatctcctt	3452
gatacaacat	tgtcatgaca	tgagaagaga	ctctgctggg	ctttttcatg	tctgtaacat	3512
gggtattggt	tatcgttttt	atctctgaag	ggcagtagcc	tgaagataac	agtgacacaag	3572
gtgggaaaag	ccagctcaga	gggtgacgtg	ccgagctact	ctgctctcta	tacctgttct	3632
ctactgggac	tttttataac	cctcaataac	tgttttttat	ttggtcttag	ggctgtctga	3692

tacttagagc tgaaggcatt ccagctgaca cagaggaata tttttctaag tgttaatggt 3752
ctatatggta attaggggga agaattatctt cttttcacaa gttaatatag ggatggctgt 3812
ttgtatcagc catggttctt tctggtggaa aacagaattc tccaactaaa aatattttta 3872
tggcagactg attacagtgg tgtggggccag aaacaaggga cagtgaacaa cccagagact 3932
tgtatcagca ggaagccatt gccattctga gccttgaagg gcaaggaggg aaacagtgtt 3992
accagagccc agtaagaact gctgtcatga aggagggggc accttgtaag agacatcatt 4052
actaccagaa ctgtggtgcc aaattgctgg tgtctctctt tggagaaacc aaccagatac 4112
atctgctgga gagcccaggt gggcacagag aagggtggag agagaatctg ggaagagaaa 4172
tggagaataa gcagcacagt gttattcatt tctgtaaatt cctatgtaga aggctcagtg 4232
ttagaaataa agttattcta ctagttgcaa aaaaaaaaaa 4272

<210> 587
<211> 1631
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (66)..(650)
<220>
<221> misc_feature
<222> (1)...(1631)
<223> n = a,t,c or g

<400> 587
tcggtaccgg ccgagatc cagcgtgcg cccacgcgtc cgcccgcgcc cctggctccc 60
gggcc atg gcg ctg agg gag ctc aaa gtg tgt ctg ctc ggg gat aca 107
Met Ala Leu Arg Glu Leu Lys Val Cys Leu Leu Gly Asp Thr
1 5 10
ggt gta ggt aaa tcg agt att gtg tgg cgg ttt gtg gaa gac agt ttt 155
Gly Val Gly Lys Ser Ser Ile Val Trp Arg Phe Val Glu Asp Ser Phe
15 20 25 30
gat cca aac atc aac cca aca ata ggg gca tct ttt atg acc aag act 203
Asp Pro Asn Ile Asn Pro Thr Ile Gly Ala Ser Phe Met Thr Lys Thr
31 36 41 46
gtc cag tac caa aat gag cta cat aaa ttc cta atc tgg gat aca gct 251
Val Gln Tyr Gln Asn Glu Leu His Lys Phe Leu Ile Trp Asp Thr Ala
47 52 57 62

gga caa gaa cga ttt cgt gcc tta gca cca atg tac tat cga ggg tcg	299
Gly Gln Glu Arg Phe Arg Ala Leu Ala Pro Met Tyr Tyr Arg Gly Ser	
63 68 73 78	
gct gca gct ata atc gtt tat gat atc aca aaa gaa gag aca ttt tca	347
Ala Ala Ala Ile Ile Val Tyr Asp Ile Thr Lys Glu Glu Thr Phe Ser	
79 84 89 94	
aca tta aag aat tgg gtg aaa gag ctt cga cag cat ggc cca cct aat	395
Thr Leu Lys Asn Trp Val Lys Glu Leu Arg Gln His Gly Pro Pro Asn	
95 100 105 110	
att gta gtt gcc att gca gga aat aaa tgt gat ctt atc gat gta aga	443
Ile Val Val Ala Ile Ala Gly Asn Lys Cys Asp Leu Ile Asp Val Arg	
111 116 121 126	
gaa gtc atg gag aga gat gca aag gac tac gcc gac tct att cat gca	491
Glu Val Met Glu Arg Asp Ala Lys Asp Tyr Ala Asp Ser Ile His Ala	
127 132 137 142	
att ttt gta gag acc agc gca aaa aac gcg ata aac ata aat gaa ctc	539
Ile Phe Val Glu Thr Ser Ala Lys Asn Ala Ile Asn Ile Asn Glu Leu	
143 148 153 158	
ttt ata gaa att agt cga aga att cca tcc act gac gcc aac ctg cca	587
Phe Ile Glu Ile Ser Arg Arg Ile Pro Ser Thr Asp Ala Asn Leu Pro	
159 164 169 174	
tct ggc ggt aag ggc ttc aaa ctc cga aga cag cct tca gag cca aag	635
Ser Gly Gly Lys Gly Phe Lys Leu Arg Arg Gln Pro Ser Glu Pro Lys	
175 180 185 190	
cgg agc tgc tgc tga ccgaacctca gcctctcaga cttgatgatg aagtaggtgg	690
Arg Ser Cys Cys *	
191	
tcctgaaagt taacaggagg gctgggggtcc ctgccaccag ttttcaccta gccagtcttg	750
agtcttctcc gtgcaaaaag gattcacaga aatggaccag ttctgttctc caaagactgc	810
agcaatgata tttcagtctg tgaacttcta ttatgtaaag aatctctagt gtacaaaggg	870
actacatcgt tggcttttga ccttgctgaa aaggaacata taattgtatg gatggtagga	930
ttaagttggt gagtagtttt gtaatcaaga ttttatgtaa catttgtaaa gggaaaatta	990
gcacttttgt ggttcttaag ggaaaagaaa cagaccttgt ggagattata atttccttgg	1050
tttctgttac cactgttaga gggagttgta tcatttnaca tatagtagga tagtttaagt	1110
gtagggagga caattattgt ctgaagctaa aatgggttat ttataggact gatggaaatg	1170
atttcacctc tgccatctct aaagcacttt tcattgaaca tgtagccta ggatacgtac	1230
agtaaattaa caatgatagc agcagatgcc tagctcatcc tgggtttgct totgaccttg	1290
tcatgtgtgt gccaccaaac acgttattgg ccccttttta aataagctct catgatcaag	1350

atggtgatgg taaagaagct gcccggaata aactgaattt catatgttct aaaatgccta 1410
gcaatggttt aaaaaggaaa aagagtggaa gtgaaaaagg tggataaat gctgtcaatt 1470
ttttttttaa cccaagtatt ttgggtggga aaagcaagta tctattgctt agcatatgta 1530
aagttgtagt ctatatatat ggggccattg cttaaagatt ataaattatg taaatacatt 1590
aataaatttt aagtttcctt tgcccttcca aaaaaaaaaa a 1631

<210> 588
<211> 1503
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (575)..(1000)

<400> 588
cccccttgaa cgctgtggt accggtccgg aattcccggg tcgacccaag cgtccgggca 60
accgggaccc tggcccggta tggctgaagt cagcatcgac cagtccaagc tgccctggagt 120
caaggaagta tgccgagatt ttgctgtcct ggaggaccac accctggctc acagcctgca 180
ggaacaagag attgagcatc atttggcatc gaacgttcag cggaaccgtt tggctcagca 240
tgatctccag gtggctaagc agctccaaga ggaagatctg aaagcgcagg ccagctcca 300
gaagcgtac aaagaccttg aacaacaaga ctgtgaaatt gctcaggaaa ttcaggagaa 360
gctggctatt gaggcagaga gacgacgcat tcaggagaag aaggatgagg acatagctcg 420
ccttttgcaa gaaaaggagt tacaggaaga gaaaaagaga aagaaacact ttccagagtt 480
ccctgcaacc cgtgcttatg cagatagtta ctattatgaa gatggaggaa tgaagccaag 540
agtgatgaaa gaagctgtat ctactccatc acga atg gcc cac agg gat cag 592
Met Ala His Arg Asp Gln

1

gaa tgg tat gat gct gaa att gcc aga aaa ctg caa gaa gaa gaa ctt 640
Glu Trp Tyr Asp Ala Glu Ile Ala Arg Lys Leu Gln Glu Glu Glu Leu
7 12 17 22
ttg gct acc cag gtg gac atg aga gcc gct caa gta gct caa gat gaa 688
Leu Ala Thr Gln Val Asp Met Arg Ala Ala Gln Val Ala Gln Asp Glu
23 28 33 38
gaa atc gct cga ctt cta atg gct gaa gaa aag aaa gct tac aaa aaa 736
Glu Ile Ala Arg Leu Leu Met Ala Glu Glu Lys Lys Ala Tyr Lys Lys
39 44 49 54

gcc aag gag cgg gag aaa tca tct ttg gac aaa aga aag caa gac ccc	784
Ala Lys Glu Arg Glu Lys Ser Ser Leu Asp Lys Arg Lys Gln Asp Pro	
55 60 65 70	
gag tgg aag cca aaa aca gct aaa gca gca aat tca aag tca aaa gag	832
Glu Trp Lys Pro Lys Thr Ala Lys Ala Ala Asn Ser Lys Ser Lys Glu	
71 76 81 86	
agt gat gaa cct cac cat tct aag aat gaa agg cca gca cgg cca cca	880
Ser Asp Glu Pro His His Ser Lys Asn Glu Arg Pro Ala Arg Pro Pro	
87 92 97 102	
cca cct atc atg aca gat ggt gaa gat gcg gat tac act cat ttt aca	928
Pro Pro Ile Met Thr Asp Gly Glu Asp Ala Asp Tyr Thr His Phe Thr	
103 108 113 118	
aac cag cag agt tcc aca cgg cat ttc tca aaa tca gag tcc tct cat	976
Asn Gln Gln Ser Ser Thr Arg His Phe Ser Lys Ser Glu Ser Ser His	
119 124 129 134	
aaa ggt ttt cat tac aaa cat taa aaacctagga atctgccttg aaaatggact	1030
Lys Gly Phe His Tyr Lys His *	
135 140	
cactatagca aatattactg ggtgatacag aatgaattct acacttactt tttttctcct	1090
gtgtttgcat tcctgggatt tctcctcaag tgcatttctg accataagta attttaattc	1150
atttcaaatg ttttggttat tcatgatcac ttgggcagta taagaaaatg tagcttctga	1210
atattggcca cctctatgct gcatatactt cttgggatat agtatctaag acctttgtaa	1270
actgccattt tgtaggtat ggagtttggg atctaggag taggccttat ttagcaattc	1330
aaattttatg gagatgaatg atcaaagtga aacaatgttt ggatgcaacg cagaataaaa	1390
gaatataaga aatagctttt tgttgcatta atgtatgata ttttgaagga cagagccttt	1450
gctttttgta ttctttaaga aaagcacaac cataaagtat tttaaaaaaa aaa	1503

<210> 589
 <211> 2045
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (102)..(1847)

<400> 589	
accggtccgg aattcccggg tcgaccacg cgtccgggcc tgagtgccac agccagggcc	60
tctgctctgt acacagaccg ggcaaggtcc ccagggccag g atg tca ggc ctg	113

Met Ser Gly Leu

1

gtg	ttg	ggg	cag	cgg	gat	gag	cct	gca	ggc	cac	cgg	ctc	agc	caa	gag	161
Val	Leu	Gly	Gln	Arg	Asp	Glu	Pro	Ala	Gly	His	Arg	Leu	Ser	Gln	Glu	
5					10					15					20	
gag	atc	ctg	ggg	agc	aca	cgg	ctg	gtc	agc	caa	ggg	cta	gag	gcc	cta	209
Glu	Ile	Leu	Gly	Ser	Thr	Arg	Leu	Val	Ser	Gln	Gly	Leu	Glu	Ala	Leu	
21					26					31					36	
cgc	agt	gaa	cac	cag	gcc	gtg	ctg	caa	agc	ctg	tcc	cag	acc	att	gag	257
Arg	Ser	Glu	His	Gln	Ala	Val	Leu	Gln	Ser	Leu	Ser	Gln	Thr	Ile	Glu	
37					42					47					52	
tgt	ctg	cag	cag	gga	ggc	cat	gag	gaa	ggg	ctg	gtg	cat	gag	aag	gcc	305
Cys	Leu	Gln	Gln	Gly	Gly	His	Glu	Glu	Gly	Leu	Val	His	Glu	Lys	Ala	
53					58					63					68	
cgg	cag	ctt	cgc	cgt	tct	atg	gaa	aac	att	gag	ctc	ggg	ctg	agt	gag	353
Arg	Gln	Leu	Arg	Arg	Ser	Met	Glu	Asn	Ile	Glu	Leu	Gly	Leu	Ser	Glu	
69					74					79					84	
gcc	cag	gtg	atg	ctg	gct	cta	gcc	agc	cac	ctg	agc	aca	gtg	gag	tcg	401
Ala	Gln	Val	Met	Leu	Ala	Leu	Ala	Ser	His	Leu	Ser	Thr	Val	Glu	Ser	
85					90					95					100	
gag	aaa	cag	aag	ctg	cgg	gct	cag	gtg	cgg	cgg	cta	tgc	cag	gag	aac	449
Glu	Lys	Gln	Lys	Leu	Arg	Ala	Gln	Val	Arg	Arg	Leu	Cys	Gln	Glu	Asn	
101					106					111					116	
cag	tgg	ctg	cgg	gat	gag	ctg	gct	ggc	acc	cag	cag	cgg	cta	cag	cgc	497
Gln	Trp	Leu	Arg	Asp	Glu	Leu	Ala	Gly	Thr	Gln	Gln	Arg	Leu	Gln	Arg	
117					122					127					132	
agt	gaa	cag	gct	gtg	gct	cag	ctg	gag	gag	gaa	aag	aag	cac	ctg	gag	545
Ser	Glu	Gln	Ala	Val	Ala	Gln	Leu	Glu	Glu	Glu	Lys	Lys	His	Leu	Glu	
133					138					143					148	
ttc	ctg	ggg	cag	ctg	cgg	cag	tat	gat	gag	gat	gga	cat	acc	tcg	gag	593
Phe	Leu	Gly	Gln	Leu	Arg	Gln	Tyr	Asp	Glu	Asp	Gly	His	Thr	Ser	Glu	
149					154					159					164	
gag	aaa	gaa	ggc	gat	gcc	acc	aag	gat	tcc	ctg	gat	gac	ctc	ttt	cct	641
Glu	Lys	Glu	Gly	Asp	Ala	Thr	Lys	Asp	Ser	Leu	Asp	Asp	Leu	Phe	Pro	
165					170					175					180	
aat	gag	gag	gaa	gag	gac	ccc	agc	aat	ggc	ttg	tcc	cgt	ggt	caa	ggt	689
Asn	Glu	Glu	Glu	Glu	Asp	Pro	Ser	Asn	Gly	Leu	Ser	Arg	Gly	Gln	Gly	
181					186					191					196	
gct	aca	gca	gct	cag	cag	ggt	gga	tat	gag	atc	cca	gca	agg	ttg	cgg	737
Ala	Thr	Ala	Ala	Gln	Gln	Gly	Gly	Tyr	Glu	Ile	Pro	Ala	Arg	Leu	Arg	
197					202					207					212	
acg	ttg	cac	aac	ctg	gtg	atc	cag	tac	gca	gcc	caa	ggt	cgc	tat	gag	785
Thr	Leu	His	Asn	Leu	Val	Ile	Gln	Tyr	Ala	Ala	Gln	Gly	Arg	Tyr	Glu	

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

213	218	223	228	
gtg gcc gtg cca ctc tgt aag cag gca cta gag gac ctg gag cgc aca				833
Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp Leu Glu Arg Thr				
229	234	239	244	
tca ggc cgt ggc cac cct gat gtc gcc acc atg ctc aac atc ctt gct				881
Ser Gly Arg Gly His Pro Asp Val Ala Thr Met Leu Asn Ile Leu Ala				
245	250	255	260	
ttg gtg tat cgt gac cag aat aag tat aag gaa gct gcc cac ctg ctg				929
Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Glu Ala Ala His Leu Leu				
261	266	271	276	
aat gat gcc ctt agc atc cgg gag agc acc ttg gga cct gac cat cct				977
Asn Asp Ala Leu Ser Ile Arg Glu Ser Thr Leu Gly Pro Asp His Pro				
277	282	287	292	
gct gtg gct gcc aca ctc aac aat ttg gct gtg ctc tat ggc aaa agg				1025
Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu Tyr Gly Lys Arg				
293	298	303	308	
ggc aag tac aag gag gca gag cct ctg tgc cag cgg gca ctg gag att				1073
Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Gln Arg Ala Leu Glu Ile				
309	314	319	324	
cga gaa aag gtc ctg ggc acg aat cat cca gat gtg gca aaa cag ctg				1121
Arg Glu Lys Val Leu Gly Thr Asn His Pro Asp Val Ala Lys Gln Leu				
325	330	335	340	
aac aac ctg gcc ctc ttg tgc caa aac cag ggc aag tat gag gcc gtg				1169
Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys Tyr Glu Ala Val				
341	346	351	356	
gaa cgc tac tac cag cga gca ctg gcc atc tac gag ggg cag ctg ggg				1217
Glu Arg Tyr Tyr Gln Arg Ala Leu Ala Ile Tyr Glu Gly Gln Leu Gly				
357	362	367	372	
ccg gac aac cct aat gta gcc cgg acc aag aac aac ctg gct tcc tgt				1265
Pro Asp Asn Pro Asn Val Ala Arg Thr Lys Asn Asn Leu Ala Ser Cys				
373	378	383	388	
tac ctg aaa cag ggc aaa tat gct gag gct gag aca cta tac aaa gag				1313
Tyr Leu Lys Gln Gly Lys Tyr Ala Glu Ala Glu Thr Leu Tyr Lys Glu				
389	394	399	404	
atc ctg acc cgt gcc cat gta cag gag ttt ggg tct gtg gat gat gac				1361
Ile Leu Thr Arg Ala His Val Gln Glu Phe Gly Ser Val Asp Asp Asp				
405	410	415	420	
cac aag ccc atc tgg atg cat gca gag gag cgg gag gaa atg agc aaa				1409
His Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu Glu Met Ser Lys				
421	426	431	436	
agc cgg cac cat gag ggt ggg aca ccc tat gct gag tat gga ggc tgg				1457
Ser Arg His His Glu Gly Gly Thr Pro Tyr Ala Glu Tyr Gly Gly Trp				
437	442	447	452	

tac aag gcc tgc aaa gtg agc agc ccc aca gtg aac act act ctg aga	1505
Tyr Lys Ala Cys Lys Val Ser Ser Pro Thr Val Asn Thr Thr Leu Arg	
453 458 463 468	
aac ctg gga gct ctg tat agg cgc cag gga aag ctg gag gct gct gag	1553
Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Leu Glu Ala Ala Glu	
469 474 479 484	
acc ctg gag gaa tgt gcc ctg cgg tcc cgg aga cag ggc act gac cct	1601
Thr Leu Glu Glu Cys Ala Leu Arg Ser Arg Arg Gln Gly Thr Asp Pro	
485 490 495 500	
atc agc cag acg aaa gca gct gac att caa ccc ggc ccc cag gtc tgc	1649
Ile Ser Gln Thr Lys Ala Ala Asp Ile Gln Pro Gly Pro Gln Val Cys	
501 506 511 516	
tgg tcc ccc gtc ccc cac agc cct cac agc att ccc cat tgc tcc tgg	1697
Trp Ser Pro Val Pro His Ser Pro His Ser Ile Pro His Cys Ser Trp	
517 522 527 532	
ctc ttc ctc tcc cct agg tgg gac agt gaa ggg gag cag ttt aac cag	1745
Leu Phe Leu Ser Pro Arg Trp Asp Ser Glu Gly Glu Gln Phe Asn Gln	
533 538 543 548	
aag att gct gct gcc ctt agg gtc tca gct ccc tcc tct gga atc cct	1793
Lys Ile Ala Ala Ala Leu Arg Val Ser Ala Pro Ser Ser Gly Ile Pro	
549 554 559 564	
ctt agg aag gac cct cag gac acc ctc tct gca ccc tgt ggt cct cta	1841
Leu Arg Lys Asp Pro Gln Asp Thr Leu Ser Ala Pro Cys Gly Pro Leu	
565 570 575 580	
gag tag ctactctga ggccccaagg tgggtacaaa gcaggatatgg ccctcagaga	1897
Glu *	
581	
tgccagcctgc tgctggcttt tcagtcagag gggtgggggc tggccagcca agctgccttg	1957
ccctggccgc tcttactccc tccctctgct gtctcacttc aggtccatgt atttcacttt	2017
tcttaaataa aagaatcagg taacctta	2045

<210> 590
 <211> 5053
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (154) .. (2409)

<400> 590
 aggggaattgg acagcctggc tgacttgccg gagcggatta aaccaccata tgcaaacgga 60

ctttcaacat cccatcttag gtcattcttct gtagaagatg ttaaactaat tataagcgag	120
gggagaccta ccatagaagt tcgaagatgt agc atg cct tct gtc att tgt gaa	174
Met Pro Ser Val Ile Cys Glu	
1 5	
cat acc aaa caa ttc caa aca ata tca gaa gag agc aat caa ggt agc	222
His Thr Lys Gln Phe Gln Thr Ile Ser Glu Glu Ser Asn Gln Gly Ser	
8 13 18 23	
tta tta act gtg cca gga gat act agt cct tct ccc aaa cct gag gta	270
Leu Leu Thr Val Pro Gly Asp Thr Ser Pro Ser Pro Lys Pro Glu Val	
24 29 34 39	
ttc tca aat gtg cct gaa aga gac ctt tca aat gta tct aac ata cat	318
Phe Ser Asn Val Pro Glu Arg Asp Leu Ser Asn Val Ser Asn Ile His	
40 45 50 55	
tcc agt ttt gca act tct cca act gga gct tca aac agc aag tat gtt	366
Ser Ser Phe Ala Thr Ser Pro Thr Gly Ala Ser Asn Ser Lys Tyr Val	
56 61 66 71	
tca gct gat aga aat ctc atc aag aat act gcc cca gtg aac act gta	414
Ser Ala Asp Arg Asn Leu Ile Lys Asn Thr Ala Pro Val Asn Thr Val	
72 77 82 87	
atg gac agt cca gtg cat tta gag cca tct agt cag gtt ggt gtg atc	462
Met Asp Ser Pro Val His Leu Glu Pro Ser Ser Gln Val Gly Val Ile	
88 93 98 103	
cag aat aaa tca tgg gag atg cct gtt gat aga cta gag aca tta agc	510
Gln Asn Lys Ser Trp Glu Met Pro Val Asp Arg Leu Glu Thr Leu Ser	
104 109 114 119	
acc aga gac ttt atc tgc cca aat tct aac ata cct gat caa gaa tcc	558
Thr Arg Asp Phe Ile Cys Pro Asn Ser Asn Ile Pro Asp Gln Glu Ser	
120 125 130 135	
tct ctt cag agt ttt tgt aat tct gaa aat aag gta ttg aaa gaa aat	606
Ser Leu Gln Ser Phe Cys Asn Ser Glu Asn Lys Val Leu Lys Glu Asn	
136 141 146 151	
gct gat ttt tta tcc ctg cgc cag act gaa ctg cca gga aac tct tgt	654
Ala Asp Phe Leu Ser Leu Arg Gln Thr Glu Leu Pro Gly Asn Ser Cys	
152 157 162 167	
gct cag gat ccg gca tcc ttt atg cct cca cag cag cct tgc tct ttc	702
Ala Gln Asp Pro Ala Ser Phe Met Pro Pro Gln Gln Pro Cys Ser Phe	
168 173 178 183	
ccc agc caa tca ctt tca gat gct gaa tcg att tct aaa cat atg tct	750
Pro Ser Gln Ser Leu Ser Asp Ala Glu Ser Ile Ser Lys His Met Ser	
184 189 194 199	
ttg tca tat gtt gct aat caa gag cca ggt att tta caa caa aaa aat	798
Leu Ser Tyr Val Ala Asn Gln Glu Pro Gly Ile Leu Gln Gln Lys Asn	

200	205	210	215	
gca gtt cag att att agt tct gct tta gat act gat aat gaa tct aca				846
Ala Val Gln Ile Ile Ser Ser Ala Leu Asp Thr Asp Asn Glu Ser Thr				
216	221	226	231	
aaa gat aca gaa aat act ttt gtc cta gga gat gtt caa aaa aca gat				894
Lys Asp Thr Glu Asn Thr Phe Val Leu Gly Asp Val Gln Lys Thr Asp				
232	237	242	247	
gcc ttt gtc cca gtg tac tct gac agc act att caa gaa gca tca cca				942
Ala Phe Val Pro Val Tyr Ser Asp Ser Thr Ile Gln Glu Ala Ser Pro				
248	253	258	263	
aac ttt gag aaa gct tat act tta cct gtg tta cca tca gaa aag gac				990
Asn Phe Glu Lys Ala Tyr Thr Leu Pro Val Leu Pro Ser Glu Lys Asp				
264	269	274	279	
ttt aat gga agt gat gcc tct acc cag cta aat aca cat tat gca ttt				1038
Phe Asn Gly Ser Asp Ala Ser Thr Gln Leu Asn Thr His Tyr Ala Phe				
280	285	290	295	
agc aaa cta act tac aag tct tcc agt ggc cat gaa gtt gag aat agc				1086
Ser Lys Leu Thr Tyr Lys Ser Ser Ser Gly His Glu Val Glu Asn Ser				
296	301	306	311	
aca act gat act cag gtc att tca cat gaa aaa gaa aac aaa ctg gag				1134
Thr Thr Asp Thr Gln Val Ile Ser His Glu Lys Glu Asn Lys Leu Glu				
312	317	322	327	
agt ttg gtt tta act cat ttg agt agg tgt gat tct gat tta tgt gaa				1182
Ser Leu Val Leu Thr His Leu Ser Arg Cys Asp Ser Asp Leu Cys Glu				
328	333	338	343	
atg aat gca ggg atg cca aaa gga aac cta aat gaa caa gat cca aaa				1230
Met Asn Ala Gly Met Pro Lys Gly Asn Leu Asn Glu Gln Asp Pro Lys				
344	349	354	359	
cat tgt cct gaa agt gaa aag tgt ttg ctt tcc ata gaa gat gag gaa				1278
His Cys Pro Glu Ser Glu Lys Cys Leu Leu Ser Ile Glu Asp Glu Glu				
360	365	370	375	
tct caa caa agc att tta tca agt ctg gaa aac cat tca cag cag tca				1326
Ser Gln Gln Ser Ile Leu Ser Ser Leu Glu Asn His Ser Gln Gln Ser				
376	381	386	391	
act caa cca gaa atg cat aaa tat ggt cag tta gtt aaa gta gaa tta				1374
Thr Gln Pro Glu Met His Lys Tyr Gly Gln Leu Val Lys Val Glu Leu				
392	397	402	407	
gaa gaa aat gcc gaa gat gat aaa act gaa aac caa atc cct caa aga				1422
Glu Glu Asn Ala Glu Asp Asp Lys Thr Glu Asn Gln Ile Pro Gln Arg				
408	413	418	423	
atg act aga aac aaa gca aat aca atg gca aat caa agc aaa cag att				1470
Met Thr Arg Asn Lys Ala Asn Thr Met Ala Asn Gln Ser Lys Gln Ile				
424	429	434	439	

1945
 1946
 1947
 1948
 1949
 1950
 1951
 1952
 1953
 1954
 1955
 1956
 1957
 1958
 1959
 1960
 1961
 1962
 1963
 1964
 1965
 1966
 1967
 1968
 1969
 1970
 1971
 1972
 1973
 1974
 1975
 1976
 1977
 1978
 1979
 1980
 1981
 1982
 1983
 1984
 1985
 1986
 1987
 1988
 1989
 1990
 1991
 1992
 1993
 1994
 1995
 1996
 1997
 1998
 1999
 2000

ctt gct agc tgt aca cta tta tca gaa aaa gac agt gaa tcc tca tct	1518
Leu Ala Ser Cys Thr Leu Leu Ser Glu Lys Asp Ser Glu Ser Ser Ser	
440 445 450 455	
cct aga gga aga ata aga tta act gaa gat gac gat cct caa att cac	1566
Pro Arg Gly Arg Ile Arg Leu Thr Glu Asp Asp Asp Pro Gln Ile His	
456 461 466 471	
cat cca cgg aaa agg aaa gtg tca cgt gta cct cag cct gtg caa gtg	1614
His Pro Arg Lys Arg Lys Val Ser Arg Val Pro Gln Pro Val Gln Val	
472 477 482 487	
agt ccc tct tta cta caa gca aaa gag aaa act cag caa tct ctg gca	1662
Ser Pro Ser Leu Leu Gln Ala Lys Glu Lys Thr Gln Gln Ser Leu Ala	
488 493 498 503	
gcc att gta gat tct cta aaa cta gat gag att cag cca tac agt tca	1710
Ala Ile Val Asp Ser Leu Lys Leu Asp Glu Ile Gln Pro Tyr Ser Ser	
504 509 514 519	
gag aga gca aat cca tat ttt gaa tac ttg cac ata agg aaa aaa ata	1758
Glu Arg Ala Asn Pro Tyr Phe Glu Tyr Leu His Ile Arg Lys Lys Ile	
520 525 530 535	
gaa gaa aaa cgc aaa tta ctg tgt agt gtg att cct caa gca cct cag	1806
Glu Glu Lys Arg Lys Leu Leu Cys Ser Val Ile Pro Gln Ala Pro Gln	
536 541 546 551	
tac tat gac gaa tat gta aca ttt aac gga tca tat ctc ctg gat gga	1854
Tyr Tyr Asp Glu Tyr Val Thr Phe Asn Gly Ser Tyr Leu Leu Asp Gly	
552 557 562 567	
aac ccc tta agc aag att tgt att ccc aca att aca cca cca cct tca	1902
Asn Pro Leu Ser Lys Ile Cys Ile Pro Thr Ile Thr Pro Pro Pro Ser	
568 573 578 583	
ctg tca gat cca ctt aaa gag ctt ttt cga caa cag gaa gtt gta agg	1950
Leu Ser Asp Pro Leu Lys Glu Leu Phe Arg Gln Gln Glu Val Val Arg	
584 589 594 599	
atg aaa cta cgt ttg caa cac agt att gaa agg gaa aaa ctc att gta	1998
Met Lys Leu Arg Leu Gln His Ser Ile Glu Arg Glu Lys Leu Ile Val	
600 605 610 615	
tcc aac gaa caa gaa gtt ttg cga gtt cat tac aga gct gca aga aca	2046
Ser Asn Glu Gln Glu Val Leu Arg Val His Tyr Arg Ala Ala Arg Thr	
616 621 626 631	
ttg gca aat caa aca ctg cca ttt agt gct tgt act gtt ttg ctg gat	2094
Leu Ala Asn Gln Thr Leu Pro Phe Ser Ala Cys Thr Val Leu Leu Asp	
632 637 642 647	
gcc gaa gta tac aat gta cca ttg gac tct cag tct gat gac agt aaa	2142
Ala Glu Val Tyr Asn Val Pro Leu Asp Ser Gln Ser Asp Asp Ser Lys	
648 653 658 663	

act tct gtg agg gat cgc ttt aat gca aga caa ttc atg tct tgg tta	2190
Thr Ser Val Arg Asp Arg Phe Asn Ala Arg Gln Phe Met Ser Trp Leu	
664 669 674 679	
caa gat gtg gat gat aaa ttt gac aaa tta aag acc tgt ctt tta atg	2238
Gln Asp Val Asp Asp Lys Phe Asp Lys Leu Lys Thr Cys Leu Leu Met	
680 685 690 695	
agg caa caa cat gaa gct gcg gct tta aat gct gtc cag agg tta gaa	2286
Arg Gln Gln His Glu Ala Ala Ala Leu Asn Ala Val Gln Arg Leu Glu	
696 701 706 711	
tgg cag ctc aaa ctc cag gaa ctt gat cct gcc acc tat aaa tct atc	2334
Trp Gln Leu Lys Leu Gln Glu Leu Asp Pro Ala Thr Tyr Lys Ser Ile	
712 717 722 727	
agc att tac gaa atc cag gag ttt tat gtt ccc ctt gtt gat gtt aac	2382
Ser Ile Tyr Glu Ile Gln Glu Phe Tyr Val Pro Leu Val Asp Val Asn	
728 733 738 743	
gac gac ttt gaa ttg act cct ata tag cagtc agtacttcct gatggtattg	2434
Asp Asp Phe Glu Leu Thr Pro Ile *	
744 749	
toctaaactg gtgatgctca agcattatac tgtggaatcac tgccttttga caaaaatact	2494
catgccttta caattgttag taaagtccga ttatagttgg ttatgtagta aacactgtca	2554
ttttataaaa aatgagaatt attttggatc ttagatccaa acacagtttc taatagaaaa	2614
ctattattta tattgggaaa ggtaactatt gcattagagc atgttggcag actggttaggt	2674
atttaaaaag ttgagaatct gctaacagcg ctggaagttg ttagcgctct aagtaataag	2734
ataaccacta gtattcaaat ctctttcagg ttttattaaa aaatatatat caataaacta	2794
aaagggttcaa ttctaccaa atagttttcta atgtggggaga aaaacttggc acaaaatctc	2854
ttcagtttat tatctgtaaa ttgtacagtt ttctttttga aagttttaat attgtcttcc	2914
tttttaataa cttattttat acatattgtg cagatgtaaa tcttgtaatt aatggtcaaa	2974
ctgtataaag ggattggtag tcaaaacatg tacaaagaaa tacctgtaaa actgttttgt	3034
ctcatgtttt attggaccaa agttgtggtt tgtatggagt gtagtagtag tgtgtacagg	3094
tagaaaactt ttaaatacag catgcagggtg tttcagttag cttgttttca tcaccataac	3154
tgcaaagatg tggcttagtt gtattgcatg cttoctataa tttaactctc cataattgat	3214
gcctgcagta gtgtaaggca tttcatacta gtctcctcta gtagacctgt gacttactgt	3274
gttggaacata ttatttagac ttagtcatac aaagaaactt agctcttttt tcatctcaca	3334
gtaaagccta tttcccaggg aaaaaataa atgcctttga atgaaaattc tgaaattgta	3394
aatgtctatt ttaatatcca cctatgaaag aatctgtgaa tatatgtaaa tacgtttaat	3454

aaatTTtatt ggtcatgtta aatcattgta aaactTTTTT acattgctta atgtTTtaag	3514
cttaatagcc tttgcacttt taaaataaaa accaagtatg caaatcaaag atatttggtta	3574
gtcaaaaataa gtaaaagaaa tataggaata tTccagtcaa tctctgaaat gtttatgaaa	3634
aacaggTTaa tatgttTtat ttttttccTt gtatcaagat gcaaaacata atttgcaaaa	3694
ttttataatt gaaataaaaac ttggTatgct gttttataat aaattagcaa tatactTTaa	3754
aaaaaatcca gtttctccta taacatgatg taaattaaat attcaggaat atttcaggTc	3814
tgaaatctgc Tgctgaactt gTtagacatt tttgaaagga aaattaggTt agcgtacaat	3874
Ttatcataaa tatatgaggT aaaatttgca aaactttcca cagtactttc ttgaattata	3934
atactgaatg ttttctgttc cgatagagaa aagtgaagca aatatgtgag gaatgaagtg	3994
atctagtTca agttggTaat tccagctaTt gggagagaat gtaaatgtgc aaaggTacat	4054
attaagctta gggatttttg aattttttacg tcagtTTata ttttaattct tactgtactt	4114
ggcatgcgca ataaagcagc acatgtaaaa aaaaaaatac acagtTcaag gactttatta	4174
taaaggTtgg atgtagtTTt ccttagaaat ttaggtgaga gattttggcc ttttttattg	4234
gataaattgg gccagaaagg cagggtagat tTcgaagcac Tggttctgtt gaagttaagt	4294
ttattaagcc Tgggaacatt aaaagctaTt ttataaaagc aatactTTTT aatatgaaaa	4354
cttactgcaa agtttgtTTa tactttttgcc taaaaaggaa attggatggg atactgtggc	4414
aaatcataaa aaaccagata attgaacttt gaagtTatag aaaatcagag aggggtaagt	4474
Ttatagggca ttttgttctg atggTtcaac cagaggTctg ggaaatagca ctgttggccc	4534
aaacagaaca ggctTTtaga agataaaaagc gacaagaagg aatctggTga attttagtca	4594
Tcccagcttt ttagTctTaa ccacagTtct cactctctta aatggTacct caaaaagctg	4654
gagcctctct gccatgatta Tgcttctaca aatttctttt ataaagagac tcaaagctaa	4714
Tgatagctta aaagaaaagt taatgccttc Tcattggaaa Tgtataatca aataagtagt	4774
Taagggtttt Tggtattaaa gatattctga agctctgaaa Tgctagaaaa aaatttgga	4834
Tggagtatat gcctgaaaag gttttggatt cagaaagaaa aaggatggTt agTTtaatca	4894
gtgattcttt tTaaactctt caaatatcat gaacaagata cTaaattgta cctaaggatt	4954
Tgtatttctt tacaattTgt tctaaatata TgtTTaatga ctagtTgata tttgtgcatg	5014
Ttattttaata aagagTtata tttttataaa aaaaaaaaa	5053

<210> 591
 <211> 2430
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (230) .. (2008)

<400> 591

taccctgcgg taccgggtccg gaattcccgg gtcgacccac gcgtccgaag ccattacaaa	60
ggttgcttaa cttctaatta tttgatcact gaggaaaatc cagaaagcta cacaacactg	120
aaggggtgaa ataaaagtcc agcgatccag cgaaagaaaa gagaagtgac agaaacaact	180
ttacctggac tgaagataaa agcacagaca agagaacaat gccctggac	235
	atg gct Met Ala 1
cca gag atc cac atg aca ggc cca atg tgc ctc att gag aac act aat	283
Pro Glu Ile His Met Thr Gly Pro Met Cys Leu Ile Glu Asn Thr Asn	
3 8 13 18	
ggg gaa ctg gtg gcg aat cca gaa gct ctg aaa atc ctg tct gcc att	331
Gly Glu Leu Val Ala Asn Pro Glu Ala Leu Lys Ile Leu Ser Ala Ile	
19 24 29 34	
aca cag cct gtg gtg gtg gtg gca att gtg ggc ctc tac cgc aca gga	379
Thr Gln Pro Val Val Val Val Ala Ile Val Gly Leu Tyr Arg Thr Gly	
35 40 45 50	
aaa tcc tac ctg atg aac aag cta gct ggg aag aaa aag ggc ttc tct	427
Lys Ser Tyr Leu Met Asn Lys Leu Ala Gly Lys Lys Lys Gly Phe Ser	
51 56 61 66	
ctg ggc tcc acg gtg cag tct cac act aaa gga atc tgg atg tgg tgt	475
Leu Gly Ser Thr Val Gln Ser His Thr Lys Gly Ile Trp Met Trp Cys	
67 72 77 82	
gtg ccc cac ccc aag aag cca ggc cac atc cta gtt ctg ctg gac acc	523
Val Pro His Pro Lys Lys Pro Gly His Ile Leu Val Leu Leu Asp Thr	
83 88 93 98	
gag ggt ctg gga gat gta gag aag ggt gac aac cag aat gac tcc tgg	571
Glu Gly Leu Gly Asp Val Glu Lys Gly Asp Asn Gln Asn Asp Ser Trp	
99 104 109 114	
atc ttc gcc ctg gcc gtc ctc ctg agc agc acc ttc gtg tac aat agc	619
Ile Phe Ala Leu Ala Val Leu Leu Ser Ser Thr Phe Val Tyr Asn Ser	
115 120 125 130	
ata gga acc atc aac cag cag gct atg gac caa ctg tac tat gtg aca	667
Ile Gly Thr Ile Asn Gln Gln Ala Met Asp Gln Leu Tyr Tyr Val Thr	
131 136 141 146	

gag ctg aca cat aga atc cga tca aaa tcc tca cct gat gag aat gag	715
Glu Leu Thr His Arg Ile Arg Ser Lys Ser Ser Pro Asp Glu Asn Glu	
147 152 157 162	
aat gag gtt gag gat tca gct gac ttt gtg agc ttc ttc cca gac ttt	763
Asn Glu Val Glu Asp Ser Ala Asp Phe Val Ser Phe Phe Pro Asp Phe	
163 168 173 178	
gtg tgg aca ctg aga gat ttc tcc ctg gac ttg gaa gca gat gga caa	811
Val Trp Thr Leu Arg Asp Phe Ser Leu Asp Leu Glu Ala Asp Gly Gln	
179 184 189 194	
ccc ctc aca cca gat gag tac ctg aca tac tcc ctg aag ctg aag aaa	859
Pro Leu Thr Pro Asp Glu Tyr Leu Thr Tyr Ser Leu Lys Leu Lys Lys	
195 200 205 210	
ggg acc agt caa aaa gat gaa act ttt aac ctg ccc aga ctc tgt atc	907
Gly Thr Ser Gln Lys Asp Glu Thr Phe Asn Leu Pro Arg Leu Cys Ile	
211 216 221 226	
cgg aaa ttc ttc cca aag aaa aaa tgc ttt gtc ttt gat cgg ccc gtt	955
Arg Lys Phe Phe Pro Lys Lys Lys Cys Phe Val Phe Asp Arg Pro Val	
227 232 237 242	
cac cgc agg aag ctt gcc cag ctc gag aaa cta caa gat gaa gag ctg	1003
His Arg Arg Lys Leu Ala Gln Leu Glu Lys Leu Gln Asp Glu Glu Leu	
243 248 253 258	
gac ccc gaa ttt gtg caa caa gta gca gac ttc tgt tcc tac atc ttt	1051
Asp Pro Glu Phe Val Gln Gln Val Ala Asp Phe Cys Ser Tyr Ile Phe	
259 264 269 274	
agt aat tcc aaa act aaa act ctt tca gga ggc atc cag gtc aac ggg	1099
Ser Asn Ser Lys Thr Lys Thr Leu Ser Gly Gly Ile Gln Val Asn Gly	
275 280 285 290	
cct cgt cta gag agc ctg gtg ctg acc tac gtc aat gcc atc agc agt	1147
Pro Arg Leu Glu Ser Leu Val Leu Thr Tyr Val Asn Ala Ile Ser Ser	
291 296 301 306	
ggg gat ctg ccg tgc atg gag aac gca gtc ctg gcc ttg gcc cag ata	1195
Gly Asp Leu Pro Cys Met Glu Asn Ala Val Leu Ala Leu Ala Gln Ile	
307 312 317 322	
gag aac tca gct gca gtg caa aag gct att gcc cac tat gaa cag cag	1243
Glu Asn Ser Ala Ala Val Gln Lys Ala Ile Ala His Tyr Glu Gln Gln	
323 328 333 338	
atg ggc cag aag gtg cag ctg ccc aca gaa acc ctc cag gag ctg ctg	1291
Met Gly Gln Lys Val Gln Leu Pro Thr Glu Thr Leu Gln Glu Leu Leu	
339 344 349 354	
gac ctg cac agg gac agt gag aga gag gcc att gaa gtc ttc atc agg	1339
Asp Leu His Arg Asp Ser Glu Arg Glu Ala Ile Glu Val Phe Ile Arg	
355 360 365 370	
agt tcc ttc aaa gat gtg gac cat cta ttt caa aag gag tta gcg gcc	1387

Ser	Ser	Phe	Lys	Asp	Val	Asp	His	Leu	Phe	Gln	Lys	Glu	Leu	Ala	Ala		
371					376					381					386		
cag	cta	gaa	aaa	aag	cgg	gat	gac	ttt	tgt	aaa	cag	aat	cag	gaa	gca	1435	
Gln	Leu	Glu	Lys	Lys	Arg	Asp	Asp	Phe	Cys	Lys	Gln	Asn	Gln	Glu	Ala		
387					392					397					402		
tca	tca	gat	cgt	tgc	tca	gct	tta	ctt	cag	gtc	att	ttc	agt	cct	cta	1483	
Ser	Ser	Asp	Arg	Cys	Ser	Ala	Leu	Leu	Gln	Val	Ile	Phe	Ser	Pro	Leu		
403					408					413					418		
gaa	gaa	gaa	gtg	aag	gcg	gga	att	tat	tcg	aaa	cca	ggg	ggc	tat	cgt	1531	
Glu	Glu	Glu	Val	Lys	Ala	Gly	Ile	Tyr	Ser	Lys	Pro	Gly	Gly	Tyr	Arg		
419					424					429					434		
ctc	ttt	gtt	cag	aag	cta	caa	gac	ctg	aag	aaa	aag	tac	tat	gag	gaa	1579	
Leu	Phe	Val	Gln	Lys	Leu	Gln	Asp	Leu	Lys	Lys	Lys	Tyr	Tyr	Glu	Glu		
435					440					445					450		
ccg	agg	aag	ggg	ata	cag	gct	gaa	gag	att	ctg	cag	aca	tac	ttg	aaa	1627	
Pro	Arg	Lys	Gly	Ile	Gln	Ala	Glu	Glu	Ile	Leu	Gln	Thr	Tyr	Leu	Lys		
451					456					461					466		
tcc	aag	gag	tct	atg	act	gat	gca	att	ctc	cag	aca	gac	cag	act	ctc	1675	
Ser	Lys	Glu	Ser	Met	Thr	Asp	Ala	Ile	Leu	Gln	Thr	Asp	Gln	Thr	Leu		
467					472					477					482		
aca	gaa	aaa	gaa	aag	gag	att	gaa	gtg	gaa	cgt	gtg	aaa	gct	gag	tct	1723	
Thr	Glu	Lys	Glu	Lys	Glu	Ile	Glu	Val	Glu	Arg	Val	Lys	Ala	Glu	Ser		
483					488					493					498		
gca	cag	gct	tca	gca	aaa	atg	ttg	cag	gaa	atg	caa	aga	aag	aat	gag	1771	
Ala	Gln	Ala	Ser	Ala	Lys	Met	Leu	Gln	Glu	Met	Gln	Arg	Lys	Asn	Glu		
499					504					509					514		
cag	atg	atg	gaa	cag	aag	gag	agg	agt	tat	cag	gaa	cac	ttg	aaa	caa	1819	
Gln	Met	Met	Glu	Gln	Lys	Glu	Arg	Ser	Tyr	Gln	Glu	His	Leu	Lys	Gln		
515					520					525					530		
ctg	act	gag	aag	atg	gag	aac	gac	agg	gtc	cag	ttg	ctg	aaa	gag	caa	1867	
Leu	Thr	Glu	Lys	Met	Glu	Asn	Asp	Arg	Val	Gln	Leu	Leu	Lys	Glu	Gln		
531					536					541					546		
gag	agg	acc	ctc	gct	ctt	aaa	ctt	cag	gaa	cag	gag	caa	cta	cta	aaa	1915	
Glu	Arg	Thr	Leu	Ala	Leu	Lys	Leu	Gln	Glu	Gln	Glu	Gln	Leu	Leu	Lys		
547					552					557					562		
gag	gga	ttt	caa	aaa	gaa	agc	aga	ata	atg	aaa	aat	gag	ata	cag	gat	1963	
Glu	Gly	Phe	Gln	Lys	Glu	Ser	Arg	Ile	Met	Lys	Asn	Glu	Ile	Gln	Asp		
563					568					573					578		
ctc	cag	acg	aaa	atg	aga	cga	cga	aag	gca	tgt	acc	ata	agc	taa	aga	2011	
Leu	Gln	Thr	Lys	Met	Arg	Arg	Arg	Lys	Ala	Cys	Thr	Ile	Ser	*			
579					584					589							
ccagagcctt	cctgtcaccc	ctaaccaagg	cataattgaa	acaatttttag	aatttggaac											2071	

aagcgctcact acatttgata ataattagat cttgcatcat aacaccaaaaa gtttataaag 2131
gcattgtggta caatgatcaa aatcatgttt tttcttaaaaa aaaaaaaaaa gactgtaaat 2191
tgtgcaacaa agatgcattt acctctgtat caactcagga aatttaataa gctggtagca 2251
ctcaggagaa gtttattctt ccagatgacc agcagtagac aaatggatac tgagcagagt 2311
cttaggtaaa agtcttggga aatatttggg cattggctctg gccaaagtcta caatgtocca 2371
atatcaaggg acaccaccct agctttctta gtgagacaat gtcagttatc catagatca 2430

<210> 592
<211> 2394
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (230)..(1972)

<400> 592
taccctgcgg taccgggtccg gaattcccgg gtcgaccac gcgtccgaag ccattacaaa 60
ggttgcttaa cttctaatta tttgatcact gaggaatac cagaaagcta cacaacactg 120
aaggggtgaa ataaaagtcc agcgatccag cgaaagaaaa gagaagtgc agaaacaact 180
ttacctggac tgaagataaa agcacagaca agagaacaat gccctggac atg gct 235
Met Ala
1
cca gag atc cac atg aca ggc cca atg tgc ctc att gag aac act aat 283
Pro Glu Ile His Met Thr Gly Pro Met Cys Leu Ile Glu Asn Thr Asn
3 8 13 18
ggg gaa ctg gtg gcg aat cca gaa gct ctg aaa atc ctg tct gcc att 331
Gly Glu Leu Val Ala Asn Pro Glu Ala Leu Lys Ile Leu Ser Ala Ile
19 24 29 34
aca cag cct gtg gtg gtg gca att gtg ggc ctc tac cgc aca gga 379
Thr Gln Pro Val Val Val Val Ala Ile Val Gly Leu Tyr Arg Thr Gly
35 40 45 50
aaa tcc tac ctg atg aac aag cta gct ggg aag aaa aag ggc ttc tct 427
Lys Ser Tyr Leu Met Asn Lys Leu Ala Gly Lys Lys Lys Gly Phe Ser
51 56 61 66
ctg ggc tcc acg gtg cag tct cac act aaa gga atc tgg atg tgg tgt 475
Leu Gly Ser Thr Val Gln Ser His Thr Lys Gly Ile Trp Met Trp Cys
67 72 77 82
gtg ccc cac ccc aag aag cca ggc cac atc cta gtt ctg ctg gac acc 523
Val Pro His Pro Lys Lys Pro Gly His Ile Leu Val Leu Leu Asp Thr

83	88	93	98	
gag ggt ctg gga gat	gta gag aag ggt gac	aac cag aat gac tcc tgg		571
Glu Gly Leu Gly Asp	Val Glu Lys Gly Asp	Asn Gln Asn Asp Ser Trp		
99	104	109	114	
atc ttc gcc ctg gcc gtc	ctc ctg agc agc acc	ttc gtg tac aat agc		619
Ile Phe Ala Leu Ala Val	Leu Leu Ser Ser Thr	Phe Val Tyr Asn Ser		
115	120	125	130	
ata gga acc atc aac cag	cag gct atg gac caa	ctg tac tat gtg aca		667
Ile Gly Thr Ile Asn Gln	Gln Ala Met Asp Gln	Leu Tyr Tyr Val Thr		
131	136	141	146	
gag ctg aca cat aga atc	cga tca aaa tcc tca	cct gat gag aat gag		715
Glu Leu Thr His Arg Ile	Arg Ser Lys Ser Ser	Pro Asp Glu Asn Glu		
147	152	157	162	
aat gag gtt gag gat tca	gct gac ttt gtg agc	ttc ttc cca gac ttt		763
Asn Glu Val Glu Asp Ser	Ala Asp Phe Val Ser	Phe Phe Pro Asp Phe		
163	168	173	178	
gtg tgg aca ctg aga gat	ttc tcc ctg gac ttg	gaa gca gat gga caa		811
Val Trp Thr Leu Arg Asp	Phe Ser Leu Asp Leu	Glu Ala Asp Gly Gln		
179	184	189	194	
ccc ctc aca cca ggt acc	agt caa aaa gat gaa	act ttt aac ctg ccc		859
Pro Leu Thr Pro Gly Thr	Ser Gln Lys Asp Glu	Thr Phe Asn Leu Pro		
195	200	205	210	
aga ctc tgt atc cgg aaa	ttc ttc cca aag aaa	aaa tgc ttt gtc ttt		907
Arg Leu Cys Ile Arg Lys	Phe Phe Pro Lys Lys	Lys Cys Phe Val Phe		
211	216	221	226	
gat cgg ccc gtt cac cgc	agg aag ctt gcc cag	ctc gag aaa cta caa		955
Asp Arg Pro Val His Arg	Arg Lys Leu Ala Gln	Leu Glu Lys Leu Gln		
227	232	237	242	
gat gaa gag ctg gac ccc	gaa ttt gtg caa caa	gta gca gac ttc tgt		1003
Asp Glu Glu Leu Asp Pro	Glu Phe Val Gln Gln	Val Ala Asp Phe Cys		
243	248	253	258	
tcc tac atc ttt agt aat	tcc aaa act aaa act	ctt tca gga ggc atc		1051
Ser Tyr Ile Phe Ser Asn	Ser Lys Thr Lys Thr	Leu Ser Gly Gly Ile		
259	264	269	274	
cag gtc aac ggg cct cgt	cta gag agc ctg gtg	ctg acc tac gtc aat		1099
Gln Val Asn Gly Pro Arg	Leu Glu Ser Leu Val	Leu Thr Tyr Val Asn		
275	280	285	290	
gcc atc agc agt ggg gat	ctg ccg tgc atg gag	aac gca gtc ctg gcc		1147
Ala Ile Ser Ser Gly Asp	Leu Pro Cys Met Glu	Asn Ala Val Leu Ala		
291	296	301	306	
ttg gcc cag ata gag aac	tca gct gca gtg caa	aag gct att gcc cac		1195
Leu Ala Gln Ile Glu Asn	Ser Ala Ala Val Gln	Lys Ala Ile Ala His		
307	312	317	322	

1243
 1291
 1339
 1387
 1435
 1483
 1531
 1579
 1627
 1675
 1723
 1771
 1819
 1867

tat gaa cag cag atg ggc cag aag gtg cag ctg ccc aca gaa acc ctc	1243
Tyr Glu Gln Gln Met Gly Gln Lys Val Gln Leu Pro Thr Glu Thr Leu	
323 328 333 338	
cag gag ctg ctg gac ctg cac agg gac agt gag aga gag gcc att gaa	1291
Gln Glu Leu Leu Asp Leu His Arg Asp Ser Glu Arg Glu Ala Ile Glu	
339 344 349 354	
gtc ttc atc agg agt tcc ttc aaa gat gtg gac cat cta ttt caa aag	1339
Val Phe Ile Arg Ser Ser Phe Lys Asp Val Asp His Leu Phe Gln Lys	
355 360 365 370	
gag tta gcg gcc cag cta gaa aaa aag cgg gat gac ttt tgt aaa cag	1387
Glu Leu Ala Ala Gln Leu Glu Lys Lys Arg Asp Asp Phe Cys Lys Gln	
371 376 381 386	
aat cag gaa gca tca tca gat cgt tgc tca gct tta ctt cag gtc att	1435
Asn Gln Glu Ala Ser Ser Asp Arg Cys Ser Ala Leu Leu Gln Val Ile	
387 392 397 402	
ttc agt cct cta gaa gaa gaa gtg aag gcg gga att tat tcg aaa cca	1483
Phe Ser Pro Leu Glu Glu Glu Val Lys Ala Gly Ile Tyr Ser Lys Pro	
403 408 413 418	
ggg ggc tat cgt ctc ttt gtt cag aag cta caa gac ctg aag aaa aag	1531
Gly Gly Tyr Arg Leu Phe Val Gln Lys Leu Gln Asp Leu Lys Lys Lys	
419 424 429 434	
tac tat gag gaa ccg agg aag ggg ata cag gct gaa gag att ctg cag	1579
Tyr Tyr Glu Glu Pro Arg Lys Gly Ile Gln Ala Glu Glu Ile Leu Gln	
435 440 445 450	
aca tac ttg aaa tcc aag gag tct atg act gat gca att ctc cag aca	1627
Thr Tyr Leu Lys Ser Lys Glu Ser Met Thr Asp Ala Ile Leu Gln Thr	
451 456 461 466	
gac cag act ctc aca gaa aaa gaa aag gag att gaa gtg gaa cgt gtg	1675
Asp Gln Thr Leu Thr Glu Lys Glu Lys Glu Ile Glu Val Glu Arg Val	
467 472 477 482	
aaa gct gag tct gca cag gct tca gca aaa atg ttg cag gaa atg caa	1723
Lys Ala Glu Ser Ala Gln Ala Ser Ala Lys Met Leu Gln Glu Met Gln	
483 488 493 498	
aga aag aat gag cag atg atg gaa cag aag gag agg agt tat cag gaa	1771
Arg Lys Asn Glu Gln Met Met Glu Gln Lys Glu Arg Ser Tyr Gln Glu	
499 504 509 514	
cac ttg aaa caa ctg act gag aag atg gag aac gac agg gtc cag ttg	1819
His Leu Lys Gln Leu Thr Glu Lys Met Glu Asn Asp Arg Val Gln Leu	
515 520 525 530	
ctg aaa gag caa gag agg acc ctc gct ctt aaa ctt cag gaa cag gag	1867
Leu Lys Glu Gln Glu Arg Thr Leu Ala Leu Lys Leu Gln Glu Gln Glu	
531 536 541 546	

caa cta cta aaa gag gga ttt caa aaa gaa agc aga ata atg aaa aat 1915
 Gln Leu Leu Lys Glu Gly Phe Gln Lys Glu Ser Arg Ile Met Lys Asn
 547 552 557 562

gag ata cag gat ctc cag acg aaa atg aga cga cga aag gca tgt acc 1963
 Glu Ile Gln Asp Leu Gln Thr Lys Met Arg Arg Arg Lys Ala Cys Thr
 563 568 573 578

ata agc taa agaccag agccttcctg tcacccoctaa ccaaggcata attgaaacaa 2019
 Ile Ser *
 579

ttttagaatt tggaacaagc gtcactacat ttgataataa ttagatcttg catcataaca 2079

ccaaaagtgt ataaaggcat gtggtacaat gatcaaaatc atgttttttc ttaaaaaaaaa 2139

aaaaaagact gtaaattgtg caacaaagat gcatttacct ctgtatcaac tcaggaaatt 2199

taataagctg gtaccactca ggagaagttt attottccag atgaccagca gtagacaaat 2259

ggatactgag cagagtctta ggtaaaagtc ttgggaaata tttgggcatt ggtctggcca 2319

agtctacaat gtcccaatat caagggacac caccctagct ttcttagtga gacaatgtca 2379

gttatccata gatca 2394

<210> 593

<211> 1674

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14)..(1297)

<400> 593

atatttcgag agg atg atg tat ata act atc tat tcg atg atg aag ata 49
 Met Met Tyr Ile Thr Ile Tyr Ser Met Met Lys Ile
 1 5 10

ccc cac caa acc caa aaa aag aga tct ctc gag gat ccg aat tcg cgg 97
 Pro His Gln Thr Gln Lys Lys Arg Ser Leu Glu Asp Pro Asn Ser Arg
 13 18 23 28

ccg cgt cga cgc ggg gtc gag atg gcg gcg cct ttg agg att cag agc 145
 Pro Arg Arg Arg Gly Val Glu Met Ala Ala Pro Leu Arg Ile Gln Ser
 29 34 39 44

gac tgg gcg caa gcc ctc agg aag gat gaa ggg gag gcc tgg ctg agc 193
 Asp Trp Ala Gln Ala Leu Arg Lys Asp Glu Gly Glu Ala Trp Leu Ser
 45 50 55 60

tgt cat ccc cca ggg aaa cca tct ttg tat ggc agc ctg act tgt caa 241
 Cys His Pro Pro Gly Lys Pro Ser Leu Tyr Gly Ser Leu Thr Cys Gln

61	66	71	76	
gga att ggc cta gat ggc atc cca gag gtt aca gct tca gaa gga ttt				289
Gly Ile Gly Leu Asp Gly Ile Pro Glu Val Thr Ala Ser Glu Gly Phe				
77	82	87	92	
act gtg aat gaa ata aac aag aaa agc att cat att tca tgt cca aag				337
Thr Val Asn Glu Ile Asn Lys Lys Ser Ile His Ile Ser Cys Pro Lys				
93	98	103	108	
gaa aat gca tct tct aag ttt ttg gca cca tat act act ttt tcc aga				385
Glu Asn Ala Ser Ser Lys Phe Leu Ala Pro Tyr Thr Thr Phe Ser Arg				
109	114	119	124	
att cat aca aag agt ata aca tgc ctg gac att tcc agc aga gga ggt				433
Ile His Thr Lys Ser Ile Thr Cys Leu Asp Ile Ser Ser Arg Gly Gly				
125	130	135	140	
ctt ggt gtg tct tct agt act gac ggg acc atg aaa atc tgg cag gct				481
Leu Gly Val Ser Ser Ser Thr Asp Gly Thr Met Lys Ile Trp Gln Ala				
141	146	151	156	
tcc aat gga gaa ctc agg aga gta ttg gaa gga cat gtg ttt gat gtg				529
Ser Asn Gly Glu Leu Arg Arg Val Leu Glu Gly His Val Phe Asp Val				
157	162	167	172	
aat tgt tgc agg ttt ttc cca tca ggc ctt gtg gtc ctg agt ggg gga				577
Asn Cys Cys Arg Phe Phe Pro Ser Gly Leu Val Val Leu Ser Gly Gly				
173	178	183	188	
atg gat gcc cag ctg aag ata tgg tca gct gaa gat gct agc tgc gtg				625
Met Asp Ala Gln Leu Lys Ile Trp Ser Ala Glu Asp Ala Ser Cys Val				
189	194	199	204	
gtg acc ttc aaa ggt cac aaa gga ggt atc ctg gat aca gcc atc gtt				673
Val Thr Phe Lys Gly His Lys Gly Gly Ile Leu Asp Thr Ala Ile Val				
205	210	215	220	
gat cgg ggg agg aat gtg gtg tct gct tct cga gat ggg aca gca cga				721
Asp Arg Gly Arg Asn Val Val Ser Ala Ser Arg Asp Gly Thr Ala Arg				
221	226	231	236	
ctt tgg gat tgt ggg cgc tca gcc tgc ttg gga gtc ctt gca gat tgt				769
Leu Trp Asp Cys Gly Arg Ser Ala Cys Leu Gly Val Leu Ala Asp Cys				
237	242	247	252	
ggg tct tct atc aat gga gtg gcg gtg ggt gct gct gac aac tcc ata				817
Gly Ser Ser Ile Asn Gly Val Ala Val Gly Ala Ala Asp Asn Ser Ile				
253	258	263	268	
aac ctt ggc tcc cct gag cag atg ccc agt gaa cgg gag gtt gga aca				865
Asn Leu Gly Ser Pro Glu Gln Met Pro Ser Glu Arg Glu Val Gly Thr				
269	274	279	284	
gag gcc aaa atg/ctg ctc ttg gcc cgg gaa gat aag aaa ctt cag tgc				913
Glu Ala Lys Met Leu Leu Leu Ala Arg Glu Asp Lys Lys Leu Gln Cys				
285	290	295	300	

ttg gga cta cag agc agg cag ctg gtg ttc ctc ttt att ggc tca gac	961
Leu Gly Leu Gln Ser Arg Gln Leu Val Phe Leu Phe Ile Gly Ser Asp	
301 306 311 316	
gct ttc aac tgc tgt act ttt ctc tct ggc ttc ttg cta ttg gct ggg	1009
Ala Phe Asn Cys Cys Thr Phe Leu Ser Gly Phe Leu Leu Leu Ala Gly	
317 322 327 332	
act caa gat gga aac att tat cag ctg gat gtg agg agt cca agg gct	1057
Thr Gln Asp Gly Asn Ile Tyr Gln Leu Asp Val Arg Ser Pro Arg Ala	
333 338 343 348	
ccg gta caa gtc atc cac aga tca gga gca cca gtt cta tcc ctg cta	1105
Pro Val Gln Val Ile His Arg Ser Gly Ala Pro Val Leu Ser Leu Leu	
349 354 359 364	
agt gtc aga gat gga ttc att gct agc caa ggt gat gga agc tgt ttt	1153
Ser Val Arg Asp Gly Phe Ile Ala Ser Gln Gly Asp Gly Ser Cys Phe	
365 370 375 380	
att gtc cag caa gac tta gac tat gtc act gag ctc act ggg gct gac	1201
Ile Val Gln Gln Asp Leu Asp Tyr Val Thr Glu Leu Thr Gly Ala Asp	
381 386 391 396	
tgt gac cct gtg tac aag gta gcc aca tgg gag aag cag atc tac aca	1249
Cys Asp Pro Val Tyr Lys Val Ala Thr Trp Glu Lys Gln Ile Tyr Thr	
397 402 407 412	
tgc tgt cga gac ggt ctt gta cga cgc tac cag ctt tct gac ctc tga	1297
Cys Cys Arg Asp Gly Leu Val Arg Arg Tyr Gln Leu Ser Asp Leu *	
413 418 423 428	
cttcttggaa agagcagtc ccggttagtga aaagggttga ccctgatcaa caatgagcag	1357
aaacatcatc agtccttccc aaggaccatg gcgtttaatg tcttgggcac cccttggaaa	1417
tcacagaaag tcagctgtac tggccgtgtg gaactctcat cccaagacct actttgaact	1477
gagtaagaag gtcattgtgc ccactgcatt tgttccaact tctccttgta taaactcacc	1537
ccagcaacac agggcaagga tatagatgct tttagtttgt tcttaaacca gttttgttaa	1597
atgtttacaa ggacctcagt actaaagcct gttctctgga ggaaataaag aaaatatggt	1657
tggaggtgcc tcaatat	1674

<210> 594
 <211> 1577
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (97)..(570)

<220>

<221> misc_feature

<222> (1)...(1577)

<223> n = a,t,c or g

<400> 594

ttttggtata ggcagaccca agctggctag cgttttaact tacgcttggt accgagctcg 60

gatccactag tccagtgtgg tggaattccg ctggga atg atg aag aag aac aat 114
Met Met Lys Lys Asn Asn

1

tcc gcc aag cgg gga cct cag gat gga aac cag cag cct gca ccg ccc 162
Ser Ala Lys Arg Gly Pro Gln Asp Gly Asn Gln Gln Pro Ala Pro Pro
7 12 17 22

gag aag gtc ggc tgg gtc cgg aaa ttc tgc ggg aaa ggg att ttc agg 210
Glu Lys Val Gly Trp Val Arg Lys Phe Cys Gly Lys Gly Ile Phe Arg
23 28 33 38

gag att tgg aaa aac cgc tat gtg gtg ctg aaa ggg gac cag ctc tac 258
Glu Ile Trp Lys Asn Arg Tyr Val Val Leu Lys Gly Asp Gln Leu Tyr
39 44 49 54

atc tct gag aag gag gta aaa gat gag aaa aat att caa gag gta ttt 306
Ile Ser Glu Lys Glu Val Lys Asp Glu Lys Asn Ile Gln Glu Val Phe
55 60 65 70

gac ctg agt gac tat gag aag tgt gaa gag ctc cgg aag tcc aag agc 354
Asp Leu Ser Asp Tyr Glu Lys Cys Glu Glu Leu Arg Lys Ser Lys Ser
71 76 81 86

agg agc aag aaa aat cat agc aag ttt act ctt gcc cac tcc aaa cag 402
Arg Ser Lys Lys Asn His Ser Lys Phe Thr Leu Ala His Ser Lys Gln
87 92 97 102

ccc ggt aac acg gca ccc aac ctg atc ttc ctg gca gtg agt cca gaa 450
Pro Gly Asn Thr Ala Pro Asn Leu Ile Phe Leu Ala Val Ser Pro Glu
103 108 113 118

gag aag gaa tcg aca ggc acc caa cct gat ctt cct ggc agt gag tcc 498
Glu Lys Glu Ser Thr Gly Thr Gln Pro Asp Leu Pro Gly Ser Glu Ser
119 124 129 134

aga aga gaa gga atc gtg gat caa tgc cct caa ctc tgc cat cac ccg 546
Arg Arg Glu Gly Ile Val Asp Gln Cys Pro Gln Leu Cys His His Pro
135 140 145 150

agc caa gaa ccg tat ctt gga tga ggtcaggggg ctactgtgg ggagagggag 600
Ser Gln Glu Pro Tyr Leu Gly *
151 156

gaacgctggg gcagagggaa cagctgtgac cactgaagg gggaggattg tgcaggcccc 660

gttttatocg ctccttcac cagcgtact tctttnaccc acccttttaa aagccctgat 720

```

ottttttteta ctttctctcc aagtctcatc tgacacotcc ttttccccgc ttcattgatgg 780
gggagccagc cttgggtcag cttaaagagc ccccttcgtg tccagtaaatt ccccttgccc 840
attcagaagc agtgaatgga gtgggcacat gttcaggcct cgggatgctg ggttgggaca 900
gcgagtcgct gaagagcact catgattcac agtacatctc ttcaggtcac cgttgaggag 960
gacagctatc ttgcccattc cactcgagac agggcaaaaa tccagcactc ccgccgcccc 1020
ccaacaaggg gacacctaatt ggctgtggct tccacctcta cctcggtatgg gatgctgacc 1080
ttggacttga tccaagagga agacccttcc cctgaggaac caacctcttg tgctgagagc 1140
tttcgggttg acctggacaa gtctgtggcc cagctggcag ggagccggcg gagagcggac 1200
tcagaccgca tccagccctc cgcagaccgg gcaagcagtc tctcccgacc ttgggaaaaa 1260
acagacaaaag gggccaccta cccccccag gcaaccaaga agttgacgcc cacagagaaa 1320
ggccgctgcg cctccctgga ggagatccta tctcagcggg atgctgcctc tgcccgacc 1380
ctccagctgc gggctggagg aacccccaac cctgccctc cccaaccggg gggcagctgt 1440
cccgattca ggaccttggg tagcaaggaa acttggagga gacttcagga gctttttggc 1500
agaaggtttc aagggactgg gagatgggaa gccgaaaggg ccaaggaccc cctcggctctt 1560
cgccggattc ccnggta 1577

```

<210> 595
 <211> 1745
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (76) .. (1314)

```

<400> 595
ctgcctagcg tttaaactta agcttggtac cgagctcgga tccactagtc cagtgtggtg 60

gaattcgtga cctgg atg tct gag gag gaa gta ctt cct gca gga caa cct 111
      Met Ser Glu Glu Val Leu Pro Ala Gly Gln Pro
        1             5             10

gcc gag ggc acc acc tgc tgc ctc gag gtc act gcc cag cag gag gag 159
Ala Glu Gly Thr Thr Cys Cys Leu Glu Val Thr Ala Gln Gln Glu Glu
  13             18             23             28

aag cag gag gat gca gcc atc tgc cca gtg aca gtg ctc cct gag gag 207
Lys Gln Glu Asp Ala Ala Ile Cys Pro Val Thr Val Leu Pro Glu Glu
  29             34             39             44

```

cca gtg acc ttc cag gat gtg gct gtg gac ttc agc cgg gag gag tgg	255
Pro Val Thr Phe Gln Asp Val Ala Val Asp Phe Ser Arg Glu Glu Trp	
45 50 55 60	
ggg ctg ctg ggc ccg aca cag agg acc gag tac cgc gat gtg atg ctg	303
Gly Leu Leu Gly Pro Thr Gln Arg Thr Glu Tyr Arg Asp Val Met Leu	
61 66 71 76	
gag acc ttt ggg cac ctg gtc tct gtg ggg tgg gag act aca ctg gaa	351
Glu Thr Phe Gly His Leu Val Ser Val Gly Trp Glu Thr Thr Leu Glu	
77 82 87 92	
aat aaa gag tta gct cca aat tct gac att cct gag gaa gaa cca gcc	399
Asn Lys Glu Leu Ala Pro Asn Ser Asp Ile Pro Glu Glu Glu Pro Ala	
93 98 103 108	
ccc agc ctg aaa gta caa gaa tcc tca agg gat tgt gcc ttg tcc tct	447
Pro Ser Leu Lys Val Gln Glu Ser Ser Arg Asp Cys Ala Leu Ser Ser	
109 114 119 124	
aca tta gaa gat acc ttg cag ggt ggg gtc cag gaa gtc caa gac aca	495
Thr Leu Glu Asp Thr Leu Gln Gly Gly Val Gln Glu Val Gln Asp Thr	
125 130 135 140	
gtg ttg aag cag atg gag tct gct cag gaa aaa gac ctt cct cag aag	543
Val Leu Lys Gln Met Glu Ser Ala Gln Glu Lys Asp Leu Pro Gln Lys	
141 146 151 156	
aag cac ttt gac aac cgt gag tcc cag gca aac agt ggt gct ctt gac	591
Lys His Phe Asp Asn Arg Glu Ser Gln Ala Asn Ser Gly Ala Leu Asp	
157 162 167 172	
aca aac caa gtt tgc ctc cag aaa att gac aac cct gag tcc cag gca	639
Thr Asn Gln Val Ser Leu Gln Lys Ile Asp Asn Pro Glu Ser Gln Ala	
173 178 183 188	
aac agt ggc gct ctt gac aca aac caa gtt ttg ctc cac aaa att cct	687
Asn Ser Gly Ala Leu Asp Thr Asn Gln Val Leu Leu His Lys Ile Pro	
189 194 199 204	
cct aga aaa cga ttg cgc aaa cgt gac tca caa gtt aaa agt atg aaa	735
Pro Arg Lys Arg Leu Arg Lys Arg Asp Ser Gln Val Lys Ser Met Lys	
205 210 215 220	
cat aat tca cgt gta aaa att cat cag aag agc tgt gaa agg caa aag	783
His Asn Ser Arg Val Lys Ile His Gln Lys Ser Cys Glu Arg Gln Lys	
221 226 231 236	
gcc aag gaa ggc aat ggt tgt agg aaa acc ttc agt cgg agt act aaa	831
Ala Lys Glu Gly Asn Gly Cys Arg Lys Thr Phe Ser Arg Ser Thr Lys	
237 242 247 252	
cag att acg ttt ata aga att cac aag ggg agc caa gtt tgc cga tgc	879
Gln Ile Thr Phe Ile Arg Ile His Lys Gly Ser Gln Val Cys Arg Cys	
253 258 263 268	

agt gaa tgt ggt aaa ata ttc cgg aac cca aga tac ttt tct gtg cat	927
Ser Glu Cys Gly Lys Ile Phe Arg Asn Pro Arg Tyr Phe Ser Val His	
269 274 279 284	
aag aaa atc cat acc gga gag agg ccc tat gtg tgt caa gac tgt ggg	975
Lys Lys Ile His Thr Gly Glu Arg Pro Tyr Val Cys Gln Asp Cys Gly	
285 290 295 300	
aaa gga ttt gtt cag agc tct tcc ctc aca cag cat cag aga gtt cat	1023
Lys Gly Phe Val Gln Ser Ser Ser Leu Thr Gln His Gln Arg Val His	
301 306 311 316	
tct gga gag aga cca ttt gaa tgt cag gag tgt ggg agg acc ttc aat	1071
Ser Gly Glu Arg Pro Phe Glu Cys Gln Glu Cys Gly Arg Thr Phe Asn	
317 322 327 332	
gat cgc tca gcc atc tcc cag cac ctg agg act cac act ggc gct aag	1119
Asp Arg Ser Ala Ile Ser Gln His Leu Arg Thr His Thr Gly Ala Lys	
333 338 343 348	
ccc tac aag tgt cag gac tgt gga aaa gcc ttc cgc cag agc tcc cac	1167
Pro Tyr Lys Cys Gln Asp Cys Gly Lys Ala Phe Arg Gln Ser Ser His	
349 354 359 364	
ctc atc aga cat cag agg act cac acc ggg gag cgc cca tat gca tgc	1215
Leu Ile Arg His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Ala Cys	
365 370 375 380	
aac aaa tgt gga aag gcc ttc acc cag agc tca cac ctt att ggg cac	1263
Asn Lys Cys Gly Lys Ala Phe Thr Gln Ser Ser His Leu Ile Gly His	
381 386 391 396	
cag aga acc cac aat agg aca aag cga aag aag aaa cag cct acc tca	1311
Gln Arg Thr His Asn Arg Thr Lys Arg Lys Lys Lys Gln Pro Thr Ser	
397 402 407 412	
tag ctct caagccagtt gaagaaacct tgccttttca gcttgaccct gcaatataac	1368
*	
413	
atgcacaggc ctgcttgtga atcaggactg aatgtgaaag ggaagtattg agtgaggaca	1428
ttcccaaaac caaaggacaa ctgaggagac tgcccagcac ataataaata aataagaaaa	1488
tgagtgagga gttattaaca tcatttgga aaaagatttc ccattcactt gatattgttt	1548
gttcactcat ttagtcatta aaagtgagat taataaaatc tgaaaatgtt atataataac	1608
tttaaaaagc caggtaatta ataatactgca ctgatattac atccacagta ccacagtatt	1668
tatgtgtatg aattaaggat taaaagataa tgtggataaa taaactattg atctatgtct	1728
gtgtaaaaaa aaaaaaa	1745

<210> 596
 <211> 1963
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (84)..(1445)

<220>
 <221> misc_feature
 <222> (1)...(1963)
 <223> n = a,t,c or g

<400> 596

```

tttggatagc cctcgggtac cggcccggaa ttcccgggtc gacccaacgcg tccgcccacg      60

cgctcgctcc gacccggcgc aac      atg gcc gca gcc tcg cct ctg cgc gac      110
                                Met Ala Ala Ala Ser Pro Leu Arg Asp
                                1                                5

tgc cag gcc tgg aag gat gcg agg ctc ccg ctc tcc acc aca agc aac      158
Cys Gln Ala Trp Lys Asp Ala Arg Leu Pro Leu Ser Thr Thr Ser Asn
  10                                15                                20                                25

gaa gcc tgc aag ctg ttc gat gcc acg ctg acc cag tat gta aaa tgg      206
Glu Ala Cys Lys Leu Phe Asp Ala Thr Leu Thr Gln Tyr Val Lys Trp
  26                                31                                36                                41

acc aat gac aag agt ctc ggt ggc atc gag ggc tgc ctg tca aag ctc      254
Thr Asn Asp Lys Ser Leu Gly Gly Ile Glu Gly Cys Leu Ser Lys Leu
  42                                47                                52                                57

aaa gca gca gat cca acc ttt gtg atg ggc cac gcc atg gct act ggc      302
Lys Ala Ala Asp Pro Thr Phe Val Met Gly His Ala Met Ala Thr Gly
  58                                63                                68                                73

ctt gtg ctg att ggc act gga agc tcc gtg aag ctg gac aaa gag ctg      350
Leu Val Leu Ile Gly Thr Gly Ser Ser Val Lys Leu Asp Lys Glu Leu
  74                                79                                84                                89

gac ctg gct gtg aag aca atg gtg gag att tca aga acc cag ccg ctg      398
Asp Leu Ala Val Lys Thr Met Val Glu Ile Ser Arg Thr Gln Pro Leu
  90                                95                                100                                105

aca agg cgg gag cag ctg cac gtg tct gca gta gag aca ttt gcc aat      446
Thr Arg Arg Glu Gln Leu His Val Ser Ala Val Glu Thr Phe Ala Asn
  106                                111                                116                                121

ggg aac ttt ccg aaa gcc tgt gaa cta tgg gaa cag att ctc cag gac      494
Gly Asn Phe Pro Lys Ala Cys Glu Leu Trp Glu Gln Ile Leu Gln Asp
  122                                127                                132                                137

cac ccg aca gac atg ttg gcc ctg aaa ttt tcc cat gat gct tat ttt      542
His Pro Thr Asp Met Leu Ala Leu Lys Phe Ser His Asp Ala Tyr Phe
  138                                143                                148                                153

```

tac ctg ggc tat cag gaa cag atg aga gat tct gtt gct cga att tac	590
Tyr Leu Gly Tyr Gln Glu Gln Met Arg Asp Ser Val Ala Arg Ile Tyr	
154 159 164 169	
ccc ttc tgg aca cct gac atc ccc cta agc agc tat gtg aaa ggc atc	638
Pro Phe Trp Thr Pro Asp Ile Pro Leu Ser Ser Tyr Val Lys Gly Ile	
170 175 180 185	
tac tct ttt ggc ttg atg gaa acc aac ttc tac gac cag gca gaa aaa	686
Tyr Ser Phe Gly Leu Met Glu Thr Asn Phe Tyr Asp Gln Ala Glu Lys	
186 191 196 201	
ctc gcc aaa gag gct tta tct att aac ccg aca gac gca tgg tcg gtg	734
Leu Ala Lys Glu Ala Leu Ser Ile Asn Pro Thr Asp Ala Trp Ser Val	
202 207 212 217	
cac acc gtc gct cac atc cac gag atg aaa gca gag atc aag gat ggg	782
His Thr Val Ala His Ile His Glu Met Lys Ala Glu Ile Lys Asp Gly	
218 223 228 233	
ttg gaa ttc atg cag cac tca gag acc ctc tgg aag gac tct gat atg	830
Leu Glu Phe Met Gln His Ser Glu Thr Leu Trp Lys Asp Ser Asp Met	
234 239 244 249	
ttg gct tgt cat aac tat tgg cac tgg gct tta tat ctg att gag aag	878
Leu Ala Cys His Asn Tyr Trp His Trp Ala Leu Tyr Leu Ile Glu Lys	
250 255 260 265	
ggc gaa tat gag gcc gcg ctg acc atc tac gat acc cac atc ctt ccc	926
Gly Glu Tyr Glu Ala Ala Leu Thr Ile Tyr Asp Thr His Ile Leu Pro	
266 271 276 281	
agc ctg cag gcc aac gat gca atg ctg gac gtg gtg gac agc tgc tcc	974
Ser Leu Gln Ala Asn Asp Ala Met Leu Asp Val Val Asp Ser Cys Ser	
282 287 292 297	
atg ctc tac cgc ctg cag atg gaa gga gtg tct gtg ggc cag cgg tgg	1022
Met Leu Tyr Arg Leu Gln Met Glu Gly Val Ser Val Gly Gln Arg Trp	
298 303 308 313	
cag gat gtc ctg cct gtg gcc cgg aag cac agc cga gac cac atc ctg	1070
Gln Asp Val Leu Pro Val Ala Arg Lys His Ser Arg Asp His Ile Leu	
314 319 324 329	
ctg ttc aat gac gca cac ttc ctg atg gca tcc ctg ggt gca cac gac	1118
Leu Phe Asn Asp Ala His Phe Leu Met Ala Ser Leu Gly Ala His Asp	
330 335 340 345	
ccc cag acc aca cag gag ctg ctg acc acc ctg cgg gac gcc agc gaa	1166
Pro Gln Thr Thr Gln Glu Leu Leu Thr Thr Leu Arg Asp Ala Ser Glu	
346 351 356 361	
tcc cca ggg gag aac tgc cag cac ctc ctg gcc cga gac gtg ggg ctg	1214
Ser Pro Gly Glu Asn Cys Gln His Leu Leu Ala Arg Asp Val Gly Leu	
362 367 372 377	
ccc ctg tgc cag gcc ctg gtg gag gct gag gac ggg aac cct gac cgc	1262

Pro	Leu	Cys	Gln	Ala	Leu	Val	Glu	Ala	Glu	Asp	Gly	Asn	Pro	Asp	Arg	
378					383					388					393	
gtc ctg gag ctg ctc ctg ccc atc cgc tac cgg atc gtc cag ctc ggt																1310
Val	Leu	Glu	Leu	Leu	Leu	Pro	Ile	Arg	Tyr	Arg	Ile	Val	Gln	Leu	Gly	
394					399					404					409	
ggg agc aat gcc cag aga gac gtc ttc aac cag ctg ctg att cac gcg																1358
Gly	Ser	Asn	Ala	Gln	Arg	Asp	Val	Phe	Asn	Gln	Leu	Leu	Ile	His	Ala	
410					415					420					425	
gcc tta aac tgc acc tcc agc gtc cat aag aac gta gcc cga ggc aag																1406
Ala	Leu	Asn	Cys	Thr	Ser	Ser	Val	His	Lys	Asn	Val	Ala	Arg	Gly	Lys	
426					431					436					441	
gtc tca ctc ggt cat cca ggt tgg aat gca gtg gtg tga tcacagttca																1455
Val	Ser	Leu	Gly	His	Pro	Gly	Trp	Asn	Ala	Val	Val	*				
442					447					452						
ctgtaaactc aaactcctgg gctcaaggaa tcttcctgcc tcacacttcc atcgtgcagg																1515
gattacaggg gagccttctg atggagcgtg atgccttgaa gcccaactcg cccctgaccg																1575
agcgggtcat ccnaaggcag ctaccgtcca cctcatgcag tgagccagag cctgtttgtt																1635
agggctgtta gaggggtgatc ttcagtttta caggaagtgg gtcacggggt aattttaaat																1695
gtgattccga atctcctttc agtcctcgag aagggccaat gagcattttt cagcagtcac																1755
agccagtgtg agtgctgctc tttccacctg ccttgcaa at tctgtttccc agggggaatg																1815
tgtctactgc ctgggtgggt tcaaagggtg ggaaggcagg gcagaggtn ggggctgatt																1875
tctgtgggg acaggtcttn cagaggcagc cttcccccat tgccgtgtccc ctnccccacc																1935
agggttgcc tgggatngg acntttgt																1963

<210> 597
 <211> 2038
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (282) .. (635)

<400> 597																
cgtcacagcc	cgacgcgcca	cccagctgtt	tttgtgtca	caagctctag	cgaaaagccg											60
ccgggtatttc	tccatctggc	tctcctctac	ctccaggcag	gctcaccgga	gatccccgcc											120
ccgaaccccc	cctgcacact	cggcccagcg	ctggtgcccc	cggagcggac	gtttctgcag											180
ctattctgag	cacacctga	cgtcggctga	gggagcggga	cagggtcagc	ggcgaaggag											240

gcaggccccg cgcgggggac tcggaagccc tgcggtgcat c atg aag ttc cag 293
Met Lys Phe Gln
1

tac aag gag gac cat ccc ttt gag tat cgg aaa aag gaa gga gaa aag 341
Tyr Lys Glu Asp His Pro Phe Glu Tyr Arg Lys Lys Glu Gly Glu Lys
5 10 15 20

atc cgg aag aaa tat ccg gac agg gtc ccc gtg att gta gag aag gct 389
Ile Arg Lys Lys Tyr Pro Asp Arg Val Pro Val Ile Val Glu Lys Ala
21 26 31 36

cca aaa gcc agg gtg cct gat ctg gac aag agg aag tac cta gtg ccc 437
Pro Lys Ala Arg Val Pro Asp Leu Asp Lys Arg Lys Tyr Leu Val Pro
37 42 47 52

tct gac ctt act gtt ggc cag ttc tac ttc tta atc cgg aag aga atc 485
Ser Asp Leu Thr Val Gly Gln Phe Tyr Phe Leu Ile Arg Lys Arg Ile
53 58 63 68

cac ctg aga cct gag gac gcc tta ttc ttc ttt gtc aac aac acc atc 533
His Leu Arg Pro Glu Asp Ala Leu Phe Phe Phe Val Asn Asn Thr Ile
69 74 79 84

cct ccc acc agt gct acc atg ggc caa ctg tat gag gac aat cat gag 581
Pro Pro Thr Ser Ala Thr Met Gly Gln Leu Tyr Glu Asp Asn His Glu
85 90 95 100

gaa gac tat ttt ctg tat gtg gcc tac agt gat gag agt gtc tat ggg 629
Glu Asp Tyr Phe Leu Tyr Val Ala Tyr Ser Asp Glu Ser Val Tyr Gly
101 106 111 116

aaa tga gtggttgaa gccagcaga tgggagcacc tggacttggg ggtaggggag 685
Lys *
117

gggtgtgtgt gcgcgacatg gggaaagagg gtggctccca ccgcaaggag acagaagggtg 745

aagacatcta gaaacattac accacacaca ccgtcatcac attttcacat gctcaattga 805

tattttttgc tgcttcctcg gccagggag aaagcatgtc aggacagagc tgttggattg 865

gctttgatag aggaatgggg atgatgtaag tttacagcat tcctgggggt taattgttgt 925

gcagtttcat agatgggtca ggaggtggac aagttggggc cagagatgat ggcagtccag 985

cagcaactcc ctgtgctccc ttctctttgg gcagagattc tatttttgac atttgcacaa 1045

gacaggtagg gaaaggggac ttgtggtagt ggaccatacc tggggaccaa aagagaccca 1105

ctgtaattga tgcattgtgg ccctgatct tcctgtctc acatttcttt tctcccatcc 1165

cggttgcaat ctactcaga catcacagta ccaccccagg ggtggcagta gacaacaacc 1225

cagaaattta gacaggggac tcttaccttt ggaaaatagg ggtaggcat gaaggtgggt 1285

gtgattaaga agatggtttt gttattaaat agcattaaac tggaattgac aagagtgttg 1345
agcatccctg tctaacctgc tctttctctt tgggtgcccc ttatctcacc ccttccttgg 1405
gaatttaata agtctcaggc atttccaatt gtagactaaa accactctta gcatctcctc 1465
tagtattttc catgtatcag gacagagggtg tcttatggta ggggaggggg gcaagtatga 1525
agtaagggtg attatatact actctcattc caggattctt tgctcccatg ctgctgtccc 1585
cttcagggt cecatgccac aggaatgcta catgatggcc agctgccttc cctccttggg 1645
tatcatccca ctgcagctgc tagttagaaa ggtttggagg gatgactttt agtaaatacat 1705
ggggatttta ttgatttatt ttcacttttg ggattttgtg ggggtgggagt ggggagcagg 1765
aattgcactc agacatgaca tttcaattca tctctgctaa tgaaaagggt tctttctctt 1825
gggggaaatg tgtgtgtcag ttctgtcagc tgcaagttct tgtataatga agtcaatgcc 1885
atcaggccaa ggaaataaaa taattgctta ccttaaaaaa aaaaaaaaaa aaaaattttt 1945
atttaaccgg ccgcagccta atccctttta gggggggtaa atttaagctg ggccctggcc 2005
gccgtttaac aacgccggga cgggaaaaac ccg 2038

<210> 598
<211> 2126
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (180)..(1688)

<400> 598
aaagtacctg tcgcacgacg accggaccgg aattcccggg tcgacgattt cgtcctaccc 60
ccgtccctag tcccgtcagc atggtttgga tcccctgtgc cgtcgcctct ttctttggcg 120
acgcctccgc cgcgcctga ggaggcgagc tatccgggag ttacaccgcc accgccagg 179
atg gat aga atg aca gaa gat gct ctt cgc ttg aat ctg ttg aag cgg 227
Met Asp Arg Met Thr Glu Asp Ala Leu Arg Leu Asn Leu Leu Lys Arg
1 5 10 15
agc ttg gac cca gca gat gag cga gat gat gtc ctg gca aag cga ctc 275
Ser Leu Asp Pro Ala Asp Glu Arg Asp Asp Val Leu Ala Lys Arg Leu
17 22 27 32
aaa atg gag ggg cat gag gcc atg gaa cgt ctg aaa atg ttg gca ttg 323
Lys Met Glu Gly His Glu Ala Met Glu Arg Leu Lys Met Leu Ala Leu
33 38 43 48
ctc aaa agg aag gat ttg gca aat ctt gag gtg cca cat gag tta ccc 371

Leu Lys Arg Lys Asp Leu Ala Asn Leu Glu Val Pro His Glu Leu Pro	
49 54 59 64	
acc aaa cag gat ggc agt ggt gtc aag ggc tat gaa gaa aaa ctt aac	419
Thr Lys Gln Asp Gly Ser Gly Val Lys Gly Tyr Glu Glu Lys Leu Asn	
65 70 75 80	
ggg aat ctc agg cct cat gga gac aac agg act gct gga agg cca ggc	467
Gly Asn Leu Arg Pro His Gly Asp Asn Arg Thr Ala Gly Arg Pro Gly	
81 86 91 96	
aaa gaa aac atc aat gat gag cct gtg gat atg agt gct aga cgg agt	515
Lys Glu Asn Ile Asn Asp Glu Pro Val Asp Met Ser Ala Arg Arg Ser	
97 102 107 112	
gag cca gag cga gga agg cta act ccc tca cca gac atc att gtt ttg	563
Glu Pro Glu Arg Gly Arg Leu Thr Pro Ser Pro Asp Ile Ile Val Leu	
113 118 123 128	
tct gac aat gag gct tcc agt ccc cgt tcc agt tcc aga atg gaa gaa	611
Ser Asp Asn Glu Ala Ser Ser Pro Arg Ser Ser Ser Arg Met Glu Glu	
129 134 139 144	
aga ctc aaa gca gcc aac tta gag atg ttt aag ggg aaa ggc att gag	659
Arg Leu Lys Ala Ala Asn Leu Glu Met Phe Lys Gly Lys Gly Ile Glu	
145 150 155 160	
gag cgg cag cag ctt atc aag cag ctg agg gat gag cta cga ttg gaa	707
Glu Arg Gln Gln Leu Ile Lys Gln Leu Arg Asp Glu Leu Arg Leu Glu	
161 166 171 176	
gaa gcc cga ctg gtc ctg tta aag aaa ctg aga cag agt cag cta cag	755
Glu Ala Arg Leu Val Leu Leu Lys Lys Leu Arg Gln Ser Gln Leu Gln	
177 182 187 192	
aaa gag aat gtg gtc cag aag act cca gtt gta cag aat gca gca tct	803
Lys Glu Asn Val Val Gln Lys Thr Pro Val Val Gln Asn Ala Ala Ser	
193 198 203 208	
att gtt cag cca tct cct gcc cat gtg gga cag cag ggc cta tct aag	851
Ile Val Gln Pro Ser Pro Ala His Val Gly Gln Gln Gly Leu Ser Lys	
209 214 219 224	
ctt ccc tct cgg cct ggg gcc caa ggg gtt gaa cct caa aat ttg aga	899
Leu Pro Ser Arg Pro Gly Ala Gln Gly Val Glu Pro Gln Asn Leu Arg	
225 230 235 240	
aca tta cag ggt cac agt gtc atc cgt tca gct acc aat acc acc ctt	947
Thr Leu Gln Gly His Ser Val Ile Arg Ser Ala Thr Asn Thr Thr Leu	
241 246 251 256	
cca cac atg ttg atg tct caa cgt gtt att gca cca aac cca gcc cag	995
Pro His Met Leu Met Ser Gln Arg Val Ile Ala Pro Asn Pro Ala Gln	
257 262 267 272	
cta cag ggt cag cgg ggc ccg cct aag cct ggc ctt gta cgc acc aca	1043
Leu Gln Gly Gln Arg Gly Pro Pro Lys Pro Gly Leu Val Arg Thr Thr	

273	278	283	288	
aca ccc aac atg aat ccc gcc atc aat tat caa ccg cag tca agt tct				1091
Thr Pro Asn Met Asn Pro Ala Ile Asn Tyr Gln Pro Gln Ser Ser Ser				
289	294	299	304	
tct gtt cca tgt cag cgt aca aca tcc tct gcc atc tat atg aac ctt				1139
Ser Val Pro Cys Gln Arg Thr Thr Ser Ser Ala Ile Tyr Met Asn Leu				
305	310	315	320	
gct tct cat atc cag cca ggg acg gtg aac aga gtg tcc tcg cca ctt				1187
Ala Ser His Ile Gln Pro Gly Thr Val Asn Arg Val Ser Ser Pro Leu				
321	326	331	336	
cct agc ccc agc gcc atg act gat gct gcc aac tca cag gct gca gcc				1235
Pro Ser Pro Ser Ala Met Thr Asp Ala Ala Asn Ser Gln Ala Ala Ala				
337	342	347	352	
aaa ttg gct ctt cgc aaa cag ctg gaa aag aca ctc ctg gag atc cca				1283
Lys Leu Ala Leu Arg Lys Gln Leu Glu Lys Thr Leu Leu Glu Ile Pro				
353	358	363	368	
ccc cct aaa cct cct gct ccc tta ctt cat ttc ttg cct agt gca gcc				1331
Pro Pro Lys Pro Pro Ala Pro Leu Leu His Phe Leu Pro Ser Ala Ala				
369	374	379	384	
aat agc gag ttc atc tac atg gta ggc ttg gaa gaa gtc gta cag agt				1379
Asn Ser Glu Phe Ile Tyr Met Val Gly Leu Glu Glu Val Val Gln Ser				
385	390	395	400	
gtc att gac agc caa ggc aaa agc tgt gcc tca ctt ctg cgg gtt gaa				1427
Val Ile Asp Ser Gln Gly Lys Ser Cys Ala Ser Leu Leu Arg Val Glu				
401	406	411	416	
ccc ttt gta tgt gcc cag tgc cgc aca gat ttc acc cct cac tgg aag				1475
Pro Phe Val Cys Ala Gln Cys Arg Thr Asp Phe Thr Pro His Trp Lys				
417	422	427	432	
caa gaa aag aat ggt aag att cta tgt gag cag tgt atg acc tcc aac				1523
Gln Glu Lys Asn Gly Lys Ile Leu Cys Glu Gln Cys Met Thr Ser Asn				
433	438	443	448	
cag aaa aag gct cta aaa gct gaa cac acc aac cgg ctg aaa aat gca				1571
Gln Lys Lys Ala Leu Lys Ala Glu His Thr Asn Arg Leu Lys Asn Ala				
449	454	459	464	
ttt gtg aaa gcc cta cag cag gaa cag gta aga att ctg act gct cac				1619
Phe Val Lys Ala Leu Gln Gln Glu Gln Val Arg Ile Leu Thr Ala His				
465	470	475	480	
tgg cca cct gtc cca gtt tgt ttt ttc caa agg gtc gcg cct tct agt				1667
Trp Pro Pro Val Pro Val Cys Phe Phe Gln Arg Val Ala Pro Ser Ser				
481	486	491	496	
ttg cag gag tgg ttc atg tga tc cctacaggtc cacaggttcc ctttttgtct				1720
Leu Gln Glu Trp Phe Met *				
497	502			

ccttatcatt gtgtcctatt tccatttgag cgagtattct gattaagaac atggtaaaat 1780
 ataatggctg aggttaacag aaagggacag aaagcttggg actcttggct tttccatagc 1840
 actctattct catcttcatt ttttcctaaa acaaataata gattttggtg ggaggaattt 1900
 atatttgtgc tataaatctc tttgaaacag ttatttgcag tgcgtgtttg ataagaaatg 1960
 acgaaagaaa gagtgaatta tgaagtagcc cagtgaagag tagtggttct agagtatgtg 2020
 aacatctcat gtagcagtta taggatgaga atatcttaga gaaggaaaaa tgtgttggga 2080
 aactcagatc cttttcttcc tatttcccac tccaccatc agagtc 2126

<210> 599
 <211> 3679
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (176)..(2176)

<400> 599

cttgaaacta tatggagacc ctagctggct agcgtttaaa cttaagcttg gtaccgagct 60
 cggatccact agtccagtgt ggtggaattc cgctcctttt ctccccttct agagtgttac 120
 ggtgactctt gggtcogaag gggacggacg tcctcccacg taccatttag aagaa atg 178
 Met
 1

gag caa gag cca caa aat gga gaa cct gct gaa att aag atc atc aga 226
 Glu Gln Glu Pro Gln Asn Gly Glu Pro Ala Glu Ile Lys Ile Ile Arg
 2 7 12 17

gaa gca tat aag aag gcc ttt tta ttt gtt aac aaa ggt ctg aat aca 274
 Glu Ala Tyr Lys Lys Ala Phe Leu Phe Val Asn Lys Gly Leu Asn Thr
 18 23 28 33

gat gaa tta ggt cag aag gaa gaa gca aag aac tac tat aag caa gga 322
 Asp Glu Leu Gly Gln Lys Glu Glu Ala Lys Asn Tyr Tyr Lys Gln Gly
 34 39 44 49

ata gga cac ctg ctc aga ggg atc agc att tca tca aaa gag tct gaa 370
 Ile Gly His Leu Leu Arg Gly Ile Ser Ile Ser Ser Lys Glu Ser Glu
 50 55 60 65

cac aca ggt cct ggg tgg gaa tct gct aga cag atg caa cag aaa atg 418
 His Thr Gly Pro Gly Trp Glu Ser Ala Arg Gln Met Gln Gln Lys Met
 66 71 76 81

aaa gaa act cta cag aat gta cgc acc agg ctg gaa att cta gag aag 466

Lys	Glu	Thr	Leu	Gln	Asn	Val	Arg	Thr	Arg	Leu	Glu	Ile	Leu	Glu	Lys	
82					87					92					97	
ggc	ctt	gcc	act	tct	ctg	cag	aat	gat	ctt	cag	gag	gtg	ccc	aag	tta	514
Gly	Leu	Ala	Thr	Ser	Leu	Gln	Asn	Asp	Leu	Gln	Glu	Val	Pro	Lys	Leu	
98					103					108					113	
tat	cca	gaa	ttt	cca	cct	aaa	gac	atg	tgt	gaa	aaa	tta	cca	gag	cct	562
Tyr	Pro	Glu	Phe	Pro	Pro	Lys	Asp	Met	Cys	Glu	Lys	Leu	Pro	Glu	Pro	
114					119					124					129	
cag	tct	ttt	agt	tca	gct	cct	cag	cat	gct	gaa	gta	aat	gga	aac	acc	610
Gln	Ser	Phe	Ser	Ser	Ala	Pro	Gln	His	Ala	Glu	Val	Asn	Gly	Asn	Thr	
130					135					140					145	
tca	act	cca	agt	gca	ggg	gca	gtt	gct	gca	cct	gct	tct	ctg	tct	tta	658
Ser	Thr	Pro	Ser	Ala	Gly	Ala	Val	Ala	Ala	Pro	Ala	Ser	Leu	Ser	Leu	
146					151					156					161	
cca	tca	caa	agt	tgt	cca	gca	gaa	gct	cct	cct	gct	tat	act	cct	caa	706
Pro	Ser	Gln	Ser	Cys	Pro	Ala	Glu	Ala	Pro	Pro	Ala	Tyr	Thr	Pro	Gln	
162					167					172					177	
gct	gct	gaa	ggc	cac	tac	act	gta	tcc	tat	gga	aca	gat	tct	ggg	gag	754
Ala	Ala	Glu	Gly	His	Tyr	Thr	Val	Ser	Tyr	Gly	Thr	Asp	Ser	Gly	Glu	
178					183					188					193	
ttt	tca	tca	gtt	gga	gag	gag	ttt	tat	agg	aat	cat	tct	cag	cca	ccg	802
Phe	Ser	Ser	Val	Gly	Glu	Glu	Phe	Tyr	Arg	Asn	His	Ser	Gln	Pro	Pro	
194					199					204					209	
cct	ctt	gag	acc	tta	ggg	ctg	gat	gca	gat	gaa	ttg	att	ttg	ata	cca	850
Pro	Leu	Glu	Thr	Leu	Gly	Leu	Asp	Ala	Asp	Glu	Leu	Ile	Leu	Ile	Pro	
210					215					220					225	
aat	gga	gta	cag	att	ttt	ttt	gta	aat	cct	gca	ggg	gag	gtt	agt	gca	898
Asn	Gly	Val	Gln	Ile	Phe	Phe	Val	Asn	Pro	Ala	Gly	Glu	Val	Ser	Ala	
226					231					236					241	
cct	tgc	tat	cct	ggg	tac	ctt	cga	att	gtg	agg	ttt	ttg	gat	aat	tct	946
Pro	Ser	Tyr	Pro	Gly	Tyr	Leu	Arg	Ile	Val	Arg	Phe	Leu	Asp	Asn	Ser	
242					247					252					257	
ctc	gat	acg	gtt	cta	aac	cgt	cct	ccc	ggg	ttt	ctt	cag	gtt	tgt	gac	994
Leu	Asp	Thr	Val	Leu	Asn	Arg	Pro	Pro	Gly	Phe	Leu	Gln	Val	Cys	Asp	
258					263					268					273	
tgg	tta	tat	cct	cta	gtt	cct	gat	aga	tct	ccg	gtt	ctg	aaa	tgt	act	1042
Trp	Leu	Tyr	Pro	Leu	Val	Pro	Asp	Arg	Ser	Pro	Val	Leu	Lys	Cys	Thr	
274					279					284					289	
gcg	gga	gcc	tac	atg	ttt	cct	gat	aca	atg	cta	caa	gca	gca	gga	tgc	1090
Ala	Gly	Ala	Tyr	Met	Phe	Pro	Asp	Thr	Met	Leu	Gln	Ala	Ala	Gly	Cys	
290					295					300					305	
ttt	gtg	ggg	gtc	gtc	ctg	tcc	tct	gag	tta	cca	gag	gat	gat	aga	gag	1138
Phe	Val	Gly	Val	Val	Leu	Ser	Ser	Glu	Leu	Pro	Glu	Asp	Asp	Arg	Glu	

306	311	316	321	
ctc ttt gag gat ctg tta agg caa atg tct gac ctt cgg ctc cag gcc				1186
Leu Phe Glu Asp Leu Leu Arg Gln Met Ser Asp Leu Arg Leu Gln Ala				
322	327	332	337	
aac tgg aac aga gca gaa gaa gaa aat gaa ttc caa atc cct gga aga				1234
Asn Trp Asn Arg Ala Glu Glu Glu Asn Glu Phe Gln Ile Pro Gly Arg				
338	343	348	353	
act aga ccc tcc tct gac caa cta aaa gaa gcc tct ggc act gat gtg				1282
Thr Arg Pro Ser Ser Asp Gln Leu Lys Glu Ala Ser Gly Thr Asp Val				
354	359	364	369	
aaa cag ttg gac caa ggc aat aag gat gta cgt cat aaa gga aaa cgt				1330
Lys Gln Leu Asp Gln Gly Asn Lys Asp Val Arg His Lys Gly Lys Arg				
370	375	380	385	
gga aaa agg gct aaa gat act tca agt gaa gaa gtt aac ctg agt cac				1378
Gly Lys Arg Ala Lys Asp Thr Ser Ser Glu Glu Val Asn Leu Ser His				
386	391	396	401	
att gta cca tgt gag cca gtt cca gaa gaa aag cca aaa gaa tta cct				1426
Ile Val Pro Cys Glu Pro Val Pro Glu Glu Lys Pro Lys Glu Leu Pro				
402	407	412	417	
gaa tgg agt gaa aaa gtg gct cac aac att ttg tca ggt gct tcc tgg				1474
Glu Trp Ser Glu Lys Val Ala His Asn Ile Leu Ser Gly Ala Ser Trp				
418	423	428	433	
gtg agt tgg ggt tta gtc aaa ggt gct gag att act ggt aag gca atc				1522
Val Ser Trp Gly Leu Val Lys Gly Ala Glu Ile Thr Gly Lys Ala Ile				
434	439	444	449	
cag aaa ggt gct tct aaa ctc cga gag cgg att caa cca gaa gaa aaa				1570
Gln Lys Gly Ala Ser Lys Leu Arg Glu Arg Ile Gln Pro Glu Glu Lys				
450	455	460	465	
ccc gtg gaa gtt agt cca gct gtc acc aag gga ctt tat ata gcg aag				1618
Pro Val Glu Val Ser Pro Ala Val Thr Lys Gly Leu Tyr Ile Ala Lys				
466	471	476	481	
caa gct aca gga gga gca gca aaa gtc agt cag ttc ctg gtt gat gga				1666
Gln Ala Thr Gly Gly Ala Ala Lys Val Ser Gln Phe Leu Val Asp Gly				
482	487	492	497	
gtt tgc act gta gca aat tgc gtt gga aaa gaa cta gct cca cat gtc				1714
Val Cys Thr Val Ala Asn Cys Val Gly Lys Glu Leu Ala Pro His Val				
498	503	508	513	
aag aag cat gga agc aaa ctt gtt cca gaa tct ctt aaa aaa gac aaa				1762
Lys Lys His Gly Ser Lys Leu Val Pro Glu Ser Leu Lys Lys Asp Lys				
514	519	524	529	
gat ggg aaa tct cct ctg gat ggt gct atg gtt gta gca gca agt agt				1810
Asp Gly Lys Ser Pro Leu Asp Gly Ala Met Val Val Ala Ala Ser Ser				
530	535	540	545	

gtt caa gga ttt tca act gtc tgg caa gga ttg gaa tgt gca gct aaa	1858
Val Gln Gly Phe Ser Thr Val Trp Gln Gly Leu Glu Cys Ala Ala Lys	
546 551 556 561	
tgc atc gtt aac aat gtt tca gca gaa act gta caa act gtc aga tac	1906
Cys Ile Val Asn Asn Val Ser Ala Glu Thr Val Gln Thr Val Arg Tyr	
562 567 572 577	
aaa tac gga tat aat gca gga gaa gct acc cac cat gcg gtg gat tct	1954
Lys Tyr Gly Tyr Asn Ala Gly Glu Ala Thr His His Ala Val Asp Ser	
578 583 588 593	
gcg gtc aat gtt ggc gta act gcc tac aat att aac aac att ggt atc	2002
Ala Val Asn Val Gly Val Thr Ala Tyr Asn Ile Asn Asn Ile Gly Ile	
594 599 604 609	
aaa gca atg gtg aag aaa act gca aca caa aca gga cac act ctc ctt	2050
Lys Ala Met Val Lys Lys Thr Ala Thr Gln Thr Gly His Thr Leu Leu	
610 615 620 625	
gag gac tat cag ata gtt gat aat tct cag agg gaa aat caa gaa gga	2098
Glu Asp Tyr Gln Ile Val Asp Asn Ser Gln Arg Glu Asn Gln Glu Gly	
626 631 636 641	
gca gca aat gtc aac gtg aga ggg gag aag gat gag cag acg aag gaa	2146
Ala Ala Asn Val Asn Val Arg Gly Glu Lys Asp Glu Gln Thr Lys Glu	
642 647 652 657	
gta aag gag gca aag aag aaa gat aaa tga t gaagtgtgga gaatcactta	2197
Val Lys Glu Ala Lys Lys Lys Asp Lys *	
658 663	
taccaaagcc ttatgaaatg gatgaaattt tgttaaataag gcaaagtgtg aattcctcac	2257
agattaacca gtatttttta aatgtattca ttctacaaa ttaactttca taaattttat	2317
ggcatgtctt ctatttaaaa ggaaaagaat aagtattctt gcatctggcc ttagaaatgt	2377
gaagttatat tctcaagttt atttttttcc aagtgtagct aaaatatttt tgcaggtaaa	2437
ataaagctga tagtacatgt gttgttcaaa ccttgttaaa cctaataattg aactattttt	2497
atatctgtg tctttcagaa ggcaaatagg aaactatata ttgcttaaa aattggcatt	2557
tagtaacctt aattcttttt atagaaggaa tgacttaag tattgtcccc tctttttgca	2617
ctaattgtgg attttttttag atgcttctca aaattttcag tgtgtaagct aaacaaaaac	2677
taaaactaag aattctcaaa aaaacttggt caaacaggg aaagactgat gaaaagtaaa	2737
atggactact tttgtaactt acctgtttgt taggaaatgg aatggtctct ttgatttaaa	2797
atgaataaaa atagattatt acgtcttttg tattgagact gtattgttat gagcctagga	2857
aatttgggaa catgattgta ttgtattaaa attcgaagtg attattatca gcttaattgg	2917

attaaaaaag tacttcaaga aattatittta tcatatctgc ttctgttttt ccaaaaggtt 2977
 aaaacttgta aaaaaaatat atataaaciaa ttgagttttac taatggtaaa cattttttatt 3037
 ctgggattcg gtcattggaa tttatattaa aagacaagtt attaaaaagg aaaggttcta 3097
 ttcataatca gggtaaagaa tatgaaaacc ttagacgtaa tccatgggtg ataggcatta 3157
 tggtttccac tttggcagaa ggcagactat tcacagccct atttacttac ataggctaaa 3217
 aaactatgta actaaatacc taatgggtatt taatttttgt ttattgaatt taagagattg 3277
 gtattagttt tcatagctgt agtocattct aataatttct gatcttctag tggctactta 3337
 attagacatt atttgaagct gtctgaagaa tgcactttat gaattaaaaa actgaattgc 3397
 ctgacctcgt tatcacatga gcttatatatt tgggaacaca tagaactgat ggaggctttt 3457
 cctaaggcca aggataatgt actagttggt aaaatggaaa taaaagtga gtggtaaata 3517
 gcttacagac agtctatgct ttgtttaaga aatggaatgg cacttcatat tattctcatt 3577
 tgtgggagct aaaaattaca aataatcaaa ctttaaggaga tagagagtag aatgatgggt 3637
 accagaggct gggaggcatt gaagggatgg ggagggaagt gg 3679

<210> 600
 <211> 1941
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (172)..(1143)

<400> 600
 agattccggg attggaatca aaatgctaatt ttaaaagggtc aagtgaagct gctcctcacg 60
 ttttggcgtg ccttgctctct ctctgcaggc agaagcgaac aaagaccag caagagaagg 120
 cagaggctaa gacccatccc gtatctgctc tcttgaaata attctggagt c atg cct 177
 Met Pro
 1
 gaa atg cca gag gac atg gag cag gag gaa gtt aac atc cct aat agg 225
 Glu Met Pro Glu Asp Met Glu Gln Glu Glu Val Asn Ile Pro Asn Arg
 3 8 13 18
 agg gtt ctg gtt act ggt gcc act ggg ctt ctt ggc aga gct gta cac 273
 Arg Val Leu Val Thr Gly Ala Thr Gly Leu Leu Gly Arg Ala Val His
 19 24 29 34
 aaa gaa ttt cag cag aat aat tgg cat gca gtt ggc tgt ggt ttc aga 321
 Lys Glu Phe Gln Gln Asn Asn Trp His Ala Val Gly Cys Gly Phe Arg

35	40	45	50	
aga gca aga cca aaa ttt gaa cag gtt aat ctg ttg gat tct aat gca				369
Arg Ala Arg Pro Lys Phe Glu Gln Val Asn Leu Leu Asp Ser Asn Ala				
51	56	61	66	
gtt cat cac atc att cat gat ttt cag ccc cat gtt ata gta cat tgt				417
Val His His Ile Ile His Asp Phe Gln Pro His Val Ile Val His Cys				
67	72	77	82	
gca gca gag aga aga cca gat gtt gta gaa aat cag cca gat gct gcc				465
Ala Ala Glu Arg Arg Pro Asp Val Val Glu Asn Gln Pro Asp Ala Ala				
83	88	93	98	
tct caa ctt aat gtg gat gct tct ggg aat tta gca aag gaa gca gct				513
Ser Gln Leu Asn Val Asp Ala Ser Gly Asn Leu Ala Lys Glu Ala Ala				
99	104	109	114	
gct gtt gga gca ttt ctc atc tac att agc tca gat tat gta ttt gat				561
Ala Val Gly Ala Phe Leu Ile Tyr Ile Ser Ser Asp Tyr Val Phe Asp				
115	120	125	130	
gga aca aat cca cct tac aga gag gaa gac ata cca gct ccc cta aat				609
Gly Thr Asn Pro Pro Tyr Arg Glu Glu Asp Ile Pro Ala Pro Leu Asn				
131	136	141	146	
ttg tat ggc aaa aca aaa tta gat gga gaa aag gct gtc ctg gag aac				657
Leu Tyr Gly Lys Thr Lys Leu Asp Gly Glu Lys Ala Val Leu Glu Asn				
147	152	157	162	
aat cta gga gct gct gtt ttg agg att cct att ctg tat ggg gaa gtt				705
Asn Leu Gly Ala Ala Val Leu Arg Ile Pro Ile Leu Tyr Gly Glu Val				
163	168	173	178	
gaa aag ctc gaa gaa agt gct gtg act gtt atg ttt gat aaa gtg cag				753
Glu Lys Leu Glu Glu Ser Ala Val Thr Val Met Phe Asp Lys Val Gln				
179	184	189	194	
ttc agc aac aag tca gca aac atg gat cac tgg cag cag agg ttc ccc				801
Phe Ser Asn Lys Ser Ala Asn Met Asp His Trp Gln Gln Arg Phe Pro				
195	200	205	210	
aca cat gtc aaa gat gtg gcc act gtg tgc cgg cag cta gca gag aag				849
Thr His Val Lys Asp Val Ala Thr Val Cys Arg Gln Leu Ala Glu Lys				
211	216	221	226	
aga atg ctg gat cca tca att aag gga acc ttt cac tgg tct ggc aat				897
Arg Met Leu Asp Pro Ser Ile Lys Gly Thr Phe His Trp Ser Gly Asn				
227	232	237	242	
gaa cag atg act aag tat gaa atg gca tgt gca att gca gat gcc ttc				945
Glu Gln Met Thr Lys Tyr Glu Met Ala Cys Ala Ile Ala Asp Ala Phe				
243	248	253	258	
aac ctc ccc agc agt cac tta aga cct att act gac agc cct gtc cta				993
Asn Leu Pro Ser Ser His Leu Arg Pro Ile Thr Asp Ser Pro Val Leu				
259	264	269	274	

gga gca caa cgt ccg aga aat gct cag ctt gac tgc tcc aaa ttg gag	1041
Gly Ala Gln Arg Pro Arg Asn Ala Gln Leu Asp Cys Ser Lys Leu Glu	
275 280 285 290	
acc ttg ggc att ggc caa cga aca cca ttt cga att gga atc aaa gaa	1089
Thr Leu Gly Ile Gly Gln Arg Thr Pro Phe Arg Ile Gly Ile Lys Glu	
291 296 301 306	
tca ctt tgg cct ttc ctc att gac aag aga tgg aga caa acg gtc ttt	1137
Ser Leu Trp Pro Phe Leu Ile Asp Lys Arg Trp Arg Gln Thr Val Phe	
307 312 317 322	
cat tag tttatttgtg ttgggttctt tttttttttt aaatgaaaag tatagtatgt	1193
His *	
323	
ggcacttttt aaagaacaaa ggaaatagtt ttgtatgagt actttaattg tgactcttag	1253
gatctttcag gtaaagatg ctcttgcaat agtgaaattg tctaaagaaa ctaaagggca	1313
gtcatgccct gtttgcagta atttttcttt ttatcatttt gtttgtcctg gctaaacttg	1373
gagtttgagt atagtaaatt atgaccccta aatatttgag agtcaggatg aagcagatct	1433
gctgtagact tttcagatga aattgttcat tctcgtaacc tccatatttt caggattttt	1493
gaagctgttg accttttcat gttgattatt ttaaattgtg tgaaatagta taaaaatcat	1553
tggtgttcat tatttgcttt gcctgagctc agatcaaaat gtttgaagaa aggaacttta	1613
tttttgcaag ttacgtacag tttttatgct tgagatatatt caacatgtta tgtatatttg	1673
aacttctaca gcttgatgcc tcttgctttt atagcagttt atggggagca cttgaaagag	1733
cgtgtgtaca tgtatttttt ttctaggcaa acattgaatg caaacgtgta tttttttaat	1793
ataaatatat aactgtcctt ttcattccat gttgccgcta agtgatatatt catatgtgtg	1853
gttataactca taataatggg ccttgtaagt cttttcacca ttcattgaata ataataaata	1913
tgtactgctg gcatgtaaaa aaaaaaaaa	1941

<210> 601
 <211> 790
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (49)..(648)

<400> 601
 atttggccct cgaggccaag aattcggcac gagggataag gcgctgtc atg gag gac 57

Met Glu Asp

1

gcc gcc gcg ccg ggg cgg acc gag ggg gtc ctt gaa agg caa gga gcg Ala Ala Ala Pro Gly Arg Thr Glu Gly Val Leu Glu Arg Gln Gly Ala 4 9 14 19	105
ccg cca gct gca ggc cag gga gga gcc ctg gtg gag ctc acc ccg acc Pro Pro Ala Ala Gly Gln Gly Gly Ala Leu Val Glu Leu Thr Pro Thr 20 25 30 35	153
ccc ggc ggc ctg gcc ctg gtg agc ccc tac cac acc cac cgg gcc ggg Pro Gly Gly Leu Ala Leu Val Ser Pro Tyr His Thr His Arg Ala Gly 36 41 46 51	201
gac ccc tta gac ctc gtg gcg ctc gca gag cag gtg cag aag gct gat Asp Pro Leu Asp Leu Val Ala Leu Ala Glu Gln Val Gln Lys Ala Asp 52 57 62 67	249
gaa ttc atc cga gca aat gcc acc aac aag ctg aca gtc ata gct gag Glu Phe Ile Arg Ala Asn Ala Thr Asn Lys Leu Thr Val Ile Ala Glu 68 73 78 83	297
caa atc caa cat ttg caa gaa caa gcc agg aag gta ctg gaa gat gct Gln Ile Gln His Leu Gln Glu Gln Ala Arg Lys Val Leu Glu Asp Ala 84 89 94 99	345
cac aga gat gcc aac ctg cac cat gta gct tgt aat ata gtg aaa aaa His Arg Asp Ala Asn Leu His His Val Ala Cys Asn Ile Val Lys Lys 100 105 110 115	393
cct ggc aac att tac tat ctc tat aaa cgg gag agt ggt cag cag tat Pro Gly Asn Ile Tyr Tyr Leu Tyr Lys Arg Glu Ser Gly Gln Gln Tyr 116 121 126 131	441
ttt tcc atc att tct cca aag gaa tgg ggg aca agt tgt cca cat gac Phe Ser Ile Ile Ser Pro Lys Glu Trp Gly Thr Ser Cys Pro His Asp 132 137 142 147	489
ttc ctt ggt gcc tac aaa cta cag cat gac ttg tcc tgg act ccg tat Phe Leu Gly Ala Tyr Lys Leu Gln His Asp Leu Ser Trp Thr Pro Tyr 148 153 158 163	537
gag gac att gag aag caa gat gct aaa atc agc atg atg gac acg ttg Glu Asp Ile Glu Lys Gln Asp Ala Lys Ile Ser Met Met Asp Thr Leu 164 169 174 179	585
cta agc cag tca gtg gcc ctg cct ccg tgc act gaa ccc aac ttc cag Leu Ser Gln Ser Val Ala Leu Pro Pro Cys Thr Glu Pro Asn Phe Gln 180 185 190 195	633
gga ctg act cac tga gagggtgctt tgacaaacag ctctcacagg acctggctgt Gly Leu Thr His * 196	688
caacctcctt gttgccccca ctgttgccctt gagaattgaa gacatgtagg tgactcacia	748

acttcttggga aagagaccct gtgtgaatgt aaaaaaaaaa aa

790

<210> 602
<211> 1006
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (365)..(835)

<400> 602

gtaccggtcc ggaattcccg ggtcgaccca cgcgtccgtt ccctgctcca agtcttctgg	60
gcgctccagg ttctgtgatg tcccacggga gccccggacc cctggtctct gtaactgtgg	120
ggtgagggaa ggtgcgacct gaatgttctc cctgacctcc tagtttccta gtcttgcaacg	180
ttctattctt ccagggtca cattcaccac acccaccac tcctgtcatt cccttccctt	240
tcaccccttc tgtctcattt agctccactt tgaaaaaact gtggcatcaa aggtccctgg	300
gtagtccctt cccaaatggg ccgctgcctg gaactctaaa tgccaccctg gagcgggagc	360
cgca atg gca cgg cag cac gcc cgg acc ttg tgg tac gac agg ccc agg	409
Met Ala Arg Gln His Ala Arg Thr Leu Trp Tyr Asp Arg Pro Arg	
1 5 10	
tat gtg ttc atg gag ttt tgt gtt gag gac agc acc gat gtc cac gtg	457
Tyr Val Phe Met Glu Phe Cys Val Glu Asp Ser Thr Asp Val His Val	
16 21 26 31	
ctt att gag gat cac cgc att gtg ttc agc tgc aag aat gcc gat gga	505
Leu Ile Glu Asp His Arg Ile Val Phe Ser Cys Lys Asn Ala Asp Gly	
32 37 42 47	
gtg gag ttg tac aat gag att gag ttc tat gcc aaa gtg aac tcc aag	553
Val Glu Leu Tyr Asn Glu Ile Glu Phe Tyr Ala Lys Val Asn Ser Lys	
48 53 58 63	
gac tcc cag gat aag cgc tct tcc cgc tct att act tgt ttt gtg aga	601
Asp Ser Gln Asp Lys Arg Ser Ser Arg Ser Ile Thr Cys Phe Val Arg	
64 69 74 79	
aaa tgg aag gaa aag gtg gcc tgg ccg cgg ctt acc aag gag gat atc	649
Lys Trp Lys Glu Lys Val Ala Trp Pro Arg Leu Thr Lys Glu Asp Ile	
80 85 90 95	
aag cca gtg tgg ctg tct gtg gac ttt gat aac tgg aga gac tgg gaa	697
Lys Pro Val Trp Leu Ser Val Asp Phe Asp Asn Trp Arg Asp Trp Glu	
96 101 106 111	
ggg gat gaa gag atg gag ctg gct cat gtg gaa cat tat gca gag ctt	745
Gly Asp Glu Glu Met Glu Leu Ala His Val Glu His Tyr Ala Glu Leu	

112	117	122	127	
ttg aag aag gtc agc acc aag aga cct cca cct gcc atg gat gat ttg				793
Leu Lys Lys Val Ser Thr Lys Arg Pro Pro Pro Ala Met Asp Asp Leu				
128	133	138	143	
gat gat gat tct gac agt gct gat gat gca aca agt aat taa ctttctg				842
Asp Asp Asp Ser Asp Ser Ala Asp Asp Ala Thr Ser Asn *				
144	149	154		
tgacgcaaag ctgggaaggc agctgtggct attttccagt tgttctagaa agctagcgcc				902
taggccttaa tagggatgag aggaaagaat attattgaaa ttatatacat tgattcactt				962
attcagtgtgta gagcctgtat tctgaagaag tttgacaaaa cggt				1006

<210> 603
 <211> 1752
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (104)..(1195)

<400> 603	
catcgactca ctatagggaa tttggccctc gaggaagaa ttcggcacga gggtagggaa	60
actgtgaggg cggcaccgga agtggcgagc agtctgcgcg cgg atg gcc gca gcg	115
Met Ala Ala Ala	
1	
gcg atg gcg gca gcg gca ggt gga ggg gct ggc gcg gcc cgc tcc ctc	163
Ala Met Ala Ala Ala Ala Gly Gly Gly Ala Gly Ala Ala Arg Ser Leu	
5 10 15 20	
tgc cgc ttc cga ggc tgc ctg gct ggc gcg ctg ctc ggg gac tgc gtg	211
Ser Arg Phe Arg Gly Cys Leu Ala Gly Ala Leu Leu Gly Asp Cys Val	
21 26 31 36	
ggc tcc ttc tac gag gcc cac gac acc gtc gac ctg acg tca gtc ctg	259
Gly Ser Phe Tyr Glu Ala His Asp Thr Val Asp Leu Thr Ser Val Leu	
37 42 47 52	
cgt cat gtc cag agt ctg gag ccg gac ccc ggc acg ccc ggg agt gag	307
Arg His Val Gln Ser Leu Glu Pro Asp Pro Gly Thr Pro Gly Ser Glu	
53 58 63 68	
cgg aca gaa gcc ttg tac tac aca gat gac aca gcc atg gcc agg gcc	355
Arg Thr Glu Ala Leu Tyr Tyr Thr Asp Asp Thr Ala Met Ala Arg Ala	
69 74 79 84	
ctg gtg cag tcc ctg cta gcc aag gag gcc ttt gac gag gtg gac atg	403
Leu Val Gln Ser Leu Leu Ala Lys Glu Ala Phe Asp Glu Val Asp Met	

85	90	95	100	
gct cac aga ttt gct cag gag tac aag aaa gac cct gac agg ggc tat				451
Ala His Arg Phe Ala Gln Glu Tyr Lys Lys Asp Pro Asp Arg Gly Tyr				
101	106	111	116	
ggg gct gga gta gtc act gtc ttc aag aag ctc ctg aac ccc aaa tgt				499
Gly Ala Gly Val Val Thr Val Phe Lys Lys Leu Leu Asn Pro Lys Cys				
117	122	127	132	
cgc gat gtc ttt gag cct gcc cgg gcc cag ttt aac ggg aaa ggc tcc				547
Arg Asp Val Phe Glu Pro Ala Arg Ala Gln Phe Asn Gly Lys Gly Ser				
133	138	143	148	
tat ggc aat gga ggt gcc atg cgg gtg gct ggc atc tcc ctg gcc tat				595
Tyr Gly Asn Gly Gly Ala Met Arg Val Ala Gly Ile Ser Leu Ala Tyr				
149	154	159	164	
agc agt gtc cag gat gtg cag aag ttt gcc cgg ctc tcg gcc cag ctg				643
Ser Ser Val Gln Asp Val Gln Lys Phe Ala Arg Leu Ser Ala Gln Leu				
165	170	175	180	
aca cac gcc tcc tcc ctg ggt tac aat ggc gcc atc ctg cag gcc ctg				691
Thr His Ala Ser Ser Leu Gly Tyr Asn Gly Ala Ile Leu Gln Ala Leu				
181	186	191	196	
gct gtg cac ctg gcc ttg cag ggc gag tct tcc agc aag cac ttt ctc				739
Ala Val His Leu Ala Leu Gln Gly Glu Ser Ser Ser Lys His Phe Leu				
197	202	207	212	
aag caa ctc ctg ggc cac atg gag gat ctg gag ggt gat gcc cag tcc				787
Lys Gln Leu Leu Gly His Met Glu Asp Leu Glu Gly Asp Ala Gln Ser				
213	218	223	228	
gtc ttg gat gcc agg gag ttg ggc atg gag gag cgt cca tac tcc agc				835
Val Leu Asp Ala Arg Glu Leu Gly Met Glu Glu Arg Pro Tyr Ser Ser				
229	234	239	244	
cgc ctg aag aag att gga gag ctt cta gac cag gca tcg gtg acc agg				883
Arg Leu Lys Lys Ile Gly Glu Leu Leu Asp Gln Ala Ser Val Thr Arg				
245	250	255	260	
gag gaa gtg gtg tct gag cta ggg aat ggc att gct gcc ttt gag tcg				931
Glu Glu Val Val Ser Glu Leu Gly Asn Gly Ile Ala Ala Phe Glu Ser				
261	266	271	276	
gta ccc acc gcc atc tac tgc ttc cta cgc tgc atg gag cca gac cct				979
Val Pro Thr Ala Ile Tyr Cys Phe Leu Arg Cys Met Glu Pro Asp Pro				
277	282	287	292	
gag atc cct tct gcc ttc aat agc ctc caa agg act ctc att tat tcc				1027
Glu Ile Pro Ser Ala Phe Asn Ser Leu Gln Arg Thr Leu Ile Tyr Ser				
293	298	303	308	
atc tca ctt ggt ggg gac aca gac acc att gcc acc atg gct ggg gcc				1075
Ile Ser Leu Gly Gly Asp Thr Asp Thr Ile Ala Thr Met Ala Gly Ala				
309	314	319	324	

cg	g	g	g	t	a	c	g	a	a	c	c	t	g	t	g	a	a	g	a	t	g		256
Arg	Glu	Glu	Tyr	Glu	Glu	Tyr	Gln	Lys	Gln	Leu	Val	Glu	Glu	Lys	Met								
41					46					51					56								
g	a	g	c	a	g	t	t	c	a	c	a	g	a	a	g	g	c	a	g	c	g	g	304
Glu	Arg	Asp	Ala	Gln	Phe	Thr	Gln	Arg	Lys	Ala	Glu	Arg	Ala	Thr	Leu								
57					62					67					72								
c	g	a	c	a	c	a	a	a	t	a	c	c	a	a	a	g	a	a	g	a	a	g	352
Arg	Ser	His	Phe	Arg	Asp	Lys	Tyr	Arg	Leu	Pro	Lys	Asn	Glu	Thr	Asp								
73					78					83					88								
g	a	g	c	a	g	a	t	g	g	c	a	g	g	g	a	g	a	c	t	g	c	c	400
Glu	Ser	Gln	Ile	Gln	Met	Ala	Gly	Gly	Asp	Val	Glu	Leu	Pro	Arg	Glu								
89					94					99					104								
c	t	g	g	c	a	a	a	g	a	t	a	c	g	a	g	a	a	a	g	a	a	g	448
Leu	Ala	Lys	Met	Ile	Glu	Glu	Asp	Thr	Glu	Glu	Glu	Glu	Glu	Glu	Lys	Ala							
105					110					115					120								
t	c	a	g	t	c	c	t	t	g	g	c	a	a	c	t	g	g	c	t	c	a		496
Ser	Val	Leu	Gly	Gln	Leu	Ala	Ser	Leu	Pro	Gly	Leu	Asn	Leu	Gly	Ser								
121					126					131					136								
c	t	c	a	a	g	a	a	g	g	c	a	c	a	c	t	g	g	a	t	c	t	c	544
Leu	Lys	Asp	Lys	Ala	Gln	Ala	Thr	Leu	Gly	Asp	Leu	Lys	Gln	Ser	Ala								
137					142					147					152								
g	a	a	g	t	g	t	c	a	c	g	t	c	a	a	a	a	a	a	a	a	a	a	597
Glu	Lys	Cys	His	Val	Met	*																	
153					158																		
c	c	c	a	t	a	g	a	g	t	g	t	c	a	a	c	t	t	c	a	c	c	a	657
tt	c	c	t	t	g	c	c	c	a	a	a	c	c	t	t	c	c	a	c	c	a	a	717
g	t	t	t	t	c	c	t	c	t	t	c	a	c	c	c	a	a	a	a	a	a	a	777
c	c	a	c	a	g	c	t	c	c	c	a	a	a	a	a	a	a	a	a	a	a	a	837
c	c	a	c	a	g	c	t	c	c	c	a	a	a	a	a	a	a	a	a	a	a	a	897
a	c	c	c	t	g	g	c	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	957
g	a	g	g	c	c	a	g	t	t	c	c	c	c	c	c	c	c	c	c	c	c	c	1013

<210> 605
 <211> 1199
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (410)..(1072)

<400> 605

```
ccggtctctg ttgccatggc aacacagggt tatttacacc ataccttga tgcaagggtg 60
ggcaggggttg cggggaggga gagggagtac agtgatgtca agagcacagg gtccttggcc 120
ttcagaccag tcctcagcta cattgctgca ggcaaggccg gcaccagccc ccaggctgag 180
tcattgggttaa aggccaaagag ctgaaacaag agtttctcat gcaccaggca catttataaa 240
gcaacccatc cacctggagc ccaaaactgg gttgacagat tccagagagg caaggtcctt 300
gatgacccca taactccac tgccccttta acaagggact cttaaacacct tatgataacc 360
caaatcctaa acactgttgc ctctgccgcc tcttcagac acagaaggc atg atc 415
Met Ile
1
ctg ctg aac act ggc ctc gag gga act gtg gct gaa aac ccc gtg ccc 463
Leu Leu Asn Thr Gly Leu Glu Gly Thr Val Ala Glu Asn Pro Val Pro
3 8 13 18
att gtt cat act cca agt ggc aac atc ctg acg ctg gag tcc tgc ctg 511
Ile Val His Thr Pro Ser Gly Asn Ile Leu Thr Leu Glu Ser Cys Leu
19 24 29 34
cag cag ctg gcc aca cat ccc gga cac tgg ggc atc cat ttg caa ata 559
Gln Gln Leu Ala Thr His Pro Gly His Trp Gly Ile His Leu Gln Ile
35 40 45 50
gcg gag ccc gca gcc ctc cgg cca tcc ctg gcc ttg ctg gca cgc ctc 607
Ala Glu Pro Ala Ala Leu Arg Pro Ser Leu Ala Leu Leu Ala Arg Leu
51 56 61 66
tcc agc ctt ggc ctc ttg cat tgg cct gtg tgg gtt ggg gcc aaa atc 655
Ser Ser Leu Gly Leu Leu His Trp Pro Val Trp Val Gly Ala Lys Ile
67 72 77 82
tcc cac ggg agt ttt tgc gtc ccc ggc cat gtg gct ggc aga gag ctg 703
Ser His Gly Ser Phe Ser Val Pro Gly His Val Ala Gly Arg Glu Leu
83 88 93 98
ctt aca gct gtg gct gag gtc ttc ccc cac gtg act gtg gca cca ggc 751
Leu Thr Ala Val Ala Glu Val Phe Pro His Val Thr Val Ala Pro Gly
99 104 109 114
tgg cct gag gag gtg ctg ggc agt ggc tac agg gaa cag ctg ctc aca 799
Trp Pro Glu Glu Val Leu Gly Ser Gly Tyr Arg Glu Gln Leu Leu Thr
115 120 125 130
gat atg cta gag ttg tgc cag ggg ctc tgg caa cct gtg tcc ttc cag 847
Asp Met Leu Glu Leu Cys Gln Gly Leu Trp Gln Pro Val Ser Phe Gln
131 136 141 146
atg cag gcc atg ctg ctg ggc cac agc aca gct gga gcc ata ggc agg 895
Met Gln Ala Met Leu Leu Gly His Ser Thr Ala Gly Ala Ile Gly Arg
```

ctg ctg gca tcc tcc ccc cgg gcc acc gtc aca gtg gag cac aac cca 943
 Leu Leu Ala Ser Ser Pro Arg Ala Thr Val Thr Val Glu His Asn Pro
 163 168 173 178

gct ggg ggc gac tat gcc tct gtg agg aca gca ttg ctg gca gct agg 991
 Ala Gly Gly Asp Tyr Ala Ser Val Arg Thr Ala Leu Leu Ala Ala Arg
 179 184 189 194

gct gtg gac agg acc cga gtc tac tac agg cta ccc cag ggc tac cac 1039
 Ala Val Asp Arg Thr Arg Val Tyr Tyr Arg Leu Pro Gln Gly Tyr His
 195 200 205 210

aag gac ttg ctg gct cat gtt ggt aga aac tga gcacccag ggggtggtggg 1090
 Lys Asp Leu Leu Ala His Val Gly Arg Asn *
 211 216 221

tcagcggacc tcagggcgga ggcttccac ggggaggcag gaagaaataa aggtcgaatt 1150

ccaccacact ggactagtgg atccgagctc ggtaccaagc ttaagtttg 1199

<210> 606
 <211> 4721
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (162)..(2018)

<220>
 <221> misc_feature
 <222> (1)...(4721)
 <223> n = a,t,c or g

<400> 606
 agtggcactg agctgaagcg tcgcgacnng cnnngaantn ccgggtcgac ccacgcgtcc 60

gcaactgtca aggcattgtg aatacaccag cattcatatt actacattct aacagagtgg 120

gggaaagagg gaagacagaa gataaataat aaacatagta g atg gct ttt cgc 173
 Met Ala Phe Arg
 1

act gaa atg gga cta tat tat tcc tat ttc aag act att gtg gaa gca 221
 Thr Glu Met Gly Leu Tyr Tyr Ser Tyr Phe Lys Thr Ile Val Glu Ala
 5 10 15 20

ccc tca ttt ttg aat gga gta tgg atg att atg aat gat aaa ctg act 269
 Pro Ser Phe Leu Asn Gly Val Trp Met Ile Met Asn Asp Lys Leu Thr
 21 26 31 36

gaa tac ccc ctt gtc att aat aca tta aaa aga ttc aat ctt tac cct 317

Glu Tyr Pro Leu Val Ile Asn Thr Leu Lys Arg Phe Asn Leu Tyr Pro	
37 42 47 52	
gag gta att ttg gcc agt tgg tac cgg att tat acc aaa ata atg gac	365
Glu Val Ile Leu Ala Ser Trp Tyr Arg Ile Tyr Thr Lys Ile Met Asp	
53 58 63 68	
ttg att ggt att caa acc aag ata tgt tgg acg gtt acc aga gga gaa	413
Leu Ile Gly Ile Gln Thr Lys Ile Cys Trp Thr Val Thr Arg Gly Glu	
69 74 79 84	
gga ctc agt cct att gaa agc tgt gaa gga ttg gga gat cct gct tgc	461
Gly Leu Ser Pro Ile Glu Ser Cys Glu Gly Leu Gly Asp Pro Ala Cys	
85 90 95 100	
ttt tat gtt gct gta att ttt att tta aat gga cta atg atg gca tta	509
Phe Tyr Val Ala Val Ile Phe Ile Leu Asn Gly Leu Met Met Ala Leu	
101 106 111 116	
ttc ttc ata tat ggc aca tat tta agt ggc agc cga tta gga ggc ctg	557
Phe Phe Ile Tyr Gly Thr Tyr Leu Ser Gly Ser Arg Leu Gly Gly Leu	
117 122 127 132	
gtt aca gtg ttg tgc ttc ttt ttc aat cat gga gag tgt acc cgt gta	605
Val Thr Val Leu Cys Phe Phe Phe Asn His Gly Glu Cys Thr Arg Val	
133 138 143 148	
atg tgg aca cca cct ctc cgt gaa agc ttc tca tat cca ttt ctt gtt	653
Met Trp Thr Pro Pro Leu Arg Glu Ser Phe Ser Tyr Pro Phe Leu Val	
149 154 159 164	
ctt cag atg ttg cta gtg act cat att ctc agg gct aca aaa ctt tat	701
Leu Gln Met Leu Leu Val Thr His Ile Leu Arg Ala Thr Lys Leu Tyr	
165 170 175 180	
aga gga agc ttg att gca ctc tgc att tcc aat gta ttt ttc atg ctt	749
Arg Gly Ser Leu Ile Ala Leu Cys Ile Ser Asn Val Phe Phe Met Leu	
181 186 191 196	
cct tgg cag ttt gct cag ttt gta ctt ctt act cag att gca tca tta	797
Pro Trp Gln Phe Ala Gln Phe Val Leu Leu Thr Gln Ile Ala Ser Leu	
197 202 207 212	
ttt gca gta tat gtt gtc ggg tac att gat ata tgt aaa tta cgg aag	845
Phe Ala Val Tyr Val Val Gly Tyr Ile Asp Ile Cys Lys Leu Arg Lys	
213 218 223 228	
atc att tat ata cac atg att tct ctt gca ctt tgt ttt gtt ttg atg	893
Ile Ile Tyr Ile His Met Ile Ser Leu Ala Leu Cys Phe Val Leu Met	
229 234 239 244	
ttt ggg aac tca atg tta tta act tct tat tat gct tct tct ttg gta	941
Phe Gly Asn Ser Met Leu Leu Thr Ser Tyr Tyr Ala Ser Ser Leu Val	
245 250 255 260	
att att tgg ggt att ctg gca atg aaa cca cat ttc ctg aaa ata aat	989
Ile Ile Trp Gly Ile Leu Ala Met Lys Pro His Phe Leu Lys Ile Asn	

261	266	271	276	
gta tct gaa ctt agt tta tgg gtt att caa gga tgt ttt tgg tta ttt				1037
Val Ser Glu Leu Ser Leu Trp Val Ile Gln Gly Cys Phe Trp Leu Phe				
277	282	287	292	
gga act gtc ata ctt aaa tac ttg aca tct aaa att ttt ggt att gca				1085
Gly Thr Val Ile Leu Lys Tyr Leu Thr Ser Lys Ile Phe Gly Ile Ala				
293	298	303	308	
gat gac gct cat att ggc aac tta cta aca tca aaa ttc ttt agt tat				1133
Asp Asp Ala His Ile Gly Asn Leu Leu Thr Ser Lys Phe Phe Ser Tyr				
309	314	319	324	
aag gat ttt gat act tta ttg tat acc tgt gca gcg gag ttt gac ttt				1181
Lys Asp Phe Asp Thr Leu Leu Tyr Thr Cys Ala Ala Glu Phe Asp Phe				
325	330	335	340	
atg gaa aaa gag act cca ctg aga tac aca aag aca tta ttg ctt cca				1229
Met Glu Lys Glu Thr Pro Leu Arg Tyr Thr Lys Thr Leu Leu Leu Pro				
341	346	351	356	
gtt gtt ctt gta gtg ttt gtt gct att gtt aga aag att att agt gat				1277
Val Val Leu Val Val Phe Val Ala Ile Val Arg Lys Ile Ile Ser Asp				
357	362	367	372	
atg tgg ggt gtc tta gct aaa caa cag aca cat gta aga aaa cac cag				1325
Met Trp Gly Val Leu Ala Lys Gln Gln Thr His Val Arg Lys His Gln				
373	378	383	388	
ttt gat cat gga gag ctg gtt tac cat gca ttg caa ttg tta gca tat				1373
Phe Asp His Gly Glu Leu Val Tyr His Ala Leu Gln Leu Leu Ala Tyr				
389	394	399	404	
aca gcc ctt ggt att tta att atg aga cta aaa ctc ttc ttg aca cca				1421
Thr Ala Leu Gly Ile Leu Ile Met Arg Leu Lys Leu Phe Leu Thr Pro				
405	410	415	420	
cac atg tgt gtt atg gca tca ctg atc tgc tca aga cag cta ttt gga				1469
His Met Cys Val Met Ala Ser Leu Ile Cys Ser Arg Gln Leu Phe Gly				
421	426	431	436	
tgg ctc ttt tgc aaa gta cat cct ggt gct att gtg ttt gct ata tta				1517
Trp Leu Phe Cys Lys Val His Pro Gly Ala Ile Val Phe Ala Ile Leu				
437	442	447	452	
gca gca atg tca ata caa ggt tca gca aat ctg caa acc cag tgg aat				1565
Ala Ala Met Ser Ile Gln Gly Ser Ala Asn Leu Gln Thr Gln Trp Asn				
453	458	463	468	
att gta ggg gag ttc agc aat ttg ccc caa gaa gaa ctt ata gaa tgg				1613
Ile Val Gly Glu Phe Ser Asn Leu Pro Gln Glu Glu Leu Ile Glu Trp				
469	474	479	484	
atc aaa tat agt act aaa cca gat gca gtg ttt gcg ggt gcc atg ccc				1661
Ile Lys Tyr Ser Thr Lys Pro Asp Ala Val Phe Ala Gly Ala Met Pro				
485	490	495	500	

acg atg gca agt gtt aag ctc tct gca ctt cgg ccc att gtg aat cat	1709
Thr Met Ala Ser Val Lys Leu Ser Ala Leu Arg Pro Ile Val Asn His	
501 506 511 516	
cca cat tat gaa gac gca ggc ttg aga gcc aga aca aaa ata gta tac	1757
Pro His Tyr Glu Asp Ala Gly Leu Arg Ala Arg Thr Lys Ile Val Tyr	
517 522 527 532	
tca atg tat agt cgg aaa gca gcc gaa gaa gtg aag cga gaa ctg ata	1805
Ser Met Tyr Ser Arg Lys Ala Ala Glu Glu Val Lys Arg Glu Leu Ile	
533 538 543 548	
aag tta aaa gtg aac tat tac att cta gaa gag tca ³ tgg tgt gta aga	1853
Lys Leu Lys Val Asn Tyr Tyr Ile Leu Glu Glu Ser Trp Cys Val Arg	
549 554 559 564	
aga tcc aag cct ggt tgc agt atg cct gaa att tgg gat gta gaa gat	1901
Arg Ser Lys Pro Gly Cys Ser Met Pro Glu Ile Trp Asp Val Glu Asp	
565 570 575 580	
cct gcc aat gct ggg aaa act ccc tta tgt aac ctc ttg gtg aag gat	1949
Pro Ala Asn Ala Gly Lys Thr Pro Leu Cys Asn Leu Leu Val Lys Asp	
581 586 591 596	
tcc aaa cct cac ttc acc act gta ttc cag aac agt gtt tac aaa gtc	1997
Ser Lys Pro His Phe Thr Thr Val Phe Gln Asn Ser Val Tyr Lys Val	
597 602 607 612	
cta gaa gtt gta aaa gaa tga ct gctacatgac ctgctgccta cggagaacta	2050
Leu Glu Val Val Lys Glu *	
613 618	
catctgtaat gggttttaatg ttttgctaag tcatgtgttg ttcatatccc aaaaactttt	2110
ataggtaact gttttcaa at agaaaacggtt ttatttggtc aatttgaatg tcattcta at	2170
tataaaaatg acttacacct ttatcaattg gttactat t caatgcaccc tttaaaat t	2230
gctatgcaaa tgagtatatg cttgtacttg actttaatat ttgtgctaaa gtgagcaa ag	2290
ctacctgtat aaagaaaaca cagtgggttg tgacaaggat gacatgaaaa tacaggacaa	2350
ttctgacaat gtaggggctg at ttttatagt gtaagaacta ttaatgcccc ttgcttct t	2410
tttctgcctc ttgctcttgt cttttggaca tttcagtgat tgtaagttct tcgggtcatgt	2470
cagccccgtg catcaacttg agttacagta gatggggcag acatggagtg tttgctatat	2530
agaactatct gtttggttta cttccttggtg cgctttttgt tctctgttct cttgtta atg	2590
aagcttttcc tgcccattat taatccaaac tcttggaacct tgtgggttagg aaattccctt	2650
aacttccagc catatggcat tctcgtgtct ctttctctct ctctcttgc tctctctctc	2710
tcctcttccc catat tttct gtcaaataag tactgtttac tcatttagtt gcttatca ag	2770

tacttattct tggtttttaa aaaaattaat ggtaactgta tttttctcat ttttagcatt 2830
 attcaaagt ttatatatta atacctttaa accactttaa agttttttca tgtttaatta 2890
 tagttttaag aaaaactatt ttgaacaacc ccaaatatag tgcactctaga aactaatgta 2950
 tatttgatta gacatcattt atagtggaa agtagactgt agtacatggg aatttttctt 3010
 ttactattaa gatacaataa aacatgacta attttgctgt caaaaatgta aagaataatg 3070
 ataaatggag tttttatatt ttacttttaa gattgcctgt ctttaataag acaaagcctt 3130
 aagccttatg ttataatttt ggttctaaaa accatcattt cagtataagg aataagtata 3190
 tttcgtcctc ctctttagtt tttttcttcc tatttatatt tattttgaaa aatttctaca 3250
 ctttctttga attccttgta tgaatttttg tttcttagaa gtttaattgt gtgaaatgag 3310
 attcttcaaa acgatgaaac ctcatagctc tgagaaaagg ttttaggggt ttaaattcta 3370
 agcaaagcgt gactatggct gacagactac acatttaatt atacagcttc tctttcttaa 3430
 ccacaggcag attaacctca ttgtggattg tccttcagac cttagtcctc aggcattggg 3490
 tctggtgccc actcctggaa gccgctgttc cttttctacc ttcttaccag agcccaaggg 3550
 caggcctggg cccggggaag cagcagcttg ctgacataag tcagctgcaa aggctgagga 3610
 gtgtgcccctc agagaagcac cgccccccag tcttgtgcca gcgcctagag ccgcagctcc 3670
 cagggatgct cttccctgg aggcagccca ggagagggac tctggcagcg ttcttcagat 3730
 ttgtggccac tgtttctcat ttgctgggtg actgttttta tttcttaggc ttttgctagt 3790
 tttagaaaat aggaagcag cccttgattt gtggattaaa agcaacattt gagcgatgat 3850
 gcacaacagt ccaggaaaat gggcgggtga cacttgaggc tgaggatggg agttgacatg 3910
 agcagggaga gggagggtgc cgctgcttat ctgtgattgt tgctcacctg agtgtggctg 3970
 attgtgtaca tccagcagtt acaattttta aaaattatac ttttacattt attttatatt 4030
 tttctcacc cagtaattt cttcccaaag aagttcacat gtaataagta gaaattctgt 4090
 ataggaaaaa agcattaaaa atactattat aactgcttca tttgctggga accattaaaa 4150
 gtaatataaa ttagcttttt ccagaaggat cttttttag cagtgtttat gaatgtaacc 4210
 ccagcaaaa tatggctata tattagggga gccagtttg agcagaggcc tgaaggctcc 4270
 tgctatgcag ccgtggccac agctcgcagc ccaagcactg tggagcatcc acacctttga 4330
 tggcaatgca gattggtagc aggttcata ggcgtacaaa acagtattaa agctcagtgt 4390
 tttgcatatt gttagcattt acaaataatt ttgctttagt atgaggaaag taaggatggg 4450
 caaagaagcg atcaaaatag ctattgctac aacattttcg aaaacaaagt tggggctgta 4510

tttcttttaaa aagataagcc tctaaaaatg cttggcaaaa aaaatatagt gttaaaatag 4570
gccagtgata ttaatgagaa aatgaaagta tgtatcagga ataaagtgat attgcatagg 4630
agtattgtat ttttatgaat tttatgccag ttgtttacat gtactatata tgttaaatta 4690
aaaaaaatca tgagaaatga aaaaaaaaaa a 4721

<210> 607
<211> 2065
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (171)..(977)

<400> 607
ggaagaaaaa gcacgtcatt acttggagac cttcagagcc aagctattaa gtttgtaaatt 60
aggtttcatg aagagagaaa aaccaagctc agcctcctct tagacaatga gcgctggaag 120
caagcagatg tctcctgcag aatttcagga tcttgttgat tctctgtcag atg gga 176
Met Gly
1
aga ttg ctt tac ctg aaa aaa aaa tca gga gcc aca gaa gaa agg aaa 224
Arg Leu Leu Tyr Leu Lys Lys Lys Ser Gly Ala Thr Glu Glu Arg Lys
3 8 13 18
cca gct gaa gtt ctt att gtc gag gga caa cag tat gca gtt gtt gga 272
Pro Ala Glu Val Leu Ile Val Glu Gly Gln Gln Tyr Ala Val Val Gly
19 24 29 34
acc gta ttg ctg tta ata aga att atc ctt gaa tat tgc cag tgt gtg 320
Thr Val Leu Leu Leu Ile Arg Ile Ile Leu Glu Tyr Cys Gln Cys Val
35 40 45 50
gat aac atc cca tct gtt act act gac atg ctt act cgt ctg tca gat 368
Asp Asn Ile Pro Ser Val Thr Thr Asp Met Leu Thr Arg Leu Ser Asp
51 56 61 66
tta ttg aag tac ttc aat tca aga agt tgc cag tta gtt ctt gga gct 416
Leu Leu Lys Tyr Phe Asn Ser Arg Ser Cys Gln Leu Val Leu Gly Ala
67 72 77 82
ggt gca ctg caa gtt gtt gga cta aaa acg ata act aca aaa aat ttg 464
Gly Ala Leu Gln Val Val Gly Leu Lys Thr Ile Thr Thr Lys Asn Leu
83 88 93 98
gct ctt tct tca cga tgt ttg cag tta att gtg cac tac att cct gtg 512
Ala Leu Ser Ser Arg Cys Leu Gln Leu Ile Val His Tyr Ile Pro Val
99 104 109 114

atc cgg gct cat ttt gaa gct cga cta cca cct aag caa tat agc atg	560
Ile Arg Ala His Phe Glu Ala Arg Leu Pro Pro Lys Gln Tyr Ser Met	
115 120 125 130	
ctt agg cat ttt gat cat atc act aag gac tac cat gat cac ata gct	608
Leu Arg His Phe Asp His Ile Thr Lys Asp Tyr His Asp His Ile Ala	
131 136 141 146	
gaa ata tca gct aag ctt gta gcg ata atg gat agc tta ttt gac aag	656
Glu Ile Ser Ala Lys Leu Val Ala Ile Met Asp Ser Leu Phe Asp Lys	
147 152 157 162	
ctg tta tct aag tat gaa gtg aag gct cct gtt cct tct gcc tgt ttc	704
Leu Leu Ser Lys Tyr Glu Val Lys Ala Pro Val Pro Ser Ala Cys Phe	
163 168 173 178	
agg aat att tgt aag caa atg aca aaa atg cac gaa gct ata ttt gat	752
Arg Asn Ile Cys Lys Gln Met Thr Lys Met His Glu Ala Ile Phe Asp	
179 184 189 194	
ctc ctt cca gaa gaa caa aca cag atg tta ttt tta aga att aat gca	800
Leu Leu Pro Glu Glu Gln Thr Gln Met Leu Phe Leu Arg Ile Asn Ala	
195 200 205 210	
agt tat aaa ctc cac ttg aaa aag cag tta tct cac tta aat gtg ata	848
Ser Tyr Lys Leu His Leu Lys Lys Gln Leu Ser His Leu Asn Val Ile	
211 216 221 226	
aat gat gga gga cct caa aat ggg ttg gtc aca gca gat gta gct ttt	896
Asn Asp Gly Gly Pro Gln Asn Gly Leu Val Thr Ala Asp Val Ala Phe	
227 232 237 242	
tac act gga aat ctt caa gcc tta aaa ggc ctt aaa gat ttg gac cta	944
Tyr Thr Gly Asn Leu Gln Ala Leu Lys Gly Leu Lys Asp Leu Asp Leu	
243 248 253 258	
aat atg gcc gaa att tgg gag cag aag agg tga tgtcatcc tggaaaactg	995
Asn Met Ala Glu Ile Trp Glu Gln Lys Arg *	
259 264 269	
ggtagttcat ctgaccatgg gatgtgtttg ttatgaagaa aatctggatg cctgtgattc	1055
gagaattgaa cctgaaaccc aaagtgaact ggggtggggg aagggaaaaa ggaaagtatc	1115
aagtgttggg aaactggatt cagtgggatc tacaaggaat gtcatttttg tgcacacctac	1175
agtgaggagt aactgatcag gtgtctataa cttttttcat tctctctgga aacagactca	1235
ggttttctttg gaccaaatcc aaaagaacac atagctgtaa cacagctgta gttgactaga	1295
atgctctgta tactttatat taaaaaatgc tttgcatttc ttccagtgca atgaaattca	1355
tatgggtgtcc caccttattt aatgatggta caatttaaaa tcttagtcaa cttctgtaga	1415
aagttttctc tatgaaagta aagctgtttg aaaaattatt atttttttac agatctttct	1475

GenBank accession number: U00180.1 (Homo sapiens chromosome 22, full genome)

ataaaaaata aacatctttt gattgcttgg atttaggaat tcaatttttg tttcagtgac 1535
caatgtcaag ttgcaggctt tgtgtgttgc atatttaata tttctactac caccgtatgt 1595
caactgggta aagccttcca gagctctcta aatacctgaa agacttaagc ctttttttaa 1655
gtaattaata cttaaaaaaa aaagatcctg gcatctatct atgcaactaa atacttttca 1715
gaaatgggtat ataaaaggct acagtttaaat atctgtatct ttataaaaagt atgatgaagg 1775
gtttgggggtg tttttatttg tagcagaggt aagaatatgt attcatataa tctgcctact 1835
tttgagttct catattaaca tttagataac atatgaagta tggccccctt ggatccttgt 1895
ttttaagtta ctttcgatgt gtatacgaac aaagaccagg gagaaacaga acttttataa 1955
ctataggctg ctgtgttggg gccagaaata aggtgacaag taaagacttt tataataacct 2015
accttcaaaa ttagaatcag cagcactgta caaataaagt gcctgtgctt 2065

<210> 608
<211> 3806
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (193)..(1746)

<400> 608
aattgatcgc ctgcggtacc ggtccggaat tcccgggtcg acgatttcgt ccggcgggaag 60
agcttctcgg ctctaggctc tggagtcccg ggagcagtga ggggccaccc ggggcacagg 120
aaagggccgc taggggaggg ccgggtgcac tccgggtgtc tgggccgcgg gtctgagggg 180
tgaggagggg cc atg gcc agc gac ggg gcc agg aag caa ttc tgg aag 228
Met Ala Ser Asp Gly Ala Arg Lys Gln Phe Trp Lys
1 5 10

cgc agc aac agc aag ctc ccg ggc agc atc cag cac gtg tat ggt gcc 276
Arg Ser Asn Ser Lys Leu Pro Gly Ser Ile Gln His Val Tyr Gly Ala
13 18 23 28

cag cac ccc ccc ttt gat cca ctg tta cat ggc act ttg ctc agg tcc 324
Gln His Pro Pro Phe Asp Pro Leu Leu His Gly Thr Leu Leu Arg Ser
29 34 39 44

acg gcc aag atg ccg acc aca cca gtg aag gcc aag agg gtc agc acc 372
Thr Ala Lys Met Pro Thr Thr Pro Val Lys Ala Lys Arg Val Ser Thr
45 50 55 60

ttc cag gag ttt gag agc aat acc agc gat gcc tgg gac gct ggg gag 420
Phe Gln Glu Phe Glu Ser Asn Thr Ser Asp Ala Trp Asp Ala Gly Glu

61	66	71	76	
gac gac gat gag ctc ctg gcc atg gcg gcg gag agc ctg aac tcc gag				468
Asp Asp Asp Glu Leu Leu Ala Met Ala Ala Glu Ser Leu Asn Ser Glu				
77	82	87	92	
gtg gtc atg gag acg gcc aac cgt gtg ctg cgt aac cac agc cag cgg				516
Val Val Met Glu Thr Ala Asn Arg Val Leu Arg Asn His Ser Gln Arg				
93	98	103	108	
cag ggg cgg ccc acg ctg cag gag ggg cca ggg ctt cag cag aag ccc				564
Gln Gly Arg Pro Thr Leu Gln Glu Gly Pro Gly Leu Gln Gln Lys Pro				
109	114	119	124	
agg ccc gag gca gag ccg ccc tca ccc ccc agc ggc gac ctc cgg ctg				612
Arg Pro Glu Ala Glu Pro Pro Ser Pro Pro Ser Gly Asp Leu Arg Leu				
125	130	135	140	
gtg aag tcg gtc agt gag agc cac acg tcc tgt cct gca gaa agt gcc				660
Val Lys Ser Val Ser Glu Ser His Thr Ser Cys Pro Ala Glu Ser Ala				
141	146	151	156	
agc gat gcc gcc cct ctg cag agg tcc cag tct ctc cca cac tcg gcc				708
Ser Asp Ala Ala Pro Leu Gln Arg Ser Gln Ser Leu Pro His Ser Ala				
157	162	167	172	
acc gtc acg ctg ggt ggc aca tct gac ccc agc act ctc agc agc tca				756
Thr Val Thr Leu Gly Gly Thr Ser Asp Pro Ser Thr Leu Ser Ser Ser				
173	178	183	188	
gcg ctg agc gaa aga gag gcc tcc cgg ctc gac aag ttc aag cag ctg				804
Ala Leu Ser Glu Arg Glu Ala Ser Arg Leu Asp Lys Phe Lys Gln Leu				
189	194	199	204	
ctt gcc ggc ccc aac acg gac ctt gag gaa tta cgg agg ttg agc tgg				852
Leu Ala Gly Pro Asn Thr Asp Leu Glu Glu Leu Arg Arg Leu Ser Trp				
205	210	215	220	
tcc gga atc cct aag cca gtg cgt cca atg acg tgg aag ctc ctc tca				900
Ser Gly Ile Pro Lys Pro Val Arg Pro Met Thr Trp Lys Leu Leu Ser				
221	226	231	236	
ggt tac ctt ccc gcc aat gta gac cgg aga cca gcc act ctc cag aga				948
Gly Tyr Leu Pro Ala Asn Val Asp Arg Arg Pro Ala Thr Leu Gln Arg				
237	242	247	252	
aaa caa aaa gaa tat ttt gca ttt att gag cac tat tac gat tct agg				996
Lys Gln Lys Glu Tyr Phe Ala Phe Ile Glu His Tyr Tyr Asp Ser Arg				
253	258	263	268	
aac gac gaa gtt cac cag gac aca tac agg cag atc cac ata gac atc				1044
Asn Asp Glu Val His Gln Asp Thr Tyr Arg Gln Ile His Ile Asp Ile				
269	274	279	284	
cct cgc atg agc cct gaa gcg ttg atc ctg cag ccc aag gtg acg gag				1092
Pro Arg Met Ser Pro Glu Ala Leu Ile Leu Gln Pro Lys Val Thr Glu				
285	290	295	300	

att ttt gaa agg atc ttg ttc ata tgg gcg atc cgc cac cca gcc agt	1140
Ile Phe Glu Arg Ile Leu Phe Ile Trp Ala Ile Arg His Pro Ala Ser	
301 306 311 316	
gga tac gtt cag ggt ata aat gat ctc gtc act cct ttc ttt gtg gtc	1188
Gly Tyr Val Gln Gly Ile Asn Asp Leu Val Thr Pro Phe Phe Val Val	
317 322 327 332	
ttc att tgt gaa tac ata gag gca gag gag gtg gac acg gtg gac gtc	1236
Phe Ile Cys Glu Tyr Ile Glu Ala Glu Glu Val Asp Thr Val Asp Val	
333 338 343 348	
tcc ggc gtg ccc gca gag gtg ctg tgc aac atc gag gcc gac acc tac	1284
Ser Gly Val Pro Ala Glu Val Leu Cys Asn Ile Glu Ala Asp Thr Tyr	
349 354 359 364	
tgg tgc atg agc aag ctg ctg gat ggc att cag gac aac tac acc ttt	1332
Trp Cys Met Ser Lys Leu Leu Asp Gly Ile Gln Asp Asn Tyr Thr Phe	
365 370 375 380	
gcc caa cct ggg att caa atg aaa gtg aaa atg tta gaa gaa ctc gtg	1380
Ala Gln Pro Gly Ile Gln Met Lys Val Lys Met Leu Glu Glu Leu Val	
381 386 391 396	
agc cgg att gat gag caa gtg cac cgg cac ctg gac caa cac gaa gtg	1428
Ser Arg Ile Asp Glu Gln Val His Arg His Leu Asp Gln His Glu Val	
397 402 407 412	
aga tac ctg cag ttt gcc ttc cgc tgg atg aac aac ctg ctg atg agg	1476
Arg Tyr Leu Gln Phe Ala Phe Arg Trp Met Asn Asn Leu Leu Met Arg	
413 418 423 428	
gag gtg ccc ctg cgt tgt acc atc cgc ctg tgg gac acc tac cag tct	1524
Glu Val Pro Leu Arg Cys Thr Ile Arg Leu Trp Asp Thr Tyr Gln Ser	
429 434 439 444	
gaa ccg gac ggc ttt tct cat ttc cac ttg tac gtg tgc gct gct ttt	1572
Glu Pro Asp Gly Phe Ser His Phe His Leu Tyr Val Cys Ala Ala Phe	
445 450 455 460	
ctc gtg aga tgg agg aag gaa ata cta gaa gaa aaa gat ttt caa gag	1620
Leu Val Arg Trp Arg Lys Glu Ile Leu Glu Glu Lys Asp Phe Gln Glu	
461 466 471 476	
ctg ctg ctc ttc ctc cag aac ctg ccc aca gcc cac tgg gat gat gag	1668
Leu Leu Leu Phe Leu Gln Asn Leu Pro Thr Ala His Trp Asp Asp Glu	
477 482 487 492	
gac atc agc ctg ttg ctg gcc gag gcc tac cgc ctc aag ttt gct ttt	1716
Asp Ile Ser Leu Leu Leu Ala Glu Ala Tyr Arg Leu Lys Phe Ala Phe	
493 498 503 508	
gcc gag gcc ccc aat cac tac aag aaa tga g cccaggccca cccgcagctg	1767
Ala Asp Ala Pro Asn His Tyr Lys Lys *	
509 514	

gcctcactgt cccgggtggc gcgccccacc tgcttggtg gtggtaggcc cctgtgagct 1827

ggccccgggc tgctaaaagg ccttggtgagg tggccccacc ctccagggga gctggtgaag 1887

atggggccaca gacctggtct agggctgaca aagacaggga cagcctttgt tttctgagat 1947

accaaagaga gccaggggag ggccccgggt tcggcggcca gaggcaggtc aggggtcccc 2007

tctccctctc cctgcaatgt ccttgccaaa tgactgcctc ctgctgcccc tagtccgggg 2067

cagcctagga ggccgacct ctttgaggctc ctgctgtctg ggtgccaggg ccggaacgag 2127

gtagtggcca tctcatacct actctgaaat gcaaaacttc tattctgttg agtgaaagaa 2187

taaaatgtag acaaaatcta gaccgagacg ttgcgctgac ccgggggtctc tgtgccgcga 2247

ggccccctca cagctgtatt tcaactgctgc tggcccttcc cctccgtgtg ttttctgct 2307

tgcttggttt aaacgtggct gggaagctga aggttgaggt ccaagccgtg agcccgccga 2367

gtgcctggga ggccgtggga ccaaaggctg ggagcagagg gaggcctcgc catcgccctta 2427

ctttccacct tgaacctctt ttacaagaga gaaaccccca cctccctgag gtccagggcc 2487

aagtggcccc gccacgcagg taggcgccgg cctcagccag agcccctgga ggcccacca 2547

ggctgtcggg ccatgttggg ctggcagacg ggcagggggg cgcgtccctg tcatcaaagc 2607

cctgaaccac agtgcctctc tcaccgcagc ctggaagcgg aatgagcttt tggagacttc 2667

ctgggacttg ctgtccttgt ccaggtctgc caggtgtagg ggaggtgtga ctggttccat 2727

catggaccgg ttccctccgtg gaccggttcc gccatggaac ggttccgccca tggaccactc 2787

ctgccctgga ccaactcctc cctggaccgg ttctgccgtg gactgggttc ccgccgtggac 2847

cagttcccgc tgtatactgg ttctgccctg gactgggttc cgtgtgtggac tggttccttg 2907

gggtcttaag tgcggaaggg ccagagctg gtccctgccc agcgccctgc tagggctgtg 2967

tccttggtc caggggcctt ggagctggct tcccagcgtt ccctcgggtg gtcacaggct 3027

gcatgacccc tggaatgcgg gcagggccac agccacagtc tgtctgatcc ctgagcccag 3087

gacaggctca cgtcctcagc gaccactgg tgactgactt ccagactct cctctgtccc 3147

tcaggagcag ccgtgtcctc tcccaggccc taggacactg ccagagactg tgggacatac 3207

aggcataagt gatgtgtgtg tttctgcttc tgttttaaaa atccagggtc attacacaca 3267

gcatggaaat tagcacaaaa tgctgtgcaa acgtcagatg ctcccaaacc agcaaaggga 3327

tgggcttgct tcacatcaga tgcgggcacg ccttaaccct gccttcctg tccccacccc 3387

agggtcaagg gttcctcaga ccagccatgc ctctctctcc tgccgcctcc ttttctagat 3447

ggggagggga ttccgtcaca agaagagccg cccctcggcc gtgtgcagga agccccatgt 3507

cgctttgccg agatcagccc tgggaggatc cctttctcta gctcagatca tgccgtgtgg 3567
ccagaaggct gcggacacaa ctgacctgct tctcgagggtg gttgatgttt taaacaggaa 3627
gctccacgga gttcagccct gtgtgcattt cctcatgtat gtaaaccgcca agactgaatg 3687
tgagaggtgt tggccgcggtg ccttaagtct gagcagatcc atctggaatg ttcgggggtgt 3747
gctgtctgga tgtggtgcgc taaaaacacg gaataaagat cagtgacaaa aaaaaaaaaa 3806

<210> 609
<211> 2573
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (200)..(1840)

<400> 609

accggtccgg aattcccggtg tcgaccacg cgtccgcgga cgcgtgggggt gagtttggtg 60
tacaaaacaa atctttcttc agttggggag ctagggtagc gcactacggg tcactcttgc 120
tttctttgct tcacaggatt ggagaaggag gtgacaggag gagccccgc acaggaccta 180
agaatgctgt gaaccagaag atg gga tcg cgg aac agc agc agt gca gga tcc 232
Met Gly Ser Arg Asn Ser Ser Ser Ala Gly Ser
1 5
ggg tcc gga gac ccc tcc gag ggc ttg ccc cga aga ggg gct ggc ctg 280
Gly Ser Gly Asp Pro Ser Glu Gly Leu Pro Arg Arg Gly Ala Gly Leu
12 17 22 27
cgt cgg agt gag gaa gag gaa gaa gag gat gaa gat gtg gat ctg gcc 328
Arg Arg Ser Glu Glu Glu Glu Glu Glu Asp Glu Asp Val Asp Leu Ala
28 33 38 43
cag gta ctg gcc tat ctc ctc cgc aga ggc caa gtg agg ttg gtg cag 376
Gln Val Leu Ala Tyr Leu Leu Arg Arg Gly Gln Val Arg Leu Val Gln
44 49 54 59
gga gga ggt gca gca aat tta caa ttc att cag gcc ctc ttg gac tca 424
Gly Gly Gly Ala Ala Asn Leu Gln Phe Ile Gln Ala Leu Leu Asp Ser
60 65 70 75
gag gaa gag aat gac aga gct tgg gat ggt cgt ctt ggg gat cga tac 472
Glu Glu Glu Asn Asp Arg Ala Trp Asp Gly Arg Leu Gly Asp Arg Tyr
76 81 86 91
aac cca cct gtg gat gct acc cct gac acc cgg gag ctg gaa ttc aat 520
Asn Pro Pro Val Asp Ala Thr Pro Asp Thr Arg Glu Leu Glu Phe Asn
92 97 102 107

gag atc aag aca caa gtg gaa ctg gcc aca ggg cag ctg ggg ctt agg	568
Glu Ile Lys Thr Gln Val Glu Leu Ala Thr Gly Gln Leu Gly Leu Arg	
108 113 118 123	
cgg gcc gcc cag aag cac agc ttt cct cga atg ttg cac cag aga gaa	616
Arg Ala Ala Gln Lys His Ser Phe Pro Arg Met Leu His Gln Arg Glu	
124 129 134 139	
cgg ggc ctc tgc cat cgg gga agc ttc tcc ctt gga gaa cag tct cga	664
Arg Gly Leu Cys His Arg Gly Ser Phe Ser Leu Gly Glu Gln Ser Arg	
140 145 150 155	
gtg ata tct cac ttc ttg ccc aat gat ctg ggc ttc act gat agc tac	712
Val Ile Ser His Phe Leu Pro Asn Asp Leu Gly Phe Thr Asp Ser Tyr	
156 161 166 171	
tct cag aag gct ttc tgt ggc atc tac agc aaa gat ggt caa ata ttc	760
Ser Gln Lys Ala Phe Cys Gly Ile Tyr Ser Lys Asp Gly Gln Ile Phe	
172 177 182 187	
atg tct gct tgc caa gac cag aca atc cga ctc tat gac tgc cga tat	808
Met Ser Ala Cys Gln Asp Gln Thr Ile Arg Leu Tyr Asp Cys Arg Tyr	
188 193 198 203	
ggc cgt ttc cat aaa ttc aag agc atc aag gcc cgc gac gta ggc tgg	856
Gly Arg Phe His Lys Phe Lys Ser Ile Lys Ala Arg Asp Val Gly Trp	
204 209 214 219	
agc gtc ttg gat gtg gcc ttc acc cct gat ggg aac cac ttc ctc tac	904
Ser Val Leu Asp Val Ala Phe Thr Pro Asp Gly Asn His Phe Leu Tyr	
220 225 230 235	
tct agc tgg tct gat tac att cat atc tgc aat atc tat ggt gag gga	952
Ser Ser Trp Ser Asp Tyr Ile His Ile Cys Asn Ile Tyr Gly Glu Gly	
236 241 246 251	
gat aca cac act gcc ctg gat ctc agg cca gat gag cgt cgc ttt gct	1000
Asp Thr His Thr Ala Leu Asp Leu Arg Pro Asp Glu Arg Arg Phe Ala	
252 257 262 267	
gtc ttc tcc att gct gtc tcc tca gat gga cga gaa gta cta gga ggg	1048
Val Phe Ser Ile Ala Val Ser Ser Asp Gly Arg Glu Val Leu Gly Gly	
268 273 278 283	
gcc aat gat ggc tgc ctg tat gtc ttt gac cga gaa cag aac cgg cgc	1096
Ala Asn Asp Gly Cys Leu Tyr Val Phe Asp Arg Glu Gln Asn Arg Arg	
284 289 294 299	
acc ctt cag att gag tcc cat gag gat gat gtg aat gca gtg gcc ttt	1144
Thr Leu Gln Ile Glu Ser His Glu Asp Asp Val Asn Ala Val Ala Phe	
300 305 310 315	
gct gat ata agc tcc caa atc ctg ttc tct ggg gga gat gat gcc atc	1192
Ala Asp Ile Ser Ser Gln Ile Leu Phe Ser Gly Gly Asp Asp Ala Ile	
316 321 326 331	

tgc aaa gtg tgg gat cga cgc acc atg cgg gag gat gac ccc aag cct	1240
Cys Lys Val Trp Asp Arg Arg Thr Met Arg Glu Asp Asp Pro Lys Pro	
332 337 342 347	
gtg ggt gca ctg gct gga cac cag gat ggc atc acc ttc att gac agc	1288
Val Gly Ala Leu Ala Gly His Gln Asp Gly Ile Thr Phe Ile Asp Ser	
348 353 358 363	
aag ggt gat gcc cgg tat ctg atc tcc aac tct aaa gac cag acc atc	1336
Lys Gly Asp Ala Arg Tyr Leu Ile Ser Asn Ser Lys Asp Gln Thr Ile	
364 369 374 379	
aaa ctc tgg gat atc cga cgc ttt tcc agc cgg gaa ggc atg gaa gct	1384
Lys Leu Trp Asp Ile Arg Arg Phe Ser Ser Arg Glu Gly Met Glu Ala	
380 385 390 395	
tca cgc cag gct gcc aca cag caa aac tgg gac tat cgg tgg cag caa	1432
Ser Arg Gln Ala Ala Thr Gln Gln Asn Trp Asp Tyr Arg Trp Gln Gln	
396 401 406 411	
gtg ccc aaa aaa gcc tgg cgg aag ctg aag ctc cca ggg gac agc tcc	1480
Val Pro Lys Lys Ala Trp Arg Lys Leu Lys Leu Pro Gly Asp Ser Ser	
412 417 422 427	
ttg atg acc tac cgg ggc cac gga gtg ctg cac acc ctc atc cgc tgc	1528
Leu Met Thr Tyr Arg Gly His Gly Val Leu His Thr Leu Ile Arg Cys	
428 433 438 443	
cgg ttc tcc ccc att cat agc act ggc cag cag ttc atc tac agt ggc	1576
Arg Phe Ser Pro Ile His Ser Thr Gly Gln Gln Phe Ile Tyr Ser Gly	
444 449 454 459	
tgc tcc act ggc aaa gtg gtt gtg tac gac ctt cta agt ggc cac att	1624
Cys Ser Thr Gly Lys Val Val Val Tyr Asp Leu Leu Ser Gly His Ile	
460 465 470 475	
gtg aag aag ctg acc aac cac aag gcc tgt gtg cgt gac gtc agt tgg	1672
Val Lys Lys Leu Thr Asn His Lys Ala Cys Val Arg Asp Val Ser Trp	
476 481 486 491	
cac ccc ttt gaa gag aag att gtc agc agt tgc tgg gac ggg aac ctg	1720
His Pro Phe Glu Glu Lys Ile Val Ser Ser Trp Asp Gly Asn Leu	
492 497 502 507	
cgt ctg tgg cag tac cgc cag gct gag tac ttc cag gat gac atg cca	1768
Arg Leu Trp Gln Tyr Arg Gln Ala Glu Tyr Phe Gln Asp Asp Met Pro	
508 513 518 523	
gaa tct gag gaa tgt gcc agc gcc cct gcc cca gtg ccc caa tcc tct	1816
Glu Ser Glu Glu Cys Ala Ser Ala Pro Ala Pro Val Pro Gln Ser Ser	
524 529 534 539	
aca ccc ttt tcc tca ccc cag tag atccaacctc cagccccata tagggatgaac	1870
Thr Pro Phe Ser Ser Pro Gln *	
540 545	
ctcttgataa gctctctgcc tctctctccc tttctccctt gtggggaatg tttggaggaa	1930

tcaactggcat ttgatgggga ataacataag cctgggctct gagcctcagc tgagccctgg 1990
 aagattctcc ccatggggca gagtgggtctc cttacgtgct cacacccagt cagcttgggt 2050
 ccctatctct ggccagagtt tggcaggact gccattatct ggggtgtggc ctctgccagc 2110
 aagagaagtg tcctgggtgt ttttaatcat gtttgaatgt taggggttgg atcctagagt 2170
 agatgcctga ggccacatct gaacagacct gtcagccagg cctgccaggt cttcacgttg 2230
 aggattcaac tggccaatca caggacaggt gtcctggcct ttcttctga ggtctctagg 2290
 ggagggggcat gggtaagggt gtttctcag caccctcctg gggtagggat tatgtctgct 2350
 gtcattgtctg ggtctttagg gtaggacagg ctgtggtatg agaggcagga gtctccacaa 2410
 ggcttcatgt ggcccccttat agggcaggcc ctgccctctg ggaagggtccc ttcattgctg 2470
 aggcacacag cttaaggaa gtaggttgaa gtaggactcc ttctgtctct cactggcttt 2530
 ggctccctca ataaactgtg tgggaacctg aaaaaaaaaa aaa 2573

<210> 610
 <211> 1654
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (200)..(1618)

<400> 610
 acccgctcgg aattccccggg tcgacccacg cgtccgcgga cgcgtggggg gagtttggtg 60
 taaaaaacia atctttcttc agttggggag ctagggtagc gcactacggg tcactcttgc 120
 tttctttgct tcacaggatt ggagaaggag gtgacaggag gagccccgc acaggaccta 180
 agaatgctgt gaccagaag atg gga tcg cgg aac agc agc agt gca gga tcc 232
 Met Gly Ser Arg Asn Ser Ser Ser Ala Gly Ser
 1 5
 ggg tcc gga gac ccc tcc gag ggc ttg ccc cga aga ggg gct ggc ctg 280
 Gly Ser Gly Asp Pro Ser Glu Gly Leu Pro Arg Arg Gly Ala Gly Leu
 12 17 22 27
 cgt cgg agt gag gaa gag gaa gaa gag gat gaa gat gtg gat ctg gcc 328
 Arg Arg Ser Glu Glu Glu Glu Glu Asp Glu Asp Val Asp Leu Ala
 28 33 38 43
 cag gta ctg gcc tat ctc ctc cgc aga ggc caa gtg agg ttg gtg cag 376
 Gln Val Leu Ala Tyr Leu Leu Arg Arg Gly Gln Val Arg Leu Val Gln
 44 49 54 59

gga gga ggt gca gca aat tta caa ttc att cag gcc ctc ttg gac tca	424
Gly Gly Gly Ala Ala Asn Leu Gln Phe Ile Gln Ala Leu Leu Asp Ser	
60 65 70 75	
gag gaa gag aat gac aga gct tgg gat ggt cgt ctt ggg gat cga tac	472
Glu Glu Glu Asn Asp Arg Ala Trp Asp Gly Arg Leu Gly Asp Arg Tyr	
76 81 86 91	
aac cca cct gtg gat gct acc cct gac acc cgg gag ctg gaa ttc aat	520
Asn Pro Pro Val Asp Ala Thr Pro Asp Thr Arg Glu Leu Glu Phe Asn	
92 97 102 107	
gag atc aag aca caa gtg gaa ctg gcc aca ggg cag ctg ggg ctt agg	568
Glu Ile Lys Thr Gln Val Glu Leu Ala Thr Gly Gln Leu Gly Leu Arg	
108 113 118 123	
cgg gcc gcc cag aag cac agc ttt cct cga atg ttg cac cag aga gaa	616
Arg Ala Ala Gln Lys His Ser Phe Pro Arg Met Leu His Gln Arg Glu	
124 129 134 139	
cgg ggc ctc tgc cat cgg gga agc ttc tcc ctt gga gaa cag tct cga	664
Arg Gly Leu Cys His Arg Gly Ser Phe Ser Leu Gly Glu Gln Ser Arg	
140 145 150 155	
gtg ata tct cac ttc ttg ccc aat gat ctg ggc ttc act gat agc tac	712
Val Ile Ser His Phe Leu Pro Asn Asp Leu Gly Phe Thr Asp Ser Tyr	
156 161 166 171	
tct cag aag gct ttc tgt ggc atc tac agc aaa gat ggt caa ata ttc	760
Ser Gln Lys Ala Phe Cys Gly Ile Tyr Ser Lys Asp Gly Gln Ile Phe	
172 177 182 187	
atg tct gct tgc caa gac cag aca atc cga ctc tat gac tgc cga tat	808
Met Ser Ala Cys Gln Asp Gln Thr Ile Arg Leu Tyr Asp Cys Arg Tyr	
188 193 198 203	
ggc cgt ttc cat aaa ttc aag agc atc aag gcc cgc gac gta ggc tgg	856
Gly Arg Phe His Lys Phe Lys Ser Ile Lys Ala Arg Asp Val Gly Trp	
204 209 214 219	
agc gtc ttg gat gtg gcc ttc acc cct gat ggg aac cac ttc ctc tac	904
Ser Val Leu Asp Val Ala Phe Thr Pro Asp Gly Asn His Phe Leu Tyr	
220 225 230 235	
tct agc tgg tct gat tac att cat atc tgc aat atc tat ggt gag gga	952
Ser Ser Trp Ser Asp Tyr Ile His Ile Cys Asn Ile Tyr Gly Glu Gly	
236 241 246 251	
gat aca cac act gcc ctg gat ctc agg cca gat gag cgt cgc ttt gct	1000
Asp Thr His Thr Ala Leu Asp Leu Arg Pro Asp Glu Arg Arg Phe Ala	
252 257 262 267	
gtc ttc tcc att gct gtc tcc tca gat gga cga gaa gta cta gga ggg	1048
Val Phe Ser Ile Ala Val Ser Ser Asp Gly Arg Glu Val Leu Gly Gly	
268 273 278 283	

gcc aat gat ggc tgc ctg tat gtc ttt gac cga gaa cag aac cgg cgc	1096
Ala Asn Asp Gly Cys Leu Tyr Val Phe Asp Arg Glu Gln Asn Arg Arg	
284 289 294 299	
acc ctt cag att gag tcc cat gag gat gat gtg aat gca gtg gcc ttt	1144
Thr Leu Gln Ile Glu Ser His Glu Asp Asp Val Asn Ala Val Ala Phe	
300 305 310 315	
gct gat ata agc tcc caa atc ctg ttc tct ggg gga gat gat gcc atc	1192
Ala Asp Ile Ser Ser Gln Ile Leu Phe Ser Gly Gly Asp Asp Ala Ile	
316 321 326 331	
tgc aaa gtg tgg gat cga cgc acc atg cgg gag gat gac ccc aag cct	1240
Cys Lys Val Trp Asp Arg Arg Thr Met Arg Glu Asp Asp Pro Lys Pro	
332 337 342 347	
gtg ggt gca ctg gct gga cac cag gat ggc atc acc ttc att gac agc	1288
Val Gly Ala Leu Ala Gly His Gln Asp Gly Ile Thr Phe Ile Asp Ser	
348 353 358 363	
aag gtg ggc cag aag tca gga ctg tac agc cag gcc gct aag gtt cta	1336
Lys Val Gly Gln Lys Ser Gly Leu Tyr Ser Gln Ala Ala Lys Val Leu	
364 369 374 379	
gtt gcc cag gag ggc atg aaa gcg gac tgg tgt ggg aat ttg aca agc	1384
Val Ala Gln Glu Gly Met Lys Ala Asp Trp Cys Gly Asn Leu Thr Ser	
380 385 390 395	
tcc tta tta acc aag gtt tgt aag agt tgg agt tta ggg aag ggg ctc	1432
Ser Leu Leu Thr Lys Val Cys Lys Ser Trp Ser Leu Gly Lys Gly Leu	
396 401 406 411	
aag cca ggg aac atg aat tcc atc tgt act cac cag tcc tca agg agc	1480
Lys Pro Gly Asn Met Asn Ser Ile Cys Thr His Gln Ser Ser Arg Ser	
412 417 422 427	
agg gca ggg ctt tcc gta caa gaa aaa tgg aag acc ggt cag gta cag	1528
Arg Ala Gly Leu Ser Val Gln Glu Lys Trp Lys Thr Gly Gln Val Gln	
428 433 438 443	
cgg ctc aca cct gta atc cta gca ctt tgg gag gct gag gtg gga gga	1576
Arg Leu Thr Pro Val Ile Leu Ala Leu Trp Glu Ala Glu Val Gly Gly	
444 449 454 459	
tca ctt gag ctc agg cgt tcc aga cca gcc tgt gaa acc tag cgagacc	1625
Ser Leu Glu Leu Arg Arg Ser Arg Pro Ala Cys Glu Thr *	
460 465 470	
tcattctctat ttattttaaaa aaaaaaaaaa	1654

<210> 611
 <211> 1000
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (163)..(942)

<400> 611

ccgttgacc ggtccggaat tcccgggtcg acccagcgt ccggtcgggc agcagcggg	60
ctgtctatcc cggtgagga cccgcggcca gtgcgggtgg ctggctttgc cattagcggg	120
ggcctttcct gaggacggcg tacggagtgt ggggaatgaa gg atg gca gca tgc	174
Met Ala Ala Cys	
1	
cgt gca tta aaa gct gtt ttg gta gat ctc agt ggc aca ctt cac att	222
Arg Ala Leu Lys Ala Val Leu Val Asp Leu Ser Gly Thr Leu His Ile	
5 10 15 20	
gaa gat gca gct gtg cca ggc gca cag gaa gct ctt aaa agg tta cgt	270
Glu Asp Ala Ala Val Pro Gly Ala Gln Glu Ala Leu Lys Arg Leu Arg	
21 26 31 36	
ggg gct tct gta atc att agg ttt gtg acc aat aca acc aaa gag agc	318
Gly Ala Ser Val Ile Ile Arg Phe Val Thr Asn Thr Thr Lys Glu Ser	
37 42 47 52	
aag caa gac ctg tta gaa agg ttg aga aaa ttg gaa ttt gat atc tct	366
Lys Gln Asp Leu Leu Glu Arg Leu Arg Lys Leu Glu Phe Asp Ile Ser	
53 58 63 68	
gaa gat gaa ata ttc aca tct ctg act gca gcc aga agt tta cta gag	414
Glu Asp Glu Ile Phe Thr Ser Leu Thr Ala Ala Arg Ser Leu Leu Glu	
69 74 79 84	
cgg aaa caa gtc aga ccc atg ctg cta gtt gat gat cgg gca cta cct	462
Arg Lys Gln Val Arg Pro Met Leu Leu Val Asp Asp Arg Ala Leu Pro	
85 90 95 100	
gat ttc aaa gga ata caa aca agt gat cct aat gct gtg gtc atg gga	510
Asp Phe Lys Gly Ile Gln Thr Ser Asp Pro Asn Ala Val Val Met Gly	
101 106 111 116	
ttg gca cca gaa cat ttt cat tat caa att ctg aat caa gca ttc cgg	558
Leu Ala Pro Glu His Phe His Tyr Gln Ile Leu Asn Gln Ala Phe Arg	
117 122 127 132	
tta ctc ctg gat gga gca cct ctg ata gca atc cac aaa gcc agg tat	606
Leu Leu Leu Asp Gly Ala Pro Leu Ile Ala Ile His Lys Ala Arg Tyr	
133 138 143 148	
tac aag agg aaa gat ggc tta gcc ctg ggg cct gga cca ttt gtg act	654
Tyr Lys Arg Lys Asp Gly Leu Ala Leu Gly Pro Gly Pro Phe Val Thr	
149 154 159 164	
gct tta gag tat gcc aca gat acc aaa gcc aca gtc gtg ggg aaa cca	702
Ala Leu Glu Tyr Ala Thr Asp Thr Lys Ala Thr Val Val Gly Lys Pro	
165 170 175 180	

gag aag acg ttc ttt ttg gaa gca ttg cgg ggc act ggc tgt gaa cct	750
Glu Lys Thr Phe Phe Leu Glu Ala Leu Arg Gly Thr Gly Cys Glu Pro	
181 186 191 196	

gag gag gct gtc atg ata gga gat gat tgc agg gat gat gtt ggt ggg	798
Glu Glu Ala Val Met Ile Gly Asp Asp Cys Arg Asp Asp Val Gly Gly	
197 202 207 212	

gct caa gat gtc ggc atg ctg ggc atc tta gta aag act ggg aaa tat	846
Ala Gln Asp Val Gly Met Leu Gly Ile Leu Val Lys Thr Gly Lys Tyr	
213 218 223 228	

cga gca tca gat gaa gaa aaa att aat cca cct cct tac tta act tgt	894
Arg Ala Ser Asp Glu Glu Lys Ile Asn Pro Pro Pro Tyr Leu Thr Cys	
229 234 239 244	

gag agt ttc cct cat gct gcg gac cac att ctg cag cac cta ttg tga	942
Glu Ser Phe Pro His Ala Ala Asp His Ile Leu Gln His Leu Leu *	
245 250 255 260	

agcaatgtgt gcatctgaag caacttgaaa tgcagcttct tattgtctga atgaatcc	1000
---	------

<210> 612
 <211> 2276
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (355) .. (1236)

<400> 612	
ggggtgattt gatatgcagg accgagtgtg ttcttcccaa cgcccccgga agaacgtctt	60
tgacgggcag gtgtgagagc cagttggcgc tccaggccag gcgacagcct cgggccccag	120
gatcgtgcag caggggtcgg agcccgctgc cgagggcagg gcagggcagg tcgggggtggg	180
gcggggcggg gatcaagcag gggcagggct ggcgctgcgg cgggagatgc tgcggggccg	240
cgcgggcgct tggcagccag gagctctgca ttgaaggcac tggggtaaag tgaatgccga	300
agacagaaga tttggatgat acaccactga ctttctttgt ttggaataca cggt atg	357
Met	
1	

aac cct ttc tgg agc atg tct aca agc tct gta cgc aaa cga tct gaa	405
Asn Pro Phe Trp Ser Met Ser Thr Ser Ser Val Arg Lys Arg Ser Glu	
2 7 12 17	

ggt gaa gag aag aca tta aca ggg gac gtg aaa acc agt cct cca cga	453
Gly Glu Glu Lys Thr Leu Thr Gly Asp Val Lys Thr Ser Pro Pro Arg	
18 23 28 33	

act gca cca aag aaa cag ctg cct tct att ccc aaa aat gct ttg ccc	501
Thr Ala Pro Lys Lys Gln Leu Pro Ser Ile Pro Lys Asn Ala Leu Pro	
34 39 44 49	
ata act aag cct aca tct cct gcc cca gca gca cag tca aca aat ggc	549
Ile Thr Lys Pro Thr Ser Pro Ala Pro Ala Ala Gln Ser Thr Asn Gly	
50 55 60 65	
acg cat gcg tcc tat gga ccc ttc tac ctg gaa tac tct ctt ctt gca	597
Thr His Ala Ser Tyr Gly Pro Phe Tyr Leu Glu Tyr Ser Leu Leu Ala	
66 71 76 81	
gaa ttt acc ttg gtt gtg aag cag aag cta cca ggc gtc tat gtg cag	645
Glu Phe Thr Leu Val Val Lys Gln Lys Leu Pro Gly Val Tyr Val Gln	
82 87 92 97	
cca tct tat cgc tct gca tta atg tgg ttt gga gta ata ttc ata cgg	693
Pro Ser Tyr Arg Ser Ala Leu Met Trp Phe Gly Val Ile Phe Ile Arg	
98 103 108 113	
cat gga ctt tac caa gat ggc gta ttt aag ttt aca gtt tac atc cct	741
His Gly Leu Tyr Gln Asp Gly Val Phe Lys Phe Thr Val Tyr Ile Pro	
114 119 124 129	
gat aac tat cca gat ggt gac tgt cca cgc ttg gtg ttc gat att cct	789
Asp Asn Tyr Pro Asp Gly Asp Cys Pro Arg Leu Val Phe Asp Ile Pro	
130 135 140 145	
gtc ttt cac ccg cta gtt gat ccc acc tca ggt gag ctg gat gtg aag	837
Val Phe His Pro Leu Val Asp Pro Thr Ser Gly Glu Leu Asp Val Lys	
146 151 156 161	
aga gca ttt gca aaa tgg agg cgg aac cat aat cat att tgg cag gta	885
Arg Ala Phe Ala Lys Trp Arg Arg Asn His Asn His Ile Trp Gln Val	
162 167 172 177	
tta atg tat gca agg aga gtt ttc tac aag att gat aca gca agc ccc	933
Leu Met Tyr Ala Arg Arg Val Phe Tyr Lys Ile Asp Thr Ala Ser Pro	
178 183 188 193	
ctg aac cca gag gct gca gta ctg tat gaa aaa gat att cag ctt ttt	981
Leu Asn Pro Glu Ala Ala Val Leu Tyr Glu Lys Asp Ile Gln Leu Phe	
194 199 204 209	
aaa agt aaa gtt gtt gac agt gtt aag gtg tgc act gct cgt ttg ttt	1029
Lys Ser Lys Val Val Asp Ser Val Lys Val Cys Thr Ala Arg Leu Phe	
210 215 220 225	
gac caa cct aaa ata gaa gac ccc tat gca att agc ttt tct cca tgg	1077
Asp Gln Pro Lys Ile Glu Asp Pro Tyr Ala Ile Ser Phe Ser Pro Trp	
226 231 236 241	
aat cct tct gta cat gat gaa gcc aga gaa aag atg ctg act cag aaa	1125
Asn Pro Ser Val His Asp Glu Ala Arg Glu Lys Met Leu Thr Gln Lys	
242 247 252 257	

aag aag cct gaa gaa cag cac aat aaa agt gtt cat gtt gct ggc ctg	1173
Lys Lys Pro Glu Glu Gln His Asn Lys Ser Val His Val Ala Gly Leu	
258 263 268 273	
tca tgg gta aag cct ggc tca gta cag cct ttc agt aaa gaa gag aaa	1221
Ser Trp Val Lys Pro Gly Ser Val Gln Pro Phe Ser Lys Glu Glu Lys	
274 279 284 289	
aca gtg gcg act taa gagatggtga atctggtgca ccatgcactt tcttgctaga	1276
Thr Val Ala Thr *	
290	
ctctggccta gttcaagctg accaatggca gaggactgcc tgaagagtaa aactgtgtga	1336
acaatgactg actgccagtg ttttccatgt atgcataggt tctaacagca gggtttgaa	1396
acctgtctct aagtaatgca ttacttctgt cagaagtgtc ttaggggtggt tatctagttc	1456
agtactccaa attattgggg accttgaggc ttaagtaagt atttttctga atataatgct	1516
aaaggtaagt tgcattcatt taaactaata gaggagacag aattcagcac tacttaatag	1576
tttataaatc agtgggttca gttgtatata tgtaggaaa tggagaggta tagagagagc	1636
aggttccata gctcagcact ttttaagtga agatcatttg aatctcagtc ttcagcctgc	1696
actgatttgt agcctgcact gtcttactga tttacaaact gaaatcactg agaaatgtct	1756
ttagttcagt gagaagaaac cagaacactt gttcctagtg ttgtgttggt ttttttaagc	1816
aaattacttt acttactgta tttttatggc aggagggaga aaaagtgtta caacgggttc	1876
taatgaagtc cgggtatttaa atgataaatg actaatgtgt ttagtagaga caaaagaaac	1936
caataaatga ttgttctttg ccatttatgc aggaaactac ctttttctca atataaccaa	1996
acaaaggcta atttataaat gctttattga aaaatacact tatcttcata taaaattaca	2056
gtagcagtat cttgagaagt tttataaata tttttgcaga acactattct aattgaacaa	2116
tgtaagttcc atatttctct cagcaatatg aagttaccta gtaactttgt ttatactgat	2176
tcaatttaca attgaatttt ctccctaata agattattaa tttgacttga aaactgctgg	2236
aacaatagtg attaataaag atatgtatag ataaaaaaaa	2276

<210> 613
 <211> 3127
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (71) .. (3079)

<400> 613

accggtcgga attcccgggt cgacgatttc gttcgcgccg cgctggcccc ggctctcccc 60

cccgcgcttc atg gct gca cac gag tgg gac tgg ttc caa cgc gag gag 109
Met Ala Ala His Glu Trp Asp Trp Phe Gln Arg Glu Glu
1 5 10

ctc atc ggg cag att agc gac atc cga gtg cag aac ctg caa gtt gag 157
Leu Ile Gly Gln Ile Ser Asp Ile Arg Val Gln Asn Leu Gln Val Glu
14 19 24 29

agg gaa aat gtg cag aag agg acc ttt aca cga tgg ata aat cta cat 205
Arg Glu Asn Val Gln Lys Arg Thr Phe Thr Arg Trp Ile Asn Leu His
30 35 40 45

cta gaa aag tgc aac cca cct cta gaa gtt aaa gat tta ttc gtc gat 253
Leu Glu Lys Cys Asn Pro Pro Leu Glu Val Lys Asp Leu Phe Val Asp
46 51 56 61

ata caa gat ggc aaa atc cta atg gct ttg tta gaa gtc ctg tct ggg 301
Ile Gln Asp Gly Lys Ile Leu Met Ala Leu Leu Glu Val Leu Ser Gly
62 67 72 77

cgg aat ctg ctg cac gaa tac aaa tcc tcg tcg cat cgt att ttt cgg 349
Arg Asn Leu Leu His Glu Tyr Lys Ser Ser Ser His Arg Ile Phe Arg
78 83 88 93

ttg aac aac ata gcg aaa gca ctt aag ttt ttg gaa gat agc aat gta 397
Leu Asn Asn Ile Ala Lys Ala Leu Lys Phe Leu Glu Asp Ser Asn Val
94 99 104 109

aaa ctg gtt agc att gat gca gca gaa ata gca gat ggc aac cct tct 445
Lys Leu Val Ser Ile Asp Ala Ala Glu Ile Ala Asp Gly Asn Pro Ser
110 115 120 125

ttg gtt ctt ggg ctg ata tgg aac ata atc ctc ttc ttc cag att aag 493
Leu Val Leu Gly Leu Ile Trp Asn Ile Ile Leu Phe Phe Gln Ile Lys
126 131 136 141

gag ctc aca ggc aac ctc agc aga aac tct cca tct tcc agc ttg tcc 541
Glu Leu Thr Gly Asn Leu Ser Arg Asn Ser Pro Ser Ser Ser Leu Ser
142 147 152 157

cct ggc tca ggg ggc aca gac tca gac tca tcc ttc cca ccc aca ccc 589
Pro Gly Ser Gly Gly Thr Asp Ser Asp Ser Ser Phe Pro Pro Thr Pro
158 163 168 173

act gca gag agg agc gtg gca ata tcg gtg aaa gac cag agg aag gct 637
Thr Ala Glu Arg Ser Val Ala Ile Ser Val Lys Asp Gln Arg Lys Ala
174 179 184 189

atc aag gcc ctg ttg gcg tgg gtg cag agg aaa acg aga aag tat ggc 685
Ile Lys Ala Leu Leu Ala Trp Val Gln Arg Lys Thr Arg Lys Tyr Gly
190 195 200 205

gtg gcg gtg cag gac ttt gcg ggc agt tgg agg agt ggg ctg gct ttc 733

Val Ala Val Gln Asp Phe Ala Gly Ser Trp Arg Ser Gly Leu Ala Phe	
206 211 216 221	
ctg gcg gtg atc aag gcc att gac ccc agc ctg gtg gac atg aaa cag	781
Leu Ala Val Ile Lys Ala Ile Asp Pro Ser Leu Val Asp Met Lys Gln	
222 227 232 237	
gcc ctg gaa aat tcc aca cga gaa aat cta gag aag gct ttc agc atc	829
Ala Leu Glu Asn Ser Thr Arg Glu Asn Leu Glu Lys Ala Phe Ser Ile	
238 243 248 253	
gca cag gat gcc ctg cac atc ccc agg ctc ctg gag cca gaa gac atc	877
Ala Gln Asp Ala Leu His Ile Pro Arg Leu Leu Glu Pro Glu Asp Ile	
254 259 264 269	
atg gtt gac aca cca gac gag cag tct atc atg act tac gtg gca cag	925
Met Val Asp Thr Pro Asp Glu Gln Ser Ile Met Thr Tyr Val Ala Gln	
270 275 280 285	
ttt cta gaa cgt ttt ccg gag ttg gaa gcc gaa gat att ttc gat tca	973
Phe Leu Glu Arg Phe Pro Glu Leu Glu Ala Glu Asp Ile Phe Asp Ser	
286 291 296 301	
gat aaa gaa gtt cct atc gaa tcc act ttt gtt cgc atc aaa gaa act	1021
Asp Lys Glu Val Pro Ile Glu Ser Thr Phe Val Arg Ile Lys Glu Thr	
302 307 312 317	
cct tct gaa cag gag agc aaa gtc ttc gtt ctg act gaa aat ggg gag	1069
Pro Ser Glu Gln Glu Ser Lys Val Phe Val Leu Thr Glu Asn Gly Glu	
318 323 328 333	
cgt acc tac act gtt aac cat gaa acc agc cac cca cca ccc tcc aaa	1117
Arg Thr Tyr Thr Val Asn His Glu Thr Ser His Pro Pro Pro Ser Lys	
334 339 344 349	
gtc ttt gtc tgt gac aag ccc gag agc atg aag gaa ttc cgc ctg gat	1165
Val Phe Val Cys Asp Lys Pro Glu Ser Met Lys Glu Phe Arg Leu Asp	
350 355 360 365	
ggg gtt tcc agc cat gcg ctg tca gac agc tcc acc gag ttc atg cac	1213
Gly Val Ser Ser His Ala Leu Ser Asp Ser Ser Thr Glu Phe Met His	
366 371 376 381	
cag att att gac cag gtc ctg caa ggg ggc cca ggt aag acc agc gac	1261
Gln Ile Ile Asp Gln Val Leu Gln Gly Gly Pro Gly Lys Thr Ser Asp	
382 387 392 397	
atc agt gag cca tct cca gaa tcc tcc att tta tca tcc aga aag gag	1309
Ile Ser Glu Pro Ser Pro Glu Ser Ser Ile Leu Ser Ser Arg Lys Glu	
398 403 408 413	
aac ggg agg tcc aac tct ttg ccg atc aag aaa aca gtt cac ttt gag	1357
Asn Gly Arg Ser Asn Ser Leu Pro Ile Lys Lys Thr Val His Phe Glu	
414 419 424 429	
gct gac acc tac aag gat cct ttc tgc agt aag aac ctg tcc ctt tgc	1405
Ala Asp Thr Tyr Lys Asp Pro Phe Cys Ser Lys Asn Leu Ser Leu Cys	

430	435	440	445	
ttt gaa ggg agc cca aga gtg gca aag gaa tca ttg agg cag gat gga				1453
Phe Glu Gly Ser Pro Arg Val Ala Lys Glu Ser Leu Arg Gln Asp Gly				
446	451	456	461	
cat gtc ttg gca gtt gag gtt gct gag gaa aag gaa cag aaa cag gaa				1501
His Val Leu Ala Val Glu Val Ala Glu Glu Lys Glu Gln Lys Gln Glu				
462	467	472	477	
tcc tcg aag att cca gaa tcc tcc tct gac aag gtc gct ggt gac att				1549
Ser Ser Lys Ile Pro Glu Ser Ser Ser Asp Lys Val Ala Gly Asp Ile				
478	483	488	493	
ttt ttg gtg gag ggc aca aac aat aat tct cag tct tct tcc tgt aat				1597
Phe Leu Val Glu Gly Thr Asn Asn Asn Ser Gln Ser Ser Ser Cys Asn				
494	499	504	509	
ggg gct tta gag agt aca gcc cgc cac gat gaa gaa agt cac tct ctt				1645
Gly Ala Leu Glu Ser Thr Ala Arg His Asp Glu Glu Ser His Ser Leu				
510	515	520	525	
tta ccc cca gga gaa aat act gtg atg gcc gat tcc ttc cag atc aag				1693
Leu Pro Pro Gly Glu Asn Thr Val Met Ala Asp Ser Phe Gln Ile Lys				
526	531	536	541	
gtt aac ctg atg act gta gaa gct tta gag gag gga gac tat ttt gaa				1741
Val Asn Leu Met Thr Val Glu Ala Leu Glu Glu Gly Asp Tyr Phe Glu				
542	547	552	557	
gcc atc cca tta aaa gcc tca aaa ttt aac agc gac cta ata gat ttt				1789
Ala Ile Pro Leu Lys Ala Ser Lys Phe Asn Ser Asp Leu Ile Asp Phe				
558	563	568	573	
gct tct acc agc cag gct ttc aac aaa gtt cct tca cct cat gag aca				1837
Ala Ser Thr Ser Gln Ala Phe Asn Lys Val Pro Ser Pro His Glu Thr				
574	579	584	589	
aaa cct gac gag gat gct gag gct ttt gag aat cat gct gaa aaa cta				1885
Lys Pro Asp Glu Asp Ala Glu Ala Phe Glu Asn His Ala Glu Lys Leu				
590	595	600	605	
ggg aaa agg agt att aaa tct gct cac aaa aag aag gat tcg cca gag				1933
Gly Lys Arg Ser Ile Lys Ser Ala His Lys Lys Lys Asp Ser Pro Glu				
606	611	616	621	
cct caa gtt aag atg gac aaa cat gaa cct cat cag gac tcc gga gaa				1981
Pro Gln Val Lys Met Asp Lys His Glu Pro His Gln Asp Ser Gly Glu				
622	627	632	637	
gaa gct gaa ggc tgt cct tca gcc cca gaa gag aca cca gtg gat aaa				2029
Glu Ala Glu Gly Cys Pro Ser Ala Pro Glu Glu Thr Pro Val Asp Lys				
638	643	648	653	
aag cca gag gtg cat gaa aag gcc aag aga aag tcc acc cgt cct cat				2077
Lys Pro Glu Val His Glu Lys Ala Lys Arg Lys Ser Thr Arg Pro His				
654	659	664	669	

tat gag gaa gag gga gaa gac gat gac ctc cag ggt gtg ggc gag gaa Tyr Glu Glu Glu Gly Glu Asp Asp Asp Leu Gln Gly Val Gly Glu Glu 670 675 680 685	2125
tta tct tcc agc ccc cca agc agc tgt gtc agc ttg gag acc ctt ggg Leu Ser Ser Ser Pro Pro Ser Ser Cys Val Ser Leu Glu Thr Leu Gly 686 691 696 701	2173
agt cac agc gaa gaa ggc ctg gat ttc aag ccc tcc cca ccc ctc tca Ser His Ser Glu Glu Gly Leu Asp Phe Lys Pro Ser Pro Pro Leu Ser 702 707 712 717	2221
aag gtt tcc gtc att ccc cac gac ctc ttc tat ttc cca cac tat gag Lys Val Ser Val Ile Pro His Asp Leu Phe Tyr Phe Pro His Tyr Glu 718 723 728 733	2269
gtt ccc ctg gct gca gtt ttg gag gct tat gta gaa gac ccg gag gat Val Pro Leu Ala Ala Val Leu Glu Ala Tyr Val Glu Asp Pro Glu Asp 734 739 744 749	2317
cta aaa aat gaa gaa atg gat ctc gaa gag cca gag ggc tat atg cca Leu Lys Asn Glu Glu Met Asp Leu Glu Glu Pro Glu Gly Tyr Met Pro 750 755 760 765	2365
gac ctg gac tcc agg gag gag gag gcc gat ggc tct cag agc agc tcc Asp Leu Asp Ser Arg Glu Glu Glu Ala Asp Gly Ser Gln Ser Ser Ser 766 771 776 781	2413
agt tcc tcg gtg cca gga gag agc ctc ccc agt gcc agc gac cag gtg Ser Ser Ser Val Pro Gly Glu Ser Leu Pro Ser Ala Ser Asp Gln Val 782 787 792 797	2461
ctg tat ctc agc agg ggt ggt gtg ggt acc aca cca gcc tca gaa ccc Leu Tyr Leu Ser Arg Gly Gly Val Gly Thr Thr Pro Ala Ser Glu Pro 798 803 808 813	2509
gct cca ctg gcc ccc cat gag gac cac cag caa agg gag acc aaa gag Ala Pro Leu Ala Pro His Glu Asp His Gln Gln Arg Glu Thr Lys Glu 814 819 824 829	2557
aat gac ccc atg gac agc cat cag tcc cag gaa tcc cca aac ctg gaa Asn Asp Pro Met Asp Ser His Gln Ser Gln Glu Ser Pro Asn Leu Glu 830 835 840 845	2605
aac ata gca aac ccc cta gaa gaa aat gta acg aaa gaa tca atc agt Asn Ile Ala Asn Pro Leu Glu Glu Asn Val Thr Lys Glu Ser Ile Ser 846 851 856 861	2653
agt aaa aaa aag gaa aaa agg aaa cat gtg gac cac gta gaa agt tca Ser Lys Lys Lys Glu Lys Arg Lys His Val Asp His Val Glu Ser Ser 862 867 872 877	2701
cta ttt gta gca cca gga agt gtt caa tcc tca gat gac cta gaa gaa Leu Phe Val Ala Pro Gly Ser Val Gln Ser Ser Asp Asp Leu Glu Glu 878 883 888 893	2749

gac agt agc gac tac agc att cct tcc agg act agt cac agt gac tcc	2797
Asp Ser Ser Asp Tyr Ser Ile Pro Ser Arg Thr Ser His Ser Asp Ser	
894 899 904 909	
agc att tac ctt cga cga cat act cat agg tct tcg gaa tcg gat cat	2845
Ser Ile Tyr Leu Arg Arg His Thr His Arg Ser Ser Glu Ser Asp His	
910 915 920 925	
ttt agc tat gtt cag ttg agg aac gca gca gat ctg gat gac aga aga	2893
Phe Ser Tyr Val Gln Leu Arg Asn Ala Ala Asp Leu Asp Asp Arg Arg	
926 931 936 941	
aac cga ata tta acc agg aag gcc aac agc tca gga gaa gcc atg tca	2941
Asn Arg Ile Leu Thr Arg Lys Ala Asn Ser Ser Gly Glu Ala Met Ser	
942 947 952 957	
ctg ggg agc cac agc ccg cag agt gac tcc ctg aca cag ctt gtc cag	2989
Leu Gly Ser His Ser Pro Gln Ser Asp Ser Leu Thr Gln Leu Val Gln	
958 963 968 973	
cag ccg gat atg atg tat ttt att ctc ttc ctg tgg ctc ctg gtg tac	3037
Gln Pro Asp Met Met Tyr Phe Ile Leu Phe Leu Trp Leu Leu Val Tyr	
974 979 984 989	
tgc ttg ctg ctc ttc cca caa ctg gat gtt agc agg ctc tga tacgtgt	3086
Cys Leu Leu Leu Phe Pro Gln Leu Asp Val Ser Arg Leu *	
990 995 1000	
gtctggataa taaaaaagac aggaccctga aaaaaaaaaa a	3127

<210> 614
 <211> 1440
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (387)..(1187)

<400> 614	
aagcttggca cgaggggtgca gctgggctca gctccccgtg ccctaccttt ctgttctctt	60
ccttggtttc cctactctc ctctgcccc aagcagtgcc tgatgccgag ttccgtctct	120
cgggtctttt cctggtccca ggcaaagcgg agcggagatc ctcaaacggc ctagtgcctc	180
gcgcttccgg aggaaaatca gcggtctaataa taattcctct ggtttggtga agcagttacc	240
aagaatcttc aaccctttcc cacaaaagct aattgagtac acgttctctgt tgagtacacg	300
ttcctgttga ttacaaaag gtgcaggtat gagcaggtct gaagactaac attttgtgaa	360
gttgtaaaac agaaaacctg ttagaa atg tgg tgg ttt cag caa ggc ctc agt	413
Met Trp Trp Phe Gln Gln Gly Leu Ser	

ttc ctt cct tca gcc ctt gta att tgg aca tct gct gct ttc ata ttt	461
Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser Ala Ala Phe Ile Phe	
10 15 20 25	
tca tac att act gca gta aca ctc cac cat ata gac ccg gct tta cct	509
Ser Tyr Ile Thr Ala Val Thr Leu His His Ile Asp Pro Ala Leu Pro	
26 31 36 41	
tat atc agt gac act ggt aca gta gct cca gaa aaa tgc tta ttt ggg	557
Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Glu Lys Cys Leu Phe Gly	
42 47 52 57	
gca atg cta aat att gcg gca gtt tta tgc att gct acc att tat gtt	605
Ala Met Leu Asn Ile Ala Ala Val Leu Cys Ile Ala Thr Ile Tyr Val	
58 63 68 73	
cgt tat aag caa gtt cat gct ctg agt cct gaa gag aac gtt atc atc	653
Arg Tyr Lys Gln Val His Ala Leu Ser Pro Glu Glu Asn Val Ile Ile	
74 79 84 89	
aaa tta aac aag gct ggc ctt gta ctt gga ata ctg agt tgt tta gga	701
Lys Leu Asn Lys Ala Gly Leu Val Leu Gly Ile Leu Ser Cys Leu Gly	
90 95 100 105	
ctt tct att gtg gca aac ttc cag aaa aca acc ctt ttt gct gca cat	749
Leu Ser Ile Val Ala Asn Phe Gln Lys Thr Thr Leu Phe Ala Ala His	
106 111 116 121	
gta agt gga gct gtg ctt acc ttt ggt atg ggc tca tta tat atg ttt	797
Val Ser Gly Ala Val Leu Thr Phe Gly Met Gly Ser Leu Tyr Met Phe	
122 127 132 137	
gtt cag acc atc ctt tcc tac caa atg cag ccc aaa atc cat ggc aaa	845
Val Gln Thr Ile Leu Ser Tyr Gln Met Gln Pro Lys Ile His Gly Lys	
138 143 148 153	
caa gtc ttc tgg atc aga ctg ttg ttg gtt atc tgg tgt gga gta agt	893
Gln Val Phe Trp Ile Arg Leu Leu Leu Val Ile Trp Cys Gly Val Ser	
154 159 164 169	
gca ctt agc atg ctg act tgc tca tca gtt ttg cac agt ggc aat ttt	941
Ala Leu Ser Met Leu Thr Cys Ser Ser Val Leu His Ser Gly Asn Phe	
170 175 180 185	
ggg act gat tta gaa cag aaa ctc cat tgg aac ccc gag gac aaa ggt	989
Gly Thr Asp Leu Glu Gln Lys Leu His Trp Asn Pro Glu Asp Lys Gly	
186 191 196 201	
tat gtg ctt cac atg atc act act gca gca gaa tgg tct atg tca ttt	1037
Tyr Val Leu His Met Ile Thr Thr Ala Ala Glu Trp Ser Met Ser Phe	
202 207 212 217	
tcc ttc ttt ggt ttt ttc ctg act tac att cgt gat ttt cag aaa att	1085
Ser Phe Phe Gly Phe Phe Leu Thr Tyr Ile Arg Asp Phe Gln Lys Ile	
218 223 228 233	

Phe	Leu	Arg	Met	Pro	Leu	Asp	Lys	His	Met	Glu	Met	Glu	Asn	Ile	Ser		
61					66					71					76		
tca	gaa	gaa	gtt	gtg	gaa	ata	gaa	tac	gtg	gag	aag	tat	act	gca	ccc	471	
Ser	Glu	Glu	Val	Val	Glu	Ile	Glu	Tyr	Val	Glu	Lys	Tyr	Thr	Ala	Pro		
77					82					87					92		
cag	cca	gag	caa	tgc	atg	ttc	cat	gat	gac	tgg	atc	agt	tca	att	aaa	519	
Gln	Pro	Glu	Gln	Cys	Met	Phe	His	Asp	Asp	Trp	Ile	Ser	Ser	Ile	Lys		
93					98					103					108		
ggg	gca	gag	gaa	tgg	atc	ttg	act	ggt	tct	tat	gat	aag	act	tct	cgg	567	
Gly	Ala	Glu	Glu	Trp	Ile	Leu	Thr	Gly	Ser	Tyr	Asp	Lys	Thr	Ser	Arg		
109					114					119					124		
atc	tgg	tcc	ttg	gaa	gga	aag	tca	ata	atg	aca	att	gtg	gga	cat	acg	615	
Ile	Trp	Ser	Leu	Glu	Gly	Lys	Ser	Ile	Met	Thr	Ile	Val	Gly	His	Thr		
125					130					135					140		
gat	gtt	gta	aaa	gat	gtg	gcc	tgg	gtg	aaa	aaa	gat	agt	ttg	tcc	tgc	663	
Asp	Val	Val	Lys	Asp	Val	Ala	Trp	Val	Lys	Lys	Asp	Ser	Leu	Ser	Cys		
141					146					151					156		
tta	tta	ttg	agt	gct	tct	atg	gat	cag	act	att	ctc	tta	tgg	gag	tgg	711	
Leu	Leu	Leu	Ser	Ala	Ser	Met	Asp	Gln	Thr	Ile	Leu	Leu	Trp	Glu	Trp		
157					162					167					172		
aat	gta	gag	aga	aac	aaa	gtg	aaa	gcc	cta	cac	tgc	tgt	aga	ggt	cat	759	
Asn	Val	Glu	Arg	Asn	Lys	Val	Lys	Ala	Leu	His	Cys	Cys	Arg	Gly	His		
173					178					183					188		
gct	gga	agt	gta	gat	tct	ata	gct	gtt	gat	ggc	tca	gga	act	aaa	ttt	807	
Ala	Gly	Ser	Val	Asp	Ser	Ile	Ala	Val	Asp	Gly	Ser	Gly	Thr	Lys	Phe		
189					194					199					204		
tgc	agt	ggc	tcc	tgg	gat	aag	atg	cta	aag	atc	tgg	tct	aca	gtc	cct	855	
Cys	Ser	Gly	Ser	Trp	Asp	Lys	Met	Leu	Lys	Ile	Trp	Ser	Thr	Val	Pro		
205					210					215					220		
aca	gat	gaa	gaa	gat	gaa	atg	gag	gag	tcc	aca	aat	cga	cca	aga	aag	903	
Thr	Asp	Glu	Glu	Asp	Glu	Met	Glu	Glu	Ser	Thr	Asn	Arg	Pro	Arg	Lys		
221					226					231					236		
aaa	cag	aag	aca	gaa	cag	ttg	gga	cta	aca	agg	act	ccc	ata	gtg	acc	951	
Lys	Gln	Lys	Thr	Glu	Gln	Leu	Gly	Leu	Thr	Arg	Thr	Pro	Ile	Val	Thr		
237					242					247					252		
ctc	tct	ggc	cac	atg	gag	gca	gtt	tcc	tca	gtt	ctg	tgg	tca	gat	gct	999	
Leu	Ser	Gly	His	Met	Glu	Ala	Val	Ser	Ser	Val	Leu	Trp	Ser	Asp	Ala		
253					258					263					268		
gaa	gaa	atc	tgc	agt	gca	tct	tgg	gac	cat	aca	att	aga	gtg	tgg	gat	1047	
Glu	Glu	Ile	Cys	Ser	Ala	Ser	Trp	Asp	His	Thr	Ile	Arg	Val	Trp	Asp		
269					274					279					284		
gtt	gag	tct	ggc	agt	ctt	aag	tca	act	ttg	aca	gga	aat	aaa	gtg	ttt	1095	
Val	Glu	Ser	Gly	Ser	Leu	Lys	Ser	Thr	Leu	Thr	Gly	Asn	Lys	Val	Phe		

285	290	295	300	
aat tgt att tcc tat tct cca ctt tgt aaa cgt tta gca tct gga agc				1143
Asn Cys Ile Ser Tyr Ser Pro Leu Cys Lys Arg Leu Ala Ser Gly Ser				
301	306	311	316	
aca gat agg cat atc aga ctg tgg gat ccc cga act aaa gat ggt tct				1191
Thr Asp Arg His Ile Arg Leu Trp Asp Pro Arg Thr Lys Asp Gly Ser				
317	322	327	332	
ttg gtg tcg ctg tcc cta acg tca cat act ggt tgg gtg aca tca gta				1239
Leu Val Ser Leu Ser Leu Thr Ser His Thr Gly Trp Val Thr Ser Val				
333	338	343	348	
aaa tgg tct cct acc cat gaa cag cag ctg att tca gga tct tta gat				1287
Lys Trp Ser Pro Thr His Glu Gln Gln Leu Ile Ser Gly Ser Leu Asp				
349	354	359	364	
aac att gtt aag ctg tgg gat aca aga agt tgt aag gct cct ctc tat				1335
Asn Ile Val Lys Leu Trp Asp Thr Arg Ser Cys Lys Ala Pro Leu Tyr				
365	370	375	380	
gat ctg gct gct cat gaa gac aaa gtt ctg agt gta gac tgg aca gac				1383
Asp Leu Ala Ala His Glu Asp Lys Val Leu Ser Val Asp Trp Thr Asp				
381	386	391	396	
aca ggg cta ctt ctg agt gga gga gca gac aat aaa ttg tat tcc tac				1431
Thr Gly Leu Leu Leu Ser Gly Gly Ala Asp Asn Lys Leu Tyr Ser Tyr				
397	402	407	412	
aga tat tca cct acc act tcc cat gtt ggg gca tga aagt gaacaataat				1481
Arg Tyr Ser Pro Thr Thr Ser His Val Gly Ala *				
413	418	423		
ttgactatag agattatttc tgtaaatgaa attggtagag aaccatgaaa ttacatagat				1541
gcagatgcag aaagcagcct tttgaagttt atataatgtt ttcccccttc ataacagcta				1601
acgtatcact ttttcttatt ttgtatttat aataagatag gttgtgttta taaaatacaa				1661
actgtggcat acattctcta tacaaacttg aaattaaact gagttttaca tttctcttta				1721
aaggtaaaaa aaaaaaa				1738

<210> 616
 <211> 3084
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (633) .. (1883)

<400> 616

Pro Cys Gly His Ser Phe Cys Lys Asn Cys Leu Glu Arg Cys Leu Asp	
136 141 146 151	
cat gca cca tat tgt cct ctt tgc aaa gaa agc tta aaa gag tat cta	1133
His Ala Pro Tyr Cys Pro Leu Cys Lys Glu Ser Leu Lys Glu Tyr Leu	
152 157 162 167	
gca gat agg agg tac tgt gtc aca cag ctg ttg gaa gaa tta ata gtg	1181
Ala Asp Arg Arg Tyr Cys Val Thr Gln Leu Leu Glu Glu Leu Ile Val	
168 173 178 183	
aag tat ctg cct gat gaa ctg tct gag aga aaa aaa ata tat gat gaa	1229
Lys Tyr Leu Pro Asp Glu Leu Ser Glu Arg Lys Lys Ile Tyr Asp Glu	
184 189 194 199	
gaa act gct gaa ctc tca cac ttg acc aag aat gtt cca ata ttt gtt	1277
Glu Thr Ala Glu Leu Ser His Leu Thr Lys Asn Val Pro Ile Phe Val	
200 205 210 215	
tgc act atg gcc tac ccc act gtg cct tgc cct ctc cat gta ttt gag	1325
Cys Thr Met Ala Tyr Pro Thr Val Pro Cys Pro Leu His Val Phe Glu	
216 221 226 231	
cca aga tac aga ttg atg att cga aga agt ata cag act gga acc aaa	1373
Pro Arg Tyr Arg Leu Met Ile Arg Arg Ser Ile Gln Thr Gly Thr Lys	
232 237 242 247	
cag ttt ggc atg tgt gtc agt gat aca caa aat agt ttt gca gat tat	1421
Gln Phe Gly Met Cys Val Ser Asp Thr Gln Asn Ser Phe Ala Asp Tyr	
248 253 258 263	
ggg tgt atg tta caa att aga aac gtg cat ttc tta ccg gac gga agg	1469
Gly Cys Met Leu Gln Ile Arg Asn Val His Phe Leu Pro Asp Gly Arg	
264 269 274 279	
tct gtg gtt gat aca gtt gga gga aag cgg ttt agg gtt tta aaa aga	1517
Ser Val Val Asp Thr Val Gly Gly Lys Arg Phe Arg Val Leu Lys Arg	
280 285 290 295	
gga atg aaa gat gga tat tgc act gcc gac att gaa tat ctg gaa gat	1565
Gly Met Lys Asp Gly Tyr Cys Thr Ala Asp Ile Glu Tyr Leu Glu Asp	
296 301 306 311	
gtt aag gtt gag aat gaa gat gag att aag aat ctc aga gag ctt cat	1613
Val Lys Val Glu Asn Glu Asp Glu Ile Lys Asn Leu Arg Glu Leu His	
312 317 322 327	
gat ttg gtt tac tct caa gcc tgc agc tgg ttt cag aat tta aga gac	1661
Asp Leu Val Tyr Ser Gln Ala Cys Ser Trp Phe Gln Asn Leu Arg Asp	
328 333 338 343	
aga ttt cga agc caa att ctt cag cat ttc gga tca atg ccc gag agg	1709
Arg Phe Arg Ser Gln Ile Leu Gln His Phe Gly Ser Met Pro Glu Arg	
344 349 354 359	
gag gaa aac ctt cag gca gcc cct aat gga cct gca tgg tgt tgg tgg	1757
Glu Glu Asn Leu Gln Ala Ala Pro Asn Gly Pro Ala Trp Cys Trp Trp	

360	365	370	375	
ctt ctt gca gtt ctc cct gta gac cca cga tac cag ctg tcg gtt ttg				1805
Leu Leu Ala Val Leu Pro Val Asp Pro Arg Tyr Gln Leu Ser Val Leu				
376	381	386	391	
tca atg aag tct ttg aaa gaa cgg ttg acc aag ata cag cat ata ctg				1853
Ser Met Lys Ser Leu Lys Glu Arg Leu Thr Lys Ile Gln His Ile Leu				
392	397	402	407	
acc tat ttt tct aga gac caa tct aag taa c taactctttg gatctccctt				1904
Thr Tyr Phe Ser Arg Asp Gln Ser Lys *				
408	413			
taaagtgacc ctaatctggc tgcattgatg gccagattgt ctgctgcctt tgcacatcta				1964
gtgctgggttt cagaaattta atgaaacttt tctttttcct tcgacctcct gaatcatgtg				2024
gttctgcaaa tgaatacctt caactaggat ttagaccact aagaacttgc acagaaaaac				2084
acgcattgaa tgtgtgtcga acctctacat tgtgaagttg cactatgtac catactctaa				2144
aatgaaataa gaactcttta tgtctgtgag agagtgtgtg tgtgtgtgtg cgtgogtgtg				2204
tgcttgtggg gggtgggtag tgtgtgtgta ttttctctgg ctttaaaatt ttaaaacaaa				2264
caaacaaaaa agccatagag agcagaactt gccgaggggc atttattgcc caagtttaca				2324
agagtagcga tacaagtttt tgcaaattga atttgccctca gatatatctg tctaatgct				2384
tatatttgca caagtatgta aaatatcgtg ttgaggatca ttctttgttg gaaatactgc				2444
tcttgctgaa ctgtcttgac cattgactat gacacagttt cttatttatg taaatacttg				2504
catcacagtg gccgacaggc attggatgca gaacctagag ccagttttca ggaacaattg				2564
taaacctgac atgggtactgt gcatctattc ataaaacact caaaactgtg aaaatatggg				2624
ttacatttaa ttgtacataa aggtaaaggg agaactcaat tcagtaccag ttagtttgta				2684
cattttaggg ggcttttcac attaaactgcc catttgtgta atttatagtt tgacatgatg				2744
tgtttgtttt aaaaaaaaaat gcatagtata aaccatttaa ggatctggga aaagagaaga				2804
agtttaatat agaactaagc ttttaaagtt tgtttttggt ttaattctg gtctcggtgc				2864
aaatgtagt tatgccttat tcatatcaca gttagatcac catgctgcaa catggtttat				2924
attcatgctg ccctagaaac ttttgtaatt atttggtgca aatttggtgac tgccttatt				2984
aactttcttt tatgtaagta atttgtaaaa gtttcttaaa atttttgott ttgcttattt				3044
aattttgaat aaaagctaaa ttcctaataa aaaaaaaaaa				3084

<210> 617
 <211> 907
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (61)..(747)

<400> 617
 atttggccct cgaggccaag aattcggcac gagggtaact tgcttttggg agccagcggg 60
 atg gcg tgc ggc tgc aag att ggc ccg tcc atc ctc aac agc gac ctg 108
 Met Ala Ser Gly Cys Lys Ile Gly Pro Ser Ile Leu Asn Ser Asp Leu
 1 5 10 15
 gcc aat tta ggg gcc gag tgc ctc cgg atg cta gac tct ggg gcc gat 156
 Ala Asn Leu Gly Ala Glu Cys Leu Arg Met Leu Asp Ser Gly Ala Asp
 17 22 27 32
 tat ctg cac ctg gac gta atg gac ggg cat ttt gtt ccc aac atc acc 204
 Tyr Leu His Leu Asp Val Met Asp Gly His Phe Val Pro Asn Ile Thr
 33 38 43 48
 ttt ggt cac cct gtg gta gaa agc ctt cga aag cag cta ggc cag gac 252
 Phe Gly His Pro Val Val Glu Ser Leu Arg Lys Gln Leu Gly Gln Asp
 49 54 59 64
 cct ttc ttt gac atg cac atg atg gtg tcc aag cca gaa cag tgg gta 300
 Pro Phe Phe Asp Met His Met Met Val Ser Lys Pro Glu Gln Trp Val
 65 70 75 80
 aag cca atg gct gta gca gga gcc aat cag tac acc ttt cat ctc gag 348
 Lys Pro Met Ala Val Ala Gly Ala Asn Gln Tyr Thr Phe His Leu Glu
 81 86 91 96
 gct act gag aac cca ggg gct ttg att aaa gac att cgg gag aat ggg 396
 Ala Thr Glu Asn Pro Gly Ala Leu Ile Lys Asp Ile Arg Glu Asn Gly
 97 102 107 112
 atg aag gtt ggc ctt gcc atc aaa cca gga acc tca gtt gag tat ttg 444
 Met Lys Val Gly Leu Ala Ile Lys Pro Gly Thr Ser Val Glu Tyr Leu
 113 118 123 128
 gca cca tgg gct aat cag ata gat atg gcc ttg gtt atg aca gtg gaa 492
 Ala Pro Trp Ala Asn Gln Ile Asp Met Ala Leu Val Met Thr Val Glu
 129 134 139 144
 ccg ggg ttt gga ggg cag aaa ttc atg gaa gat atg atg cca aag gtt 540
 Pro Gly Phe Gly Gly Gln Lys Phe Met Glu Asp Met Met Pro Lys Val
 145 150 155 160
 cac tgg ttg agg acc cag ttc cca tct ttg gat ata gag gtc gat ggt 588
 His Trp Leu Arg Thr Gln Phe Pro Ser Leu Asp Ile Glu Val Asp Gly
 161 166 171 176
 gga gta ggt cct gac act gtc cat aaa tgt gca gag gca gga gct aac 636

gct act gag aac cca ggg gct ttg att aaa gac att cgg gag aat ggg	396
Ala Thr Glu Asn Pro Gly Ala Leu Ile Lys Asp Ile Arg Glu Asn Gly	
97 102 107 112	
atg aag tct tgc tct gtc acc cag gct gaa gtg cag tgg cac agt cag	444
Met Lys Ser Cys Ser Val Thr Gln Ala Glu Val Gln Trp His Ser Gln	
113 118 123 128	
ggc cca ttg cag gtt ggc ctt gcc atc aaa cca gga acc tca gtt gag	492
Gly Pro Leu Gln Val Gly Leu Ala Ile Lys Pro Gly Thr Ser Val Glu	
129 134 139 144	
tat ttg gca cca tgg gct aat cag ata gat atg gcc ttg gtt atg aca	540
Tyr Leu Ala Pro Trp Ala Asn Gln Ile Asp Met Ala Leu Val Met Thr	
145 150 155 160	
gtg gaa ccg ggg ttt gga ggg cag aaa ttc atg gaa gat atg atg cca	588
Val Glu Pro Gly Phe Gly Gly Gln Lys Phe Met Glu Asp Met Met Pro	
161 166 171 176	
aag gtt cac tgg ttg agg acc cag ttc cca tct ttg gat ata gag gtc	636
Lys Val His Trp Leu Arg Thr Gln Phe Pro Ser Leu Asp Ile Glu Val	
177 182 187 192	
gat ggt gga gta ggt cct gac act gtc cat aaa tgt gca gag gca gga	684
Asp Gly Gly Val Gly Pro Asp Thr Val His Lys Cys Ala Glu Ala Gly	
193 198 203 208	
gct aac atg att gtg tct ggc agt gct att atg agg agt gaa gac ccc	732
Ala Asn Met Ile Val Ser Gly Ser Ala Ile Met Arg Ser Glu Asp Pro	
209 214 219 224	
aga tct gtg atc aat cta tta aga aat gtt tgc tca gaa gct gct cag	780
Arg Ser Val Ile Asn Leu Leu Arg Asn Val Cys Ser Glu Ala Ala Gln	
225 230 235 240	
aaa cgt tct ctt gat cgg tga aa ccataaggag cccagtgttc ctgttcatga	833
Lys Arg Ser Leu Asp Arg *	
241 246	
aatctccott ttactggaaa acaggaatat tgactaccaa atcacaatgc aattgaagcc	893
gtactgcttt tttagcagt tattcattcc agtgattaaa actgattgtg cagaataaaa	953
aaaaaaaa	961

<210> 619
 <211> 5531
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (108) .. (1856)

<400> 619

```
agacctggg gaggtggctg ctggagttt atgagacggt tgccccacc ctggcgtgcc      60

tgccccggcc gcggctgagg aggaggagga ggaggaggag gaggagg  atg atc tcc      116
                               Met Ile Ser
                               1

aga tac act cgg aag gcg gtg cca cag agc ttg gag ctg aaa gga ata      164
Arg Tyr Thr Arg Lys Ala Val Pro Gln Ser Leu Glu Leu Lys Gly Ile
 4                               9                               14                               19

aca aaa cat gct ctt aac cat cat ccc cct cca gag123 aag ctg gag gaa      212
Thr Lys His Ala Leu Asn His His Pro Pro Pro Glu Lys Leu Glu Glu
 20                               25                               30                               35

att tcc ccc acc agt gac agt cat gag aaa gac aca agt tcc caa agc      260
Ile Ser Pro Thr Ser Asp Ser His Glu Lys Asp Thr Ser Ser Gln Ser
 36                               41                               46                               51

aag tct gac atc aca aga gaa tca tct ttt aca tca gcc gac act ggg      308
Lys Ser Asp Ile Thr Arg Glu Ser Ser Phe Thr Ser Ala Asp Thr Gly
 52                               57                               62                               67

aat tca ctg tct gct ttt cca agt tat aca ggc gca ggg ata tct act      356
Asn Ser Leu Ser Ala Phe Pro Ser Tyr Thr Gly Ala Gly Ile Ser Thr
 68                               73                               78                               83

gaa gga agc tcg gac ttc tcc tgg gga tat ggt gaa ctc gat caa aat      404
Glu Gly Ser Ser Asp Phe Ser Trp Gly Tyr Gly Glu Leu Asp Gln Asn
 84                               89                               94                               99

gcc act gaa aaa gtc cag aca atg ttc aca gcc att gat gaa ctc ttg      452
Ala Thr Glu Lys Val Gln Thr Met Phe Thr Ala Ile Asp Glu Leu Leu
100                               105                               110                               115

tat gag cag aag ttg agt gtg cat acc aag agt cta caa gaa gag tgc      500
Tyr Glu Gln Lys Leu Ser Val His Thr Lys Ser Leu Gln Glu Glu Cys
116                               121                               126                               131

caa cag tgg aca gct agc ttt cct cac ctc agg att cta ggt agg cag      548
Gln Gln Trp Thr Ala Ser Phe Pro His Leu Arg Ile Leu Gly Arg Gln
132                               137                               142                               147

ata atc act cca agt gaa ggt tat aga ttg tat cct aga tcc cct tct      596
Ile Ile Thr Pro Ser Glu Gly Tyr Arg Leu Tyr Pro Arg Ser Pro Ser
148                               153                               158                               163

gct gtt tcc gct tca tat gaa aca acc ttg tct caa gaa aga gat tct      644
Ala Val Ser Ala Ser Tyr Glu Thr Thr Leu Ser Gln Glu Arg Asp Ser
164                               169                               174                               179

act ata ttt ggt ata agg gga aag aag tta cat ttt tca tct tct tat      692
Thr Ile Phe Gly Ile Arg Gly Lys Lys Leu His Phe Ser Ser Ser Tyr
180                               185                               190                               195
```

gct cat aaa gca tct tcc att gcc aaa tcc tcc agc ttt tgt tct atg	740
Ala His Lys Ala Ser Ser Ile Ala Lys Ser Ser Ser Phe Cys Ser Met	
196 201 206 211	
gaa aga gat gag gaa gac tct ata atc gtc tca gaa gga ata att gag	788
Glu Arg Asp Glu Glu Asp Ser Ile Ile Val Ser Glu Gly Ile Ile Glu	
212 217 222 227	
gaa tac cta gca ttc gat cac ata gat ata gaa gag gga ttt cat ggg	836
Glu Tyr Leu Ala Phe Asp His Ile Asp Ile Glu Glu Gly Phe His Gly	
228 233 238 243	
aag aaa tca gaa gca gct aca gag aaa cag aaa tta ggg tat cct ccc	884
Lys Lys Ser Glu Ala Ala Thr Glu Lys Gln Lys Leu Gly Tyr Pro Pro	
244 249 254 259	
att gct cca ttt tac tgc atg aaa gaa gat gtc ctt gct tat gtg ttt	932
Ile Ala Pro Phe Tyr Cys Met Lys Glu Asp Val Leu Ala Tyr Val Phe	
260 265 270 275	
gac agt gta tgg tgc aag gtt gtg agc tgt atg gag cag ttg aca cgt	980
Asp Ser Val Trp Cys Lys Val Val Ser Cys Met Glu Gln Leu Thr Arg	
276 281 286 291	
agt cac tgg gaa gga ttt gcc tct gat gat gag agt aat gtt gca gtt	1028
Ser His Trp Glu Gly Phe Ala Ser Asp Asp Glu Ser Asn Val Ala Val	
292 297 302 307	
acc aga ccc gat tca gaa agt tcc tgt gtg ctg agt gaa cta cat cct	1076
Thr Arg Pro Asp Ser Glu Ser Ser Cys Val Leu Ser Glu Leu His Pro	
308 313 318 323	
ttg gtg tta ccg cga gtg cca cag tct aag gtg ctg tac att acc tca	1124
Leu Val Leu Pro Arg Val Pro Gln Ser Lys Val Leu Tyr Ile Thr Ser	
324 329 334 339	
aat ccg atg agt ctc tgt caa gca agc aga cat cag cca aat gtg aat	1172
Asn Pro Met Ser Leu Cys Gln Ala Ser Arg His Gln Pro Asn Val Asn	
340 345 350 355	
gat ctc ttg gtt cat gga atg cct cta cag cca aga aat ctc tcc cta	1220
Asp Leu Leu Val His Gly Met Pro Leu Gln Pro Arg Asn Leu Ser Leu	
356 361 366 371	
atg gac aag ctc cta gat ctt gat gac aag cta ctt atg agg cct ggg	1268
Met Asp Lys Leu Leu Asp Leu Asp Asp Lys Leu Leu Met Arg Pro Gly	
372 377 382 387	
tcc agt acc atc ctt tca act cga aat tgg cca aat cga gct gtg gag	1316
Ser Ser Thr Ile Leu Ser Thr Arg Asn Trp Pro Asn Arg Ala Val Glu	
388 393 398 403	
ttt agt aca tca tct ctg tca tac aca gtg cag tcc acc agg aga cgc	1364
Phe Ser Thr Ser Ser Leu Ser Tyr Thr Val Gln Ser Thr Arg Arg Arg	
404 409 414 419	
aat cca cca cca cga act ctt cat ccg atc agc acg agc cat tca tgt	1412

Asn Pro Pro Pro Arg Thr Leu His Pro Ile Ser Thr Ser His Ser Cys	
420 425 430 435	
gct gaa aca cca aga tct gtg gaa gaa atc ctc aga gga gcc cga gtc	1460
Ala Glu Thr Pro Arg Ser Val Glu Glu Ile Leu Arg Gly Ala Arg Val	
436 441 446 451	
cca gtg gca ccc gac tcg ctc tcc tct ccc tca ccg acg ccc ctg agt	1508
Pro Val Ala Pro Asp Ser Leu Ser Ser Pro Ser Pro Thr Pro Leu Ser	
452 457 462 467	
cga aat aat ctg cta cca cct att ggc aca gct gaa gtg gaa cat gtg	1556
Arg Asn Asn Leu Leu Pro Pro Ile Gly Thr Ala Glu Val Glu His Val	
468 473 478 483	
agc act gtg ggg cca caa aga cag atg aaa ccc cat ggc gac tct agt	1604
Ser Thr Val Gly Pro Gln Arg Gln Met Lys Pro His Gly Asp Ser Ser	
484 489 494 499	
cga gct caa agt gcg gtg gtg gat gaa cct aac tat cag cag cca caa	1652
Arg Ala Gln Ser Ala Val Val Asp Glu Pro Asn Tyr Gln Gln Pro Gln	
500 505 510 515	
gaa agg ctc ctt ttg ccc gac ttt ttc ccc agg ccc aac aca act caa	1700
Glu Arg Leu Leu Leu Pro Asp Phe Phe Pro Arg Pro Asn Thr Thr Gln	
516 521 526 531	
tca ttt ttg ctg gat aca cag tat cgt cgc tca tgt gca gtt gag tat	1748
Ser Phe Leu Leu Asp Thr Gln Tyr Arg Arg Ser Cys Ala Val Glu Tyr	
532 537 542 547	
cct cat cag gcc cga cct ggc agg gga tct gca ggt cct cag tta cat	1796
Pro His Gln Ala Arg Pro Gly Arg Gly Ser Ala Gly Pro Gln Leu His	
548 553 558 563	
ggg tct aca aaa tct caa agc gga ggc aga cca gtc tct cga acc agg	1844
Gly Ser Thr Lys Ser Gln Ser Gly Gly Arg Pro Val Ser Arg Thr Arg	
564 569 574 579	
cag gga cca taa ggc aaatgagaag aatctatcag gctgcaggaa acacgagatt	1899
Gln Gly Pro *	
580	
tcataagca gtattcagtc atcaagtgat gcagagcttg tatagaagat cgactagaaa	1959
tcattctcat gaagagtgat ttggcaciaa gtgaccgaag aacaaaacac catagcagcc	2019
aaaaatgaca tgagtgttgt ttctatctcc agttactgtc tctttcagca gaaattaacc	2079
tatcccattg gaaaggcaag ttgtacca aagatgcaac agtgaataat acccaaatca	2139
ctgctcatgt tatctcttaa caatgatcag ttcaatcata taggatttga tgagctcaca	2199
catacacaaa aagcagcaaa tcatcagtga caatatcact ggcttcagaa tacttcagcc	2259
tgtgttcatt tctggagagt tgtactcagt ttttaagtcatt ttgctgttg aaaatctgac	2319

ctcatcaaat	agatgtcatt	cctaaaactc	tctttagatg	tcctacccta	tcagcagatt	2379
aaaatggaag	gggtgtgtaa	ctaaaaacat	aaatgttaag	cattagtata	aagtaacttc	2439
tgtataaat	tatatcgcat	atTTTTtCag	ataggacagc	tcaaccttac	gatgcctacc	2499
tgatgccagg	tgatgcttat	tttcttccta	aagtaggtta	ctggtcatat	cttttttcca	2559
aatattaaat	gcaccttgcc	agatattctc	ctgcagctct	aaggaaagga	aatcaattta	2619
aaaataatTT	gtagaatcta	ctattgagcc	accaaagtat	aattccctaa	aagtTTaaga	2679
aaccttgcca	attaattcag	cataaacata	tcctataaac	agcaggagag	gttcagcttt	2739
ctgattttac	tgtggacctt	ttcctaaggg	cattcatgaa	tgcagcaaca	gttttaacta	2799
tggcttacat	ttattttaaa	tttcactaaa	tacaaatctt	gattgtcatg	ccagttttag	2859
atcttattaa	ttttcagaat	ggataaatTC	aaataatcat	aaattacggT	aactttttat	2919
tataccaagg	tgttctaattg	ccatcatatg	aagacagatg	cttcaaacaa	cctgcattaa	2979
attatatTTT	taataaaatt	aaaatctatt	tttaacctat	ttgtagtcac	aaaccgaaaa	3039
cgtgtcgtct	ttaccttaga	gctaaaggct	tacttttatgc	atacggtata	tttaatagtc	3099
tacaaatcaa	agattttaaC	agtcctctaa	aaattccata	tattctcata	ccaactcatc	3159
tacatagaaa	tgaaaatctc	tattgttctc	acaaaccatt	accatgagtt	cactataaca	3219
actggatcaa	tatggcttgc	ctttcaaagt	taaagaatca	gaaagggggc	tgtagaaggt	3279
catttagccc	aattccctca	ccctgtgtgt	tttccctcaa	agccagtgcA	atTTTTTTTT	3339
aaccaaaaaa	ctggacatgt	ttaatacata	cagtttgaca	aatttggaTT	tcactctttg	3399
ttttgatgta	gtaactcttt	tataaaaggg	aacagattca	gacaagctca	gtggcccaac	3459
tgaagacatt	cagcaattaa	tggcaggact	tcagtaatca	gtggcaggac	tacaacatac	3519
atctcttcat	gctagggaaa	ccaggctctc	tattataaag	ctgaccaggg	ctattgtttt	3579
ccccttttct	ctcatcctaa	acaccattca	tatttttctt	aggtcacatt	ttagtgggat	3639
catttacaaa	gccccagaa	cttaatcatc	atgtttttacc	ttttttattg	aattatatac	3699
acctcttaca	aaaatgcttg	aagtaattta	acacctgtac	atcagtacaa	aacctggctg	3759
agtaaaatga	agagaggatc	tattcaagat	cattaagacc	aaatgtaaac	tgggaagtat	3819
gtggaagata	gctgtccagc	aagtgtctgg	aaggtgttct	agctgggtag	agagcctatt	3879
ctaacagaca	cgcacatcgc	agaaagcagc	atgaacagaa	ccacatccta	gataagagtt	3939
ctgtgtacag	aagatccatg	gaggcaagtg	ctgtcaggaa	ggacactgcc	tcctccacc	3999
ctcccaaattg	tcaccaccaa	gttccttcag	gtgagacctc	acacaatgtc	aagtgccttc	4059

<213> Homo sapiens

<220>

<221> CDS

<222> (43)..(1161)

<400> 620

atttggccct cgaggccaag aattcggcac gaggtcgcca ag atg gcg tcc tcc 54
Met Ala Ser Ser
1

gcc tcc gcc cgg act ccg gca ggg aag cga gtg ata aat cag gaa gaa 102
Ala Ser Ala Arg Thr Pro Ala Gly Lys Arg Val Ile Asn Gln Glu Glu
5 10 15 20

ttg cgg cgg tta atg aag gag aag cag cgt ctg agc acc agt cgg aaa 150
Leu Arg Arg Leu Met Lys Glu Lys Gln Arg Leu Ser Thr Ser Arg Lys
21 26 31 36

cgg ata gaa tct cca ttc gcg aag tac aac cgt ttg ggg cag ctg agt 198
Arg Ile Glu Ser Pro Phe Ala Lys Tyr Asn Arg Leu Gly Gln Leu Ser
37 42 47 52

tgt gcc ctg tgt aac act ccg gtt aag agc gag ctc ctg tgg cag act 246
Cys Ala Leu Cys Asn Thr Pro Val Lys Ser Glu Leu Leu Trp Gln Thr
53 58 63 68

cac gtc ctg gga aag cag cac cga gag aaa gtg gcc gag ctg aaa ggc 294
His Val Leu Gly Lys Gln His Arg Glu Lys Val Ala Glu Leu Lys Gly
69 74 79 84

gcg aag gaa gcc agc cag ggt tgc tcc gcc agt tca gcg cct cag tcc 342
Ala Lys Glu Ala Ser Gln Gly Ser Ser Ala Ser Ser Ala Pro Gln Ser
85 90 95 100

gtc aag agg aaa gcg ccg gac gca gac gac caa gat gtc aag aga gcg 390
Val Lys Arg Lys Ala Pro Asp Ala Asp Asp Gln Asp Val Lys Arg Ala
101 106 111 116

aag gcc acc ttg gtg cct cag gta cag ccc tcc aca tct gcg tgg acc 438
Lys Ala Thr Leu Val Pro Gln Val Gln Pro Ser Thr Ser Ala Trp Thr
117 122 127 132

acc aac ttt gac aaa ata gga aag gag ttc att aga gcg act ccc agt 486
Thr Asn Phe Asp Lys Ile Gly Lys Glu Phe Ile Arg Ala Thr Pro Ser
133 138 143 148

aag cct tca gga ctc agt tta ctc ccc gat tat gaa gat gag gag gag 534
Lys Pro Ser Gly Leu Ser Leu Leu Pro Asp Tyr Glu Asp Glu Glu Glu
149 154 159 164

gag gaa gag gag gag gaa gga gat gga gaa aga aaa agg ggg gac gcc 582
Glu Glu Glu Glu Glu Glu Gly Asp Gly Glu Arg Lys Arg Gly Asp Ala
165 170 175 180

agc aag ccg ctc tcc gac gca cag ggc aag gag cac tca gtt tcc tct 630
Ser Lys Pro Leu Ser Asp Ala Gln Gly Lys Glu His Ser Val Ser Ser

181	186	191	196	
tca cgg gag gta aca	agt agt gtg ctg cca	aac gat ttc ttt agt act		678
Ser Arg Glu Val Thr	Ser Ser Val Leu Pro	Asn Asp Phe Phe Ser Thr		
197	202	207	212	
aat cct ccc aag gcc	ccc ata att cct cat	tca ggg tca att gag aaa		726
Asn Pro Pro Lys Ala	Pro Ile Ile Pro His	Ser Gly Ser Ile Glu Lys		
213	218	223	228	
gca gaa ata cat gaa	aaa gtg gtg gaa agg	aga gaa aac acc gcg gaa		774
Ala Glu Ile His Glu	Lys Val Val Glu Arg	Arg Glu Asn Thr Ala Glu		
229	234	239	244	
gcg tta ccg gaa ggt	ttt ttt gac gac cct	gag gta gat gca aga gta		822
Ala Leu Pro Glu Gly	Phe Phe Asp Asp Pro	Glu Val Asp Ala Arg Val		
245	250	255	260	
cga aag gtt gat gct	cca aaa gat cag atg	gac aaa gag tgg gac gaa		870
Arg Lys Val Asp Ala	Pro Lys Asp Gln Met	Asp Lys Glu Trp Asp Glu		
261	266	271	276	
ttc caa aaa gcc atg	agg cag gtc aac act	att tcc gaa gcc ata gtt		918
Phe Gln Lys Ala Met	Arg Gln Val Asn Thr	Ile Ser Glu Ala Ile Val		
277	282	287	292	
gcc gaa gag gat gag	gag gga cgg ttg gac	cgc cag att ggg gag atc		966
Ala Glu Glu Asp Glu	Glu Gly Arg Leu Asp	Arg Gln Ile Gly Glu Ile		
293	298	303	308	
gat gag cag ata gag	tgt tac cga cgg gtg	gaa aag cta cgg aat cgc		1014
Asp Glu Gln Ile Glu	Cys Tyr Arg Arg Val	Glu Lys Leu Arg Asn Arg		
309	314	319	324	
cag gat gaa ata aaa	aat aaa ctt aaa gaa	atc ctg acc ata aaa gaa		1062
Gln Asp Glu Ile Lys	Asn Lys Leu Lys Glu	Ile Leu Thr Ile Lys Glu		
325	330	335	340	
ctg cag aaa aag gaa	gaa gag aat gct gac	agc gat gat gag ggg gaa		1110
Leu Gln Lys Lys Glu	Glu Glu Asn Ala Asp	Ser Asp Asp Glu Gly Glu		
341	346	351	356	
cta cag gat ttg ttg	tct cag gat tgg agg	gtg aaa ggg gca ttg tta		1158
Leu Gln Asp Leu Leu	Ser Gln Asp Trp Arg	Val Lys Gly Ala Leu Leu		
357	362	367	372	
tag gggt ttaaagaccc	aagggtttcta acagcctctg	ctgttgtata aaaagtgtctg		1215
*				
373				
tctctcagta gtatagcgg	tacttcatgc ctcaagattt	gggtacctgg attgctaaac		1275
tggtattgttg agataaaatg	agccagtgag ctacagcact	ttggaaaatt tgtgtaacat		1335
gtttttgagg taaagttgtt	tttgaaattt ctgaagtgtt	atataccaaa atgccaacat		1395
ttccacgaca gacttaactg	tataatttcg ttgtaaaatc	tgtaagttgt aaatattgta		1455

catagttaaa tctgtattct gttttgaatt tttttaatta atagaaagac caaccggcaa 1515
actttcaaaa aaaaaaaaaa 1534

<210> 621
<211> 2315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (257)..(937)

<400> 621

aaggatcctt aattaaatta atcccccccc cccggtcccc gccgctgcag ccgtcgctt 60
cggagcgaag ggtaccgacc cggcagaagc tcggagctct cgggggtatcg aggaggcagg 120
cccgcgggcg cacgggagag cgggccggga gccggagcgg cggaggagcc ggcagcageg 180
gcgcggcggg ctccaggcga ggcggtcgac gtcctgaaa acttgcgcg gcgctcgcg 240
cactgcgccc ggagcg atg aag atg gtc gcg ccc tgg acg cgg ttc tac 289
Met Lys Met Val Ala Pro Trp Thr Arg Phe Tyr
1 5
tcc aac agc tgc tgc ttg tgc tgc cat gtc cgc acc ggc acc atc ctg 337
Ser Asn Ser Cys Cys Leu Cys Cys His Val Arg Thr Gly Thr Ile Leu
12 17 22 27
ctc ggc gtc tgg tat ctg atc atc aat gct gtg gta ctg ttg att tta 385
Leu Gly Val Trp Tyr Leu Ile Ile Asn Ala Val Val Leu Leu Ile Leu
28 33 38 43
ttg agt gcc ctg gct gat ccg gat cag tat aac ttt tca agt tct gaa 433
Leu Ser Ala Leu Ala Asp Pro Asp Gln Tyr Asn Phe Ser Ser Ser Glu
44 49 54 59
ctg gga ggt gac ttt gag ttc atg gat gat gcc aac atg tgc att gcc 481
Leu Gly Gly Asp Phe Glu Phe Met Asp Asp Ala Asn Met Cys Ile Ala
60 65 70 75
att gcg att tct ctt ctc atg atc ctg ata tgt gct atg gct act tac 529
Ile Ala Ile Ser Leu Leu Met Ile Leu Ile Cys Ala Met Ala Thr Tyr
76 81 86 91
gga gcg tac aag caa cgc gca gcc tgg atc atc cca ttc ttc tgt tac 577
Gly Ala Tyr Lys Gln Arg Ala Ala Trp Ile Ile Pro Phe Phe Cys Tyr
92 97 102 107
cag atc ttt gac ttt gcc ctg aac atg ttg gtt gca atc act gtg ctt 625
Gln Ile Phe Asp Phe Ala Leu Asn Met Leu Val Ala Ile Thr Val Leu
108 113 118 123

att tat cca aac tcc att cag gaa tac ata cgg caa ctg cct cct aat	673
Ile Tyr Pro Asn Ser Ile Gln Glu Tyr Ile Arg Gln Leu Pro Pro Asn	
124 129 134 139	
ttt ccc tac aga gat gat gtc atg tca gtg aat cct acc tgt ttg gtc	721
Phe Pro Tyr Arg Asp Asp Val Met Ser Val Asn Pro Thr Cys Leu Val	
140 145 150 155	
ctt att att ctt ctg ttt att agc att atc ttg act ttt aag ggt tac	769
Leu Ile Ile Leu Leu Phe Ile Ser Ile Ile Leu Thr Phe Lys Gly Tyr	
156 161 166 171	
ttg att agc tgt gtt tgg aac tgc tac cga tac atc aat ggt agg aac	817
Leu Ile Ser Cys Val Trp Asn Cys Tyr Arg Tyr Ile Asn Gly Arg Asn	
172 177 182 187	
tcc tct gat gtc ctg gtt tat gtt acc agc aat gac act acg gtg ctg	865
Ser Ser Asp Val Leu Val Tyr Val Thr Ser Asn Asp Thr Thr Val Leu	
188 193 198 203	
cta ccc ccg tat gat gat gcc act gtg aat ggt gct gcc aag gag cca	913
Leu Pro Pro Tyr Asp Asp Ala Thr Val Asn Gly Ala Ala Lys Glu Pro	
204 209 214 219	
ccg cca cct tac gtg tct gcc taa gccttcaagt gggcggagct gagggcagca	967
Pro Pro Pro Tyr Val Ser Ala *	
220 225	
gottgacttt gcagacatct gagcaatagt tctgttattt cacttttgcc atgagcctct	1027
ctgagcttgt ttgttgctga aatgctactt tttaaaattt agatgttaga ttgaaaactg	1087
tagttttcaa catatgcttt gctagaacac tgtgatagat taactgtaga attcttcctg	1147
taagattggg gatataacgg gcttcaactaa ccttccttag gcattgaaac ttcccccaaa	1207
tctgatggac ctagaagtct gcttttgtac ctgctgggcc ccaaagttgg gcatttttct	1267
ctctgttccc tctcttttga aaatgtaaaa taaaacccaa aatagacaac tttttcttca	1327
gccattccat catagagaac aaaaccttat ggaaacagga atgtcaattg tgtaatcatt	1387
gttctaatta ggtaaataga agtccttatg tatgtgttac aagaatttcc cccacaacat	1447
cctttatgac tgaagttcaa tgacagtttg tgtttggtgg taaaggattt tctccatggc	1507
ctgaattaag accattagaa agcaccaggc cgtgggagca gtgaccatct gctgactgtt	1567
cttgtggatc ttgtgtccag ggacatgggg tgacatgcct cgtatgtgtt agagggtgga	1627
atggatgtgt ttggcgctgc atgggatctg gtgcccctct tctoctggat tcacatcccc	1687
accaggggcc cgcttttact aagtgttctg ccctagattg gttcaaggag gtcaccaac	1747
tgacttttat caagtggaat tgggatatat ttgatatact tctgcctaac aacatggaaa	1807

59	64	69	74	
acc atc cat gcc aag ttc acc gac tgg aag ggc tac ctc atg aaa cgg				532
Thr Ile His Ala Lys Phe Thr Asp Trp Lys Gly Tyr Leu Met Lys Arg				
75	80	85	90	
ctg gtg ggc tcc agg acg ctt ccc gtg gat ttc cac atc aag atg gtg				580
Leu Val Gly Ser Arg Thr Leu Pro Val Asp Phe His Ile Lys Met Val				
91	96	101	106	
gag agc atg aag tac ccc ttt agg cag ggc atg cgg ctg gaa gtg gtg				628
Glu Ser Met Lys Tyr Pro Phe Arg Gln Gly Met Arg Leu Glu Val Val				
107	112	117	122	
gac aag tcc cag gtg tca cgc act cgc atg gct gtg gtg gac aca gta				676
Asp Lys Ser Gln Val Ser Arg Thr Arg Met Ala Val Val Asp Thr Val				
123	128	133	138	
atc ggg ggt cgc cta cgg ctc ctc tac gag gat ggt gac agt gac gac				724
Ile Gly Gly Arg Leu Arg Leu Leu Tyr Glu Asp Gly Asp Ser Asp Asp				
139	144	149	154	
gac ttc tgg tgc cac atg tgg agc ccc ctg atc cac cca gtg ggt tgg				772
Asp Phe Trp Cys His Met Trp Ser Pro Leu Ile His Pro Val Gly Trp				
155	160	165	170	
tca cga cgt gtg ggc cac ggc atc aag atg tca gag agg cga agt gac				820
Ser Arg Arg Val Gly His Gly Ile Lys Met Ser Glu Arg Arg Ser Asp				
171	176	181	186	
atg gcc cat cac ccc acc ttc cgg aag atc tac tgt gat gcc gtt cct				868
Met Ala His His Pro Thr Phe Arg Lys Ile Tyr Cys Asp Ala Val Pro				
187	192	197	202	
tac ctc ttc aag aag gta cga gca gtc tac aca gaa ggc ggt tgg ttt				916
Tyr Leu Phe Lys Lys Val Arg Ala Val Tyr Thr Glu Gly Gly Trp Phe				
203	208	213	218	
gag gaa ggg atg aag ctg gag gcc att gac ccc ctg aat ctg ggc aac				964
Glu Glu Gly Met Lys Leu Glu Ala Ile Asp Pro Leu Asn Leu Gly Asn				
219	224	229	234	
atc tgc gtg gca act gtc tgt aag gtt ctc ctg gat gga tac ctg atg				1012
Ile Cys Val Ala Thr Val Cys Lys Val Leu Leu Asp Gly Tyr Leu Met				
235	240	245	250	
atc tgt gtg gac ggg ggg ccc tcc aca gat ggc ttg gac tgg ttc tgc				1060
Ile Cys Val Asp Gly Gly Pro Ser Thr Asp Gly Leu Asp Trp Phe Cys				
251	256	261	266	
tac cat gcc tct tcc cac gcc atc ttc cgg gcc acc ttc tgt cag aag				1108
Tyr His Ala Ser Ser His Ala Ile Phe Pro Ala Thr Phe Cys Gln Lys				
267	272	277	282	
aat gac att gag ctc aca ccg cca aaa ggt tat gag gca cag act ttc				1156
Asn Asp Ile Glu Leu Thr Pro Pro Lys Gly Tyr Glu Ala Gln Thr Phe				
283	288	293	298	

aac tgg gag aac tac ttg gag aag acc aag tcg aaa gcc gct cca tcg	1204
Asn Trp Glu Asn Tyr Leu Glu Lys Thr Lys Ser Lys Ala Ala Pro Ser	
299 304 309 314	
aga ctc ttt aac atg gat tgc cca aac cat ggc ttc aag gtg ggc atg	1252
Arg Leu Phe Asn Met Asp Cys Pro Asn His Gly Phe Lys Val Gly Met	
315 320 325 330	
aag ctg gag gcc gtg gac ctg atg gag ccc cgg ctc atc tgt gtg gcc	1300
Lys Leu Glu Ala Val Asp Leu Met Glu Pro Arg Leu Ile Cys Val Ala	
331 336 341 346	
acg gtg aaa cga gtg gtg cat cgg ctc ctc agc atc cac ttt gac ggc	1348
Thr Val Lys Arg Val Val His Arg Leu Leu Ser Ile His Phe Asp Gly	
347 352 357 362	
tgg gac agc gag tac gac cag tgg gtg gac tgc gag tcc cca gac atc	1396
Trp Asp Ser Glu Tyr Asp Gln Trp Val Asp Cys Glu Ser Pro Asp Ile	
363 368 373 378	
tac ccc gtc ggc tgg tgt gag ctc acc ggc tac cag ctc cag cct cct	1444
Tyr Pro Val Gly Trp Cys Glu Leu Thr Gly Tyr Gln Leu Gln Pro Pro	
379 384 389 394	
gtg gcc gca gaa ccg gcc aca ccg ctg aag gcc aaa gag gcc aca aag	1492
Val Ala Ala Glu Pro Ala Thr Pro Leu Lys Ala Lys Glu Ala Thr Lys	
395 400 405 410	
aag aaa aag aaa cag ttt ggg aag aaa agg aaa aga atc ccg ccc act	1540
Lys Lys Lys Lys Gln Phe Gly Lys Lys Arg Lys Arg Ile Pro Pro Thr	
411 416 421 426	
aag acg cga ccc ctc aga cag ggg tcc aag aag ccc ctg ctg gag gac	1588
Lys Thr Arg Pro Leu Arg Gln Gly Ser Lys Lys Pro Leu Leu Glu Asp	
427 432 437 442	
gac cct cag ggt gcc agg aag atc tcg tcg gag cct gtt cct ggc gag	1636
Asp Pro Gln Gly Ala Arg Lys Ile Ser Ser Glu Pro Val Pro Gly Glu	
443 448 453 458	
atc att gct gtg cgt gtg aag gaa gag cat cta gac gtg gcc tcg ccc	1684
Ile Ile Ala Val Arg Val Lys Glu Glu His Leu Asp Val Ala Ser Pro	
459 464 469 474	
gac aag gct tca agt cca gag ctg cct gtc tcc gtc gag aac atc aag	1732
Asp Lys Ala Ser Ser Pro Glu Leu Pro Val Ser Val Glu Asn Ile Lys	
475 480 485 490	
cag gaa aca gac gac tga gccttc ctgcctccag cctggcttct agctggaagc	1786
Gln Glu Thr Asp Asp *	
491 496	
cagcccagcg tttctctacc accaccacca tgccctccacc tgactttggc ttggagactg	1846
atcctctctg tgtaaattct gcccggtgct gtgaaggctg gacggtggag gacctgctgg	1906

```

ggctctcctgg gacccgcctg ttgcttctgc cctccctgt ggaaaggtct atatgacggg 1966
ccgcctgagg cccagaact cgtctgtgaa ccaccttttc cagccagagt tcccaaagct 2026
ggaacgctag ctgcctgctc ttccttaaga tggcctcccc ccgacccgcc acggccctca 2086
gttgccaggg atggggccac cactgtcaca ctgtggaata caagacagtg aactctgtct 2146
gcctgaacga gtcattgtaa ttaagttcta gagcagctct ctgagcagga taagggtccc 2206
tgacagtgag ttgtgtggtg ggggcagcct ctgcctcaaa aattcaccaa gcagaatgcc 2266
tctcagcctc atgtgttggc cctctgtctc tctagctcc ccagggatgt tggggaccca 2326
gcttgtctcg gcagctaaga agcagtgacc aggatgtgga ttttggcgac ctgtgtggtg 2386
gccttgagct gctttctgtg tttgtgagga ctgactccca tttcctaaag gaaatgcccc 2446
cggggaggac attgggagga agatggcctg agtgtgcact ttggctctgc tacctgctcc 2506
tgaagccccg ctaaaaataa ttcattccaag attcctttgt agttaagggg tccagttctg 2566
attggagcct ctagagagct gggcttgat gttcttttgg ccttttgttc ctacctaaat 2626
gaagaaacca tgcctggagg ggccgtgaac acagaaccct caagacaagg atgacagagc 2686
tgaggagcac atctagctgc cattgcaacc tcaactgggct cccagactc tgtgtgtgag 2746
aaattaaacc cctgcttgc ttgaaaaaaa aaaaa 2781

```

```

<210> 623
<211> 5310
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (311)..(1606)

```

```

<400> 623
gggtgtgtgcg tcatcgatcg cctgoggtac cgggtccggaa ttcccgggtc gaccacgcg 60
tccgccacg cgtccgccca cgcgtccggt ctgactgcac ctgcatcctt agctcagagc 120
atccccggag catcttaaga gctgagcgca gctgacaact agggggccgga ccgtcgcagg 180
aggcgtccgc tggatacctt ccccttccc tgacctagag ctctacagct gctgcctcgg 240
tactgaccga gggttcccag agctgtctca ccattgcaaa aacgttatag caacagcctc 300
tgattacgac atg gct gag atc acc aat atc cga cct agc ttt gat gtg 349
Met Ala Glu Ile Thr Asn Ile Arg Pro Ser Phe Asp Val
1 5 10

```

tca ccg gtg gtg gcc ggc ctc atc ggg gcc tct gtg ctg gtg gtg tgt	397
Ser Pro Val Val Ala Gly Leu Ile Gly Ala Ser Val Leu Val Val Cys	
14 19 24 29	
gtc tcg gtg acc gtc ttt gtc tgg tca tgc tgc cac cag cag gca gag	445
Val Ser Val Thr Val Phe Val Trp Ser Cys Cys His Gln Gln Ala Glu	
30 35 40 45	
aag aag cac aag aac cca cca tac aag ttt att cac atg ctc aaa ggc	493
Lys Lys His Lys Asn Pro Pro Tyr Lys Phe Ile His Met Leu Lys Gly	
46 51 56 61	
atc agc ata tac cca gag acc ctc agc aac aag aag aaa atc atc aaa	541
Ile Ser Ile Tyr Pro Glu Thr Leu Ser Asn Lys Lys Lys Ile Ile Lys	
62 67 72 77	
gtg cgg aga gac aaa gat ggt cct ggg agg gaa ggt gga cgt agg aac	589
Val Arg Arg Asp Lys Asp Gly Pro Gly Arg Glu Gly Gly Arg Arg Asn	
78 83 88 93	
ctg ttg gtg gac gca gca gag gct ggc ctg cta agc cga gac aaa gat	637
Leu Leu Val Asp Ala Ala Glu Ala Gly Leu Leu Ser Arg Asp Lys Asp	
94 99 104 109	
ccc agg ggg cct agc tct gga tct tgt ata gac caa tta ccc atc aaa	685
Pro Arg Gly Pro Ser Ser Gly Ser Cys Ile Asp Gln Leu Pro Ile Lys	
110 115 120 125	
atg gac tat ggg gaa gaa cta agg agc cct att aca agc ctg acc cct	733
Met Asp Tyr Gly Glu Glu Leu Arg Ser Pro Ile Thr Ser Leu Thr Pro	
126 131 136 141	
ggg gag agc aaa acc acc tct cca tca tct cca gag gag gat gtc atg	781
Gly Glu Ser Lys Thr Thr Ser Pro Ser Ser Pro Glu Glu Asp Val Met	
142 147 152 157	
cta gga tcc ctc acc ttc tca gtg gac tat aac ttc ccg aaa aaa gcc	829
Leu Gly Ser Leu Thr Phe Ser Val Asp Tyr Asn Phe Pro Lys Lys Ala	
158 163 168 173	
ctg gtg gtg aca atc cag gag gcc cac ggg ctg cca gtg atg gat gac	877
Leu Val Val Thr Ile Gln Glu Ala His Gly Leu Pro Val Met Asp Asp	
174 179 184 189	
cag acc cag gga tct gac ccc tac atc aaa atg acc atc ctt cct gac	925
Gln Thr Gln Gly Ser Asp Pro Tyr Ile Lys Met Thr Ile Leu Pro Asp	
190 195 200 205	
aaa cgg cat cgg gtg aag acc aga gtg ctg cgg aag acc ctg gac cct	973
Lys Arg His Arg Val Lys Thr Arg Val Leu Arg Lys Thr Leu Asp Pro	
206 211 216 221	
gtg ttt gac gag acc ttc acc ttc tat ggc atc ccc tac agc cag ctg	1021
Val Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr Ser Gln Leu	
222 227 232 237	
cag gac ctg gtg ctg cac ttc ctt gtc ctc agc ttt gac cgc ttc tct	1069

Gln Asp Leu Val Leu His Phe Leu Val Leu Ser Phe Asp Arg Phe Ser	
238 243 248 253	
cgg gat gat gtc att ggc gag gtc atg gtg cca ctg gca ggg gtg gac	1117
Arg Asp Asp Val Ile Gly Glu Val Met Val Pro Leu Ala Gly Val Asp	
254 259 264 269	
ccc agc aca ggc aag gta caa ctg acc agg gac atc atc aaa agg aat	1165
Pro Ser Thr Gly Lys Val Gln Leu Thr Arg Asp Ile Ile Lys Arg Asn	
270 275 280 285	
atc cag aag tgc atc agc aga ggg gag ctc cag gtg tct ctg tca tat	1213
Ile Gln Lys Cys Ile Ser Arg Gly Glu Leu Gln Val Ser Leu Ser Tyr	
286 291 296 301	
cag cct gtg gca cag aga atg aca gtg gtg gtc ctc aaa gcc aga cac	1261
Gln Pro Val Ala Gln Arg Met Thr Val Val Val Leu Lys Ala Arg His	
302 307 312 317	
ttg ccg aag atg gat atc acc ggt ctc tca ggt aat cct tat gtc aag	1309
Leu Pro Lys Met Asp Ile Thr Gly Leu Ser Gly Asn Pro Tyr Val Lys	
318 323 328 333	
gtg aac gtc tac tac ggc aga aag cgc att gcc aag aag aaa acc cat	1357
Val Asn Val Tyr Tyr Gly Arg Lys Arg Ile Ala Lys Lys Lys Thr His	
334 339 344 349	
gtg aag aag tgc act ttg aac ccc atc ttc aat gaa tct ttc atc tac	1405
Val Lys Lys Cys Thr Leu Asn Pro Ile Phe Asn Glu Ser Phe Ile Tyr	
350 355 360 365	
gac atc ccc act gac ctc ctg cct gat atc agc atc gag ttc ctc gtt	1453
Asp Ile Pro Thr Asp Leu Leu Pro Asp Ile Ser Ile Glu Phe Leu Val	
366 371 376 381	
atc gac ttc gat cgc acc acc aag aat gag gtg gtg ggg agg ctg atc	1501
Ile Asp Phe Asp Arg Thr Thr Lys Asn Glu Val Val Gly Arg Leu Ile	
382 387 392 397	
ctg ggg gca cac agt gtc aca gcc agt ggt gct gaa cac tgg aga gag	1549
Leu Gly Ala His Ser Val Thr Ala Ser Gly Ala Glu His Trp Arg Glu	
398 403 408 413	
gtc tgc gag agc ccc cgc aag cct gtg gcc aag tgg cac agt ctg agc	1597
Val Cys Glu Ser Pro Arg Lys Pro Val Ala Lys Trp His Ser Leu Ser	
414 419 424 429	
gag tac taa tctgtt cttctctcct ctaatccccg ggggcccaagc tggggaggga 1653	
Glu Tyr * 430	
tgtggagggg aaaaagatga cagagaagtg gactccaaac ctcatttttag ttgtagaaga	1713
aaattttctta caaaacaaat tocacaaaga acaccctata tgaccacagc tgcagatcag	1773
ttcttagcaa tgatgttttt ttttctgctt tgcaaggcgc tagaatcttt tattttactt	1833

tattttttttt	gaggtggagt	ttcgctcttg	ttgcccgggc	tggagtgcaa	tggtgagatc	1893
tcaactcact	gcaacctctg	ccctccaggt	tcaagtgatt	ctcctccctc	agcctcccaa	1953
gtagctggga	ttacaggcac	ccacgagcat	gcccggtcaa	ttttttgtat	tttcagtaga	2013
gatggggttc	accatgttgg	ccaggctggg	ctcgaattcc	agacctcagg	tgatccaccc	2073
gcctcggcct	cccaaagtgc	tgggattaca	gggtgcgagcc	accgtgcccc	gcctctgggt	2133
ttgttttgtt	tttttttttt	aatgggggac	aaaagagagg	gaaagacccc	tataaaatct	2193
atatataaca	atgtaacct	atacttgcat	gtcttaatac	aaactgaaga	aattagccta	2253
actgccaata	tcaagttgca	gattttaatc	catggaaatt	gtgttttgtg	ctgaattgta	2313
tttgctgatt	acctgaaatt	ggcttctttt	tattgggctt	ctctggagaa	tttctccac	2373
tccccacctc	tgcagaagaa	aattttgctc	ttataaaacc	tcattgtttt	atcattccca	2433
tcttttcttt	ttattgcctc	ttatatctct	gctctttgac	ctcaaggctc	agaggctctg	2493
agtaagccaa	gaaacaaagg	tgggggtggg	gaggcaagg	ttgcaggaga	aagaggaatt	2553
gagaaatggg	gtatttttgc	tatcagctct	tctgctatga	agtagtaaaa	ggcagtctat	2613
aattaactga	cagacctaac	tgaagcacag	agaatacatc	agacttatgc	atccaagaca	2673
tcagaacttg	gatttttatca	aacttgatga	cttctctaaa	aggagctttg	gaaacttcaa	2733
attcagctat	aggatagtag	caatgaacac	atccagctga	tccccaaaag	tgttttcagg	2793
tataaggaca	aggagaggag	acaagtgcag	acagccattc	ccctttgcag	ctatctactg	2853
tagtgacagc	catttcttgg	ttgatgggtt	ggaagtcatc	agaggtttga	agaattacac	2913
tggcctttgt	ttttctggaa	atgccgacca	tggagatgct	ttagagtctt	ctcaaatagc	2973
ttagatgttg	taatgagggt	agctttgctt	cataaaacag	gggccctcag	aagtctctct	3033
taaatttttc	aataaaaatt	tagctcttaa	aaaaataaca	gtgtgactga	gtgaatgaag	3093
ataagttgga	ttctttcaga	gcattctttt	cotcaaaacg	agctgcataa	ttcttggaat	3153
ttatgtctta	ccacatgggt	gagggatgga	ggaactacag	gatgcaattc	ttcttctacc	3213
aatgggcaat	agaggttgag	agagattcag	catctttctg	ggattagaat	tcaagtctct	3273
ttactcctac	agcagctgtg	tctccaacgt	tgagactttg	cagatggcac	agactccatg	3333
gataataggt	aaacttgggg	ccgggcgcag	tggctcacgc	ctgtaatccc	agtattttgg	3393
gaggccgagg	tggaaagatc	gcttgagccc	aggagttcaa	gaccagcctg	ggctacatga	3453
cgaaactcca	tctctatcaa	aaatacaaaa	aattaactag	gtgtgggtgt	gcacgcctgt	3513
ggccccagct	attcaggagg	ctgagggtgg	aggatcattt	gagcccagag	gtagagggtg	3573

cagtgagcca	tgatcatgcc	actgcactct	gggctgggta	acagagtgag	atcctgtctc	3633
aaaaattaat	taattaatta	attaaaataa	actaggtaaa	cttggatagg	cagtagatat	3693
ttttgcccac	ctgaggagga	actcagtcaa	gctgttgctt	aacagcttga	tccagggcgt	3753
gaaaggttag	ttgagactga	agtgttcact	tccatagaag	aacatcactt	ttaaccttgc	3813
tttggcgaag	ggagtcggaa	agctgagtct	ctatggacgg	gggggtgatc	ttgctttcag	3873
tgttcctca	gcttttgtgg	atttaaaacc	attctgctcc	cccttaacct	tttgtttgat	3933
ttcagcccat	gttcttgaca	atgcagagca	attctgagca	gtcaciaaagc	ctactctctg	3993
ttcttgtccc	tgccaacccc	caccccccat	aatctgactc	acaacttcac	catcagttgg	4053
ggtcatacca	ctagtctctg	tcctataccc	catgaaatgt	aaatactgta	tcataagtag	4113
aagaaaataa	tttttgtttt	ctaaaaatgc	attttgagat	agtttaatgt	aaatctgaca	4173
ggagcattct	gaagcccat	taggaaaaaa	tttaaattgg	tcctcttcat	ogccttaatg	4233
tctaaagatc	agaaatcgct	gagcaaacc	gcttttgttt	ccttcccaga	aacaatgcaa	4293
aacaacaggt	ggagatagtc	tggctcttgc	cctgctgtgt	gtgcctctgt	agctcctcct	4353
gacaaacgtc	tgggaaaaca	gcctcacccc	actctcctct	ctcttcccca	tttccttgta	4413
gctttattcc	ttgcatcttt	gggtctactg	agcagtgggt	gctgaggtga	caggggagga	4473
accagttgtt	ctgtagccta	ggaactgcct	cagtgtcttt	gccagaaaaa	ggcaaagagg	4533
cggacagtgc	agggctcctc	cctcctacct	caggcctgat	ccatcgtgoc	cttgactttg	4593
cgtctcaaaa	gtttcttagc	tgactttggc	tttcacattt	gttctttcca	gagctaactg	4653
ataagagtgg	aggaggaatg	ccttctccta	agagtcagtt	gaaagaaaga	caagagagtc	4713
acatcttagc	ttttgcacaa	ggcattcgtg	gtcaggaata	ggttagggaa	tggtcacttc	4773
tgattttcca	acagttgctc	cttctctgaa	gagatcttga	ttcctttggg	aagacaagaa	4833
ttttcttaa	taacaaaggt	ccctttatga	gttattcctt	ctttcagttc	atctcactgg	4893
agcacagcca	agatggacat	gtttatggac	agtgtcttag	atgtgaaaac	agatagaact	4953
ggtttgtggg	acaggggcag	cttgtctcagg	agaggaata	acgcagggtc	cttttcttgg	5013
aaggcttgta	ctatggccat	gacagtgaca	ttgcctcac	catgatccct	ctccaaagtg	5073
gttgtcttcc	tttaccttgt	gtcttctctt	gtaaaaatga	aactcaaaaa	taaaataaat	5133
gtgtcaaat	ttgaaaaaaa	aagaaaactg	aaaaagctaa	catgaattgt	gtgaaattgc	5193
ataatgctgt	aatgctaate	tacaatatgt	aatgctatct	tgtatgttga	atttgtaaat	5253

gcaccacaca agtgcaaaat aaagactgat tcacattaca taggcaaaaa aaaaaaa 5310

<210> 624
<211> 2812
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (119)..(2200)

<400> 624
gtcgacgatt tcgtcgtgag tctcctcagc tctgcttacc ggtgcgacta gcggcagcga 60

cgcggtctaaa agcgaagggg cgagtgcgag tcccctgagc tgtacgaacg cggtcgcc 118
atg gac cgc cca gat gag ggg cct ccg gcc aag acc cgc cgc ctg agc 166
Met Asp Arg Pro Asp Glu Gly Pro Pro Ala Lys Thr Arg Arg Leu Ser
1 5 10 15

agc tcc gag tct cca cag cgc gac ccg ccc ccg ccg ccg ccg ccg ccg 214
Ser Ser Glu Ser Pro Gln Arg Asp Pro Pro Pro Pro Pro Pro Pro Pro
17 22 27 32

ccg ctc ctc cga ctg ccg ctg cct cca ccc cag cag cgc ccg agg ctc 262
Pro Leu Leu Arg Leu Pro Leu Pro Pro Pro Gln Gln Arg Pro Arg Leu
33 38 43 48

cag gag gaa acg gag gcg gca cag gtg ctg gcc gat atg agg ggg gtg 310
Gln Glu Glu Thr Glu Ala Ala Gln Val Leu Ala Asp Met Arg Gly Val
49 54 59 64

gga ctg ggc ccc gcg ctg ccc ccg ccg cct ccc tat gtc att ctc gag 358
Gly Leu Gly Pro Ala Leu Pro Pro Pro Pro Pro Tyr Val Ile Leu Glu
65 70 75 80

gag ggg ggg atc cgc gca tac ttc acg ctc ggt gct gag tgt ccc ggc 406
Glu Gly Gly Ile Arg Ala Tyr Phe Thr Leu Gly Ala Glu Cys Pro Gly
81 86 91 96

tgg gat tct acc atc gag tcg ggg tat ggg gag gcg ccc ccg ccc acg 454
Trp Asp Ser Thr Ile Glu Ser Gly Tyr Gly Glu Ala Pro Pro Pro Thr
97 102 107 112

gag agc ctg gaa gca ctc ccc act cct gag gcc tcg ggg ggg agc ctg 502
Glu Ser Leu Glu Ala Leu Pro Thr Pro Glu Ala Ser Gly Gly Ser Leu
113 118 123 128

gaa atc gat ttt cag gtt gta cag tcg agc agt ttt ggt gga gag ggg 550
Glu Ile Asp Phe Gln Val Gln Ser Ser Ser Phe Gly Gly Glu Gly
129 134 139 144

gcc cta gaa acc tgt agc gca gtg ggg tgg gcg ccc cag agg tta gtt 598
Ala Leu Glu Thr Cys Ser Ala Val Gly Trp Ala Pro Gln Arg Leu Val
145 150 155 160

gac ccg aag agc aag gaa gag gcg atc atc ata gtg gag gat gag gat Asp Pro Lys Ser Lys Glu Glu Ala Ile Ile Ile Val Glu Asp Glu Asp 161 166 171 176	646
gag gat gag cgg gag agt atg agg agc agc agg agg cgg cgg cgg cgg Glu Asp Glu Arg Glu Ser Met Arg Ser Ser Arg Arg Arg Arg Arg Arg 177 182 187 192	694
cgg agg agg aag cag agg aag gtg aag agg gaa agc aga gag aga aat Arg Arg Arg Lys Gln Arg Lys Val Lys Arg Glu Ser Arg Glu Arg Asn 193 198 203 208	742
gcc gag agg atg gag agc atc ctg cag gca ctg gag gat att cag ctg Ala Glu Arg Met Glu Ser Ile Leu Gln Ala Leu Glu Asp Ile Gln Leu 209 214 219 224	790
gat ctg gag gca gtg aac atc aag gca ggc aaa gcc ttc ctg cgt ctc Asp Leu Glu Ala Val Asn Ile Lys Ala Gly Lys Ala Phe Leu Arg Leu 225 230 235 240	838
aag cgc aag ttc atc cag atg cga aga ccc ttc ctg gag cgc aga gac Lys Arg Lys Phe Ile Gln Met Arg Arg Pro Phe Leu Glu Arg Arg Asp 241 246 251 256	886
ctc atc atc cag cat atc cca ggc ttc tgg gtc aaa gca ttc ctc aac Leu Ile Ile Gln His Ile Pro Gly Phe Trp Val Lys Ala Phe Leu Asn 257 262 267 272	934
cac ccc aga att tca att ttg atc aac cga cgt gat gaa gac att ttc His Pro Arg Ile Ser Ile Leu Ile Asn Arg Arg Asp Glu Asp Ile Phe 273 278 283 288	982
cgc tac ttg acc aat ctg cag gta cag gat ctc aga cat atc tcc atg Arg Tyr Leu Thr Asn Leu Gln Val Gln Asp Leu Arg His Ile Ser Met 289 294 299 304	1030
ggc tac aaa atg aag ctg tac ttc cag act aac ccc tac ttc aca aac Gly Tyr Lys Met Lys Leu Tyr Phe Gln Thr Asn Pro Tyr Phe Thr Asn 305 310 315 320	1078
atg gtg att gtc aag gag ttc cag cgc aac cgc tca ggc cgg ctg gtg Met Val Ile Val Lys Glu Phe Gln Arg Asn Arg Ser Gly Arg Leu Val 321 326 331 336	1126
tct cac tca acc cca atc cgc tgg cac cgg ggc cag gaa ccc cag gcc Ser His Ser Thr Pro Ile Arg Trp His Arg Gly Gln Glu Pro Gln Ala 337 342 347 352	1174
cgt cgt cac ggg aac cag gat gcg agc cac agc ttt ttc agc tgg ttc Arg Arg His Gly Asn Gln Asp Ala Ser His Ser Phe Phe Ser Trp Phe 353 358 363 368	1222
tca aac cat agc ctc cca gag gct gac agg att gct gag att atc aag Ser Asn His Ser Leu Pro Glu Ala Asp Arg Ile Ala Glu Ile Ile Lys 369 374 379 384	1270

aat gat ctg tgg gtt aac cct cta cgc tac tac ctg aga gaa agg ggc	1318
Asn Asp Leu Trp Val Asn Pro Leu Arg Tyr Tyr Leu Arg Glu Arg Gly	
385 390 395 400	
tcc agg ata aag aga aag aag caa gaa atg aag aaa cgt aaa acc agg	1366
Ser Arg Ile Lys Arg Lys Lys Gln Glu Met Lys Lys Arg Lys Thr Arg	
401 406 411 416	
ggc aga tgt gag gtg gtg atc atg gaa gac gcc cct gac tat tat gca	1414
Gly Arg Cys Glu Val Val Ile Met Glu Asp Ala Pro Asp Tyr Tyr Ala	
417 422 427 432	
gtg gaa gac att ttc agc gag atc tca gac att gat gag aca att cat	1462
Val Glu Asp Ile Phe Ser Glu Ile Ser Asp Ile Asp Glu Thr Ile His	
433 438 443 448	
gac atc aag atc tct gac ttc atg gag acc acc gac tac ttc gag acc	1510
Asp Ile Lys Ile Ser Asp Phe Met Glu Thr Thr Asp Tyr Phe Glu Thr	
449 454 459 464	
act gac aat gag ata act gac atc aat gag aac atc tgc gac agc gag	1558
Thr Asp Asn Glu Ile Thr Asp Ile Asn Glu Asn Ile Cys Asp Ser Glu	
465 470 475 480	
aat cct gac cac aat gag gtc ccc aac aac gag acc act gat aac aac	1606
Asn Pro Asp His Asn Glu Val Pro Asn Asn Glu Thr Thr Asp Asn Asn	
481 486 491 496	
gag agt gct gat gac cac gaa acc act gac aac aat gag agt gca gat	1654
Glu Ser Ala Asp Asp His Glu Thr Thr Asp Asn Asn Glu Ser Ala Asp	
497 502 507 512	
gac aac aac gag aat cct gaa gac aat aac aag aac act gat gac aac	1702
Asp Asn Asn Glu Asn Pro Glu Asp Asn Asn Lys Asn Thr Asp Asp Asn	
513 518 523 528	
gaa gag aac cct aac aac aac gag aac act tac ggc aac aac ttc ttc	1750
Glu Glu Asn Pro Asn Asn Asn Glu Asn Thr Tyr Gly Asn Asn Phe Phe	
529 534 539 544	
aaa ggt ggc ttc tgg ggc agc cat ggc aac aac cag gac agc agc gac	1798
Lys Gly Gly Phe Trp Gly Ser His Gly Asn Asn Gln Asp Ser Ser Asp	
545 550 555 560	
agt gac aat gaa gca gat gag gcc agt gat gat gaa gat aat gat ggc	1846
Ser Asp Asn Glu Ala Asp Glu Ala Ser Asp Asp Glu Asp Asn Asp Gly	
561 566 571 576	
aac gaa ggt gac aat gag ggc agt gat gat gat ggc aat gaa ggt gac	1894
Asn Glu Gly Asp Asn Glu Gly Ser Asp Asp Asp Gly Asn Glu Gly Asp	
577 582 587 592	
aat gaa ggc agc gat gat gac gac aga gac att gag tac tat gag aaa	1942
Asn Glu Gly Ser Asp Asp Asp Asp Arg Asp Ile Glu Tyr Tyr Glu Lys	
593 598 603 608	
gtt att gaa gac ttt gac aag gat cag gct gac tac gag gac gtg ata	1990

Val Ile Glu Asp Phe Asp Lys Asp Gln Ala Asp Tyr Glu Asp Val Ile	
609 614 619 624	
gag atc atc tca gac gaa tca gtg gaa gaa gag ggc att gag gaa ggc	2038
Glu Ile Ile Ser Asp Glu Ser Val Glu Glu Glu Gly Ile Glu Glu Gly	
625 630 635 640	
atc cag caa gat gag gac atc tat gag gaa gga aac tat gag gag gaa	2086
Ile Gln Gln Asp Glu Asp Ile Tyr Glu Glu Gly Asn Tyr Glu Glu Glu	
641 646 651 656	
gga agt gaa gat gtc tgg gaa gaa ggg gaa gat tcg gac gac tct gac	2134
Gly Ser Glu Asp Val Trp Glu Glu Gly Glu Asp Ser Asp Ser Asp	
657 662 667 672	
cta gag gat gtg ctt cag gtc cca aac ggt tgg gcc aat ccg ggg aag	2182
Leu Glu Asp Val Leu Gln Val Pro Asn Gly Trp Ala Asn Pro Gly Lys	
673 678 683 688	
agg ggg aaa acc gga taa gggttt tccccctttg gggatcacct ctctgtatcc	2236
Arg Gly Lys Thr Gly *	
689 694	
cccacccact atcccatttg cctcctcct cagctagggc cacgcggccc cacattgcac	2296
ttctgggggg tgaccgactt cgtacacggg tttaaagttt atttttatgg tttagtcatt	2356
gcagagttct tattttgggg ggaggggaaag ggggctagtc ccttctttt ggccctccgc	2416
ccccgcaggc ttctgtgtgc tgetaactgt atttattgtg atgccttggc cagggcccct	2476
ctaccacatt ctccagtc gttgtggccc cagccccctt cctgtgtctg tgtggagtgg	2536
acaccctgac cccgaagcg gggagggccg ctgtggcctt cgtcacagcc gcgcagtgcc	2596
catggaggcg ctgctgccac ctctctctcc caagttcttt ctccatccct ctctcttcc	2656
cgcgcgccc ctagcccgcc tcggtgtcta tgcaaggccg cttcgccatt gcggtattct	2716
ttgcggtatt cttgtccccg tccccagaa ggctgcctc tccccgtgga cctgttaat	2776
ccaataaaaa ttctgagcaa gttcaaaaaa aaaaaa	2812

<210> 625
 <211> 1878
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (945)..(1229)

<400> 625	
attgaacgcc tgcggtaccg gtccggaatt cccgggtcga cccacgcgtc cgcggacgcg	60

tgggctctct ctctctccct gtgtcgctta aacaacagtc ctaacttttg tgtgttgcaa	120
atataaaaagg caagccatgt gacagaggga cagaagaaca aaagcatttg gaagtaacag	180
gacctctttc tagctctcag aaaagtctga gaagaaagga gccctgcgtt cccctaagct	240
gtgcagcaga tactgtgatg atggattgca agtgcaaaga gtaagacaaa actccagcac	300
ataaaggaca atgacaacca gaaagcttca gcccgatcct gccctttcct tgaacgggac	360
tggatcctag gaggtgaagc catttccaat tttttgtcct ctgcctccct ctgctgttct	420
tctagagaag tttttcctta caacaatgag aaaacatgta ctgctgcat ccttttctat	480
gctctccctg ctgggtgataa tgggagatac agacagtaaa acggacagct cattcataat	540
ggactcggac cctcgacgct gcatgaggca ccactatgtg gattctatca gtcaccatt	600
gtacaagtgt agctcaaaga tgggtgctcct ggccagggtgc gaggggact gcagccaggc	660
gtcacgctcc gagcctttgg tgtcgttcag cactgtcctc aagcaaccct tccgttcctc	720
ctgtcactgc tgcgggcccc agacttccaa gctgaaggca ctgcggctgc gatgctcagg	780
gggcatgcca ctactgcca cctaccggta catcctctcc tgtcactgcg aggaatgcaa	840
ttcctgaggc ccgctgctgt gtgtggcttc tggatgggac aactgtagag gcagttcgac	900
cagccaggga aagactggca agaaaagagt taaggcaaaa aagg atg caa caa ttc	956
Met Gln Gln Phe	
1	
tcc cgg gac tct gca tat tct agt aat aaa gac tct aca tgc ttg ttg	1004
Ser Arg Asp Ser Ala Tyr Ser Ser Asn Lys Asp Ser Thr Cys Leu Leu	
5 10 15 20	
aca gag aga gat act ctg gga act tct ttg cag ttc cca tct cct ttc	1052
Thr Glu Arg Asp Thr Leu Gly Thr Ser Leu Gln Phe Pro Ser Pro Phe	
21 26 31 36	
tct ggt aca att tct ttt ggt tca ttt tca gat tca ggc att ttc ccc	1100
Ser Gly Thr Ile Ser Phe Gly Ser Phe Ser Asp Ser Gly Ile Phe Pro	
37 42 47 52	
ctt ggc tct caa tgc tgt ttg ggt ttc caa caa ttc agc att agt ggg	1148
Leu Gly Ser Gln Cys Cys Leu Gly Phe Gln Gln Phe Ser Ile Ser Gly	
53 58 63 68	
aaa aag tgg gcc ctc ata cac aag cgt gtc agg ctg tca gtg ttt ggt	1196
Lys Lys Trp Ala Leu Ile His Lys Arg Val Arg Leu Ser Val Phe Gly	
69 74 79 84	
gca cgc tgg gga aga att tac ttt gga aag tag aaaagccc agcttttcct	1247
Ala Arg Trp Gly Arg Ile Tyr Phe Gly Lys *	
85 90 95	


```

gggacatctt ctgttattgt tgatgttttt ttttaccttg tcatttttggc ctaaggttgc 1307
cattgctgct aaagggttacc gatttcaaag tccagatacc aagcatgtgg atatgttttag 1367
ctacgtttac tcacagccag cgaactgaca ttaaaataac taacaaacag attcttttat 1427
gtgatgctgg aactcttgac agctataatt attattcaga aatgactttt tgaaagtaaa 1487
agcagcataa agaattttgtc acaggaaggc tgtctcagat aaattatggg aaaattttgt 1547
aagggagcag actttttaag acttgcacaa atacggatcc tgcactgact ctggaaaagg 1607
catatatgta ctagtggcat ggagaatgca ccatactcat gcatgcaaatt tagacaacca 1667
agtatgaatc tatttgtggg tgtgctatag ctttagccgt gtcacgggca tcattctcta 1727
atatccactt gtccatgtga aacatgttgc caaaatgggt gcctggcttg tttctgaac 1787
gtttggttca aatgtgtttt ggtcctggag gctcaaattt tgagttattc ccacgttttg 1847
aaataaaaag agtatattca aaaaaaaaaa a 1878

```

```

<210> 626
<211> 1310
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (95)..(955)

```

```

<400> 626
tagtaccggt ccggatttcc cgggtcgacg atttcgtgct gccgccgcct ctccaagttc 60

ttgtggcccc cgcggtgcgg agtatggggc gctg      atg gcc atg gag ggc tac 112
                                   Met Ala Met Glu Gly Tyr
                                   1

tgg cgc ttc ctg gcg ctg ctg ggg tcg gca ctg ctc gtc ggc ttc ctg 160
Trp Arg Phe Leu Ala Leu Leu Gly Ser Ala Leu Leu Val Gly Phe Leu
 7              12              17              22

tcg gtg atc ttc gcc ctc gtc tgg gtc ctc cac tac cga gag ggg ctt 208
Ser Val Ile Phe Ala Leu Val Trp Val Leu His Tyr Arg Glu Gly Leu
23              28              33              38

ggc tgg gat ggg agc gca cta gag ttt aac tgg cac cca gtg ctc atg 256
Gly Trp Asp Gly Ser Ala Leu Glu Phe Asn Trp His Pro Val Leu Met
39              44              49              54

gtc acc ggc ttc gtc ttc atc cag ggc atc gcc atc atc gtc tac aga 304
Val Thr Gly Phe Val Phe Ile Gln Gly Ile Ala Ile Ile Val Tyr Arg
55              60              65              70

```

ctg ccg tgg acc tgg aaa tgc agc aag ctc ctg atg aaa tcc atc cat	352
Leu Pro Trp Thr Trp Lys Cys Ser Lys Leu Leu Met Lys Ser Ile His	
71 76 81 86	
gca ggg tta aat gca gtt gct gcc att ctt gca att atc tct gtg gtg	400
Ala Gly Leu Asn Ala Val Ala Ala Ile Leu Ala Ile Ile Ser Val Val	
87 92 97 102	
gcc gtg ttt gag aac cac aat gtt aac aat ata gcc aat atg tac agt	448
Ala Val Phe Glu Asn His Asn Val Asn Asn Ile Ala Asn Met Tyr Ser	
103 108 113 118	
ctg cac agc tgg gtt gga ctg ata gct gtc ata tgc tat ttg tta cag	496
Leu His Ser Trp Val Gly Leu Ile Ala Val Ile Cys Tyr Leu Leu Gln	
119 124 129 134	
ctt ctt tca ggt ttt tca gtc ttt ctg ctt cca tgg gct ccg ctt tct	544
Leu Leu Ser Gly Phe Ser Val Phe Leu Leu Pro Trp Ala Pro Leu Ser	
135 140 145 150	
ctc cga gca ttt ctc atg ccc ata cat gtt tat tct gga att gtc atc	592
Leu Arg Ala Phe Leu Met Pro Ile His Val Tyr Ser Gly Ile Val Ile	
151 156 161 166	
ttt gga aca gtg att gca aca gca ctt atg gga ttg aca gag aaa ctg	640
Phe Gly Thr Val Ile Ala Thr Ala Leu Met Gly Leu Thr Glu Lys Leu	
167 172 177 182	
att ttt tcc ctg aga gat cct gca tac agt aca ttc ccg cca gaa ggt	688
Ile Phe Ser Leu Arg Asp Pro Ala Tyr Ser Thr Phe Pro Pro Glu Gly	
183 188 193 198	
gtt ttc gta aat acg ctt ggc ctt ctg atc ctg gtg ttc ggg gcc ctc	736
Val Phe Val Asn Thr Leu Gly Leu Leu Ile Leu Val Phe Gly Ala Leu	
199 204 209 214	
att ttt tgg ata gtc acc aga ccg caa tgg aaa cgt cct aag gag cca	784
Ile Phe Trp Ile Val Thr Arg Pro Gln Trp Lys Arg Pro Lys Glu Pro	
215 220 225 230	
aat tct acc att ctt cat cca aat gga ggc act gaa cag gga gca aga	832
Asn Ser Thr Ile Leu His Pro Asn Gly Gly Thr Glu Gln Gly Ala Arg	
231 236 241 246	
ggg tcc atg cca gcc tac tct ggc aac aac atg gac aaa tca gat tca	880
Gly Ser Met Pro Ala Tyr Ser Gly Asn Asn Met Asp Lys Ser Asp Ser	
247 252 257 262	
gag tta aac agt gaa gta gca gca agg aaa aga aac tta gct ctg gat	928
Glu Leu Asn Ser Glu Val Ala Ala Arg Lys Arg Asn Leu Ala Leu Asp	
263 268 273 278	
gag gct ggg cag aga tct acc atg taa aatgt tgtagagata gagccatata	980
Glu Ala Gly Gln Arg Ser Thr Met *	
279 284	
acgtcacggt tcaaaactag ctctacagtt ttgcttctcc tattagccat atgataattg	1040

ggctatgtag tatcaatatt tactttaatc acaaaggatg gtttcttgaa ataatttgta 1100
 ttgattgagg cctatgaact gacctgaatt ggaaaggatg tgattaatat aaataatagc 1160
 agatataaat tgtggttatg ttacctttat cttgttgagg accacaacat tagcacggtg 1220
 ccttgtgcag aatagatact caatatgtga atatgtgtct actagtagtt aattggataa 1280
 actggcagca tccctgaaaa aaaaaaaaaa 1310

<210> 627
 <211> 1477
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (352) .. (1011)

<400> 627
 cttggaccgg ctgcatcgag tgactgatgt atataactat ctattcgatg atgaagatac 60
 cccaccaaac ccaaaaaaag agatctctcg aggatccgaa ttccgcgccg cgtcgacgcg 120
 gcctgggtac cttgtcggag ctggggctgg gcagccgtcc ccttcgggtcc ccaccgtggc 180
 ctcagcgtgc tgcttgacag gatacctcag cgggcgccac ggtggctccc agcttgtaga 240
 caaaagacgt cactctcatt ccttaatcga ccagaccttc caaacctggc ttataagaag 300
 ctaaaaggca aaagtccagg aattatcttc atccctggct atctttctta t atg aat 357
 Met Asn
 1
 ggt aca aaa gcg ttg gcg att gag gag ttt tgc aaa tct cta ggt cac 405
 Gly Thr Lys Ala Leu Ala Ile Glu Glu Phe Cys Lys Ser Leu Gly His
 3 8 13 18
 gcc tgc ata agg ttt gat tac tca gga gtt gga agt tca gat ggt aac 453
 Ala Cys Ile Arg Phe Asp Tyr Ser Gly Val Gly Ser Ser Asp Gly Asn
 19 24 29 34
 tca gag gaa agc aca ctg ggg aaa tgg aga aaa gat gtt ctt tct ata 501
 Ser Glu Glu Ser Thr Leu Gly Lys Trp Arg Lys Asp Val Leu Ser Ile
 35 40 45 50
 att gat gac tta gct gat ggg cca cag att ctt gtt gga tct agc ctt 549
 Ile Asp Asp Leu Ala Asp Gly Pro Gln Ile Leu Val Gly Ser Ser Leu
 51 56 61 66
 gga ggg tgg ctt atg ctt cat gct gca att gca cga cca gag aag gtc 597
 Gly Gly Trp Leu Met Leu His Ala Ala Ile Ala Arg Pro Glu Lys Val
 67 72 77 82